

N3027PCT\_sequ.list.txt  
SEQUENCE LISTING

<110> Technische Universität Dresden  
Medizinische Hochschule Hannover

<120> Means for treating myosin-related diseases

<130> N3027 PCT

<150> US 60/989,773

<151> 2007-11-21

<160> 109

<170> Patent In version 3.3

<210> 1

<211> 6351

<212> DNA

<213> Dictyostelium discoideum

<220>

<221> misc\_feature

<222> (1)..(6351)

<223> Myosin-2

<400> 1

at gaat ccaa t t cat gat ag aact t cagat t at cacaat act t aaaagt t aaacaaggt	60
gat t ct gat t t at t t aaact t act g t t t ca gat aagagat acat t t ggt a t aat ccagat	120
ccaaaagaaa gagat t cat a t gaat gt ggt gaaat t g t t t cagaaacct c t gat t ct t t c	180
acat t caaaa ccgt t gat gg t caagacaga caagt caaaa aggat gat gc caat caacgt	240
aat ccaat ca aat t cgat gg t gt cgaagat at gt ct gaat t at cat acct caat gaacca	300
gcagt t t t cc acaat ct ccg t gt t cgt t ac aat caagat t t aat t t acac ct at t caggt	360
ct ct t t t t gg t t gccgt caa t ccat t caag agaat t ccaa t ct aact ca agagat ggt t	420
gat at ct t ca aaggt cgt ag aagaaat gaa gt t gccccac at at t t t cgc cat t t ct gat	480
gt t gcct at c gt t caat gt t agat gat cgt caaaat caat cact ct t aat cact ggt gaa	540
t ct ggt gct g gt aagact ga aaacaccaa aaggt cat t c aat at ct t gc at ct gt cgct	600
ggg cgt aat c aagccaat gg t agt ggt gt a t t ggaacaac aaat t ct cca agccaat cca	660
at cct t gaag ct t t t ggt aa t gccaaaacc acccgt aaca acaat t cat c t cgt t t cggt	720
aaat t cat t g aaat t caat t caacagt gct ggt t t cat t a gt ggt gct t c aat t caat cc	780
t acct t t t ag agaaat cacg t gt cgt t t t c caat ct gaaa ccgaacgt aa t t at cacat t	840
t t ct at caac t ct t agct gg t gccaccgcc gaagaaaaga aagct ct t ca ct t ggct ggt	900
ccagaat cat t caact act t aaat caaagt ggt t gt gt t g at at caaagg t gt ct ct gat	960
agt gaagaat t caaaat cac t cgt caagct at ggacat t g t t ggt t t ct c acaagaagaa	1020
caaat gt caa t ct t t aagat cat t gct ggt at ct t acat t t aggt aacat caaat t cgaa	1080
aaaggt gct g gt gaaggt gc t gt cct caaa gacaaaaccg ccct caacgc t gct t caacc	1140
gt ct t t ggt g t caat ccat c agt cct t gaa aaggct ct ca t ggaaccacg t at t t t agcc	1200
ggg cgt gat t t agt t gct ca acat ct caac gt t gaaaaat cct cat cat c aagagacgct	1260

N3027PCT\_sequ.list.txt

ct t gt caaag ct ct ct at gg t cgt c t t t t c ct ct ggt t gg t caaaaagat caacaat gt c	1320
ct ct gt caag agagaaaagc t t act t t at t ggt gt t t t gg at at t t cagg t t t t gaaat t	1380
t t caaagt ca at t cat t cga acaat t at gt at caat t at a ccaat gaaaa act ccaacaa	1440
t t ct t caat c accat at gt t caaat t ggaa caagaagaat at ct t aaaga gaaaat caat	1500
t ggact t t ca t cgat t t t gg t ct t gat t ca caagccact a t cgat t t aat t gat ggt cgt	1560
caaccaccag gt at t t t agc t ct t t t ggat gaacaat ct g t t t t cccaaa t gccaccgat	1620
aat act t t aa t caccaaact ccacagt cac t t t agcaaga agaacgccaa at acgaagaa	1680
ccacgt t t ct ccaaaaccga at t t ggt gt t acccat t at g ct ggt caagt cat gt at gag	1740
at t caagat t ggt t agaaaa gaacaaagat ccat t acaac aagat ct cga act t t gct t c	1800
aaagat t cat cagacaacgt t gt caccaaa ct t t t caat g at ccaaacat t gccagt cgt	1860
gcaaagaaaag gt gcaaact t t at cact gt c gccgct caat acaaggaaca at t agcct ca	1920
ct cat ggcca ccct t gaaac caccaacca cat t t cgt t c gt t gt at cat t ccaaacaac	1980
aaacaat t ac cagccaaact cgaagat aaa gt t gt cct cg accaat t acg t t gcaat ggt	2040
gt cct cgaag gt at t cgt at t act cgt aaa ggt t t cccaa at cgt at t at ct at gccgat	2100
t t cgt caaac gt t act at t t at t agct cca aacgt t ccaa gagacgct ga agact cacia	2160
aaagccaccg at gct gt t ct caaacat ct t aacat t gat c cagaacaat a t cgt t t cggt	2220
at caccaaga t t t t ct t ccg t gccggt caa t t agct cgt a t t gaagaagc t cgt gaacaa	2280
cgt at ct ct g aaat cat caa agccat t caa gct gccact c gt ggt t ggat cgct cgt aaa	2340
gt ct acaaac aagcacgt ga acacact gt t gct gct cgt a t cat ccaaca aaat ct ccgt	2400
gct t acat t g at t t caaat c at ggccat gg t ggaaact ct t ct caaaggc t cgt ccat t a	2460
t t aaagagaa gaaact t t ga aaaggaaat c aaagaaaagg aaagagaaat ct t agaact c	2520
aaat ct aat c t caccgact c t accact caa aaggat aaat t agagaaat c act caaagat	2580
act gaat cca at gt act cga t ct ccaacgt caact caaag ct gaaaaaga aaccct caaa	2640
gct at gt acg at agcaagga t gcct t agaa gct caaaaac gt gaat t aga aat ccgt gt t	2700
gaagat at gg aat ct gaact cgacgaaaag aaat t agct t t ggaaaacct ccaaaaccaa	2760
aaacgt t cag t cgaagaaaa agt cagagac t t ggaagaag aat t acaaga ggaacaaaaa	2820
t t acgt aat a ccct t gaaaa at t aaagaag aaat acgaag aggaat t aga agaaat gaaa	2880
cgt gt caat g acggt caat c t gat accat c t ct cgt t t ag aaaaaat caa ggat gaat t a	2940
caaaaagaag t t gaagaat t aact gaaagc t t ct ct gaag aat ccaaaga t aaagggt gt t	3000
t t agaaaaga ct cgt gt cag at t acaaagt gaat t ggat g at t t aaccgt aagat t agat	3060
agt gaaacca aagacaaat c t gaat t act c cgt caaaaga agaaact cga agaagaact c	3120
aaacaagt t c aagaagct ct cgct gct gaa act gct gct a aat t agct ca agaagct gcc	3180
aacaagaaat t acaaggt ga at acact gaa t t aaacgaaa aat t caact c t gaagt cact	3240
gct cgt t caa at gt t gaaaa at caaagaag accct cgaaa gt caat t ggt t gccgt caac	3300

N3027PCT\_sequ. list.txt

aacgaat t ag at gaagagaa gaagaat cgt gat gccct t g aaaagaagaa gaaagct t t a	3360
gacgct at gt t agaggaaat gaaagat caa t t agaat cca ct ggt ggt ga aaagaaat ca	3420
ct ct at gat c t caaagt t aa acaagaat ca gat at ggagg ct t t acgt aa t caaat ct ct	3480
gaact ccaat caact at t gc caaat t agaa aagat t aaat ccact t t aga aggt gaagt t	3540
gct cgt t t ac aaggt gaat t agaagct gaa caat t agcca aat ccaacgt t gaaaaacaa	3600
aagaagaagg t t gaat t aga t t t ggaagat aaat ct gct c aat t agct ga agaaaccgcc	3660
gccaaacaag ct t t agat aa at t aaagaag aaat t agaac aagaat t at c t gaagt t caa	3720
act caact ct ct gaagccaa caacaagaat gt caact ct g at t ccacca caaacat t t g	3780
gaaacct ct t t caat aat ct caaat t agaa t t ggaagct g aacaaaaagc caaacaagct	3840
ct t gaaaaga aacgt ct cgg t t t agaat ct gaat t aaaac at gt caat ga acaat t ggaa	3900
gaagaaaaga aacaaaaaga at ccaacgaa aaacgt aaag t t gat t t aga aaaggaagt c	3960
t ct gaact ca aagaccaaat t gaagaagaa gt t gcct cca agaaagct gt cact gaagcc	4020
aagaacaaga aagaat ct ga act cgat gaa at caagagac aat at gct ga t gt t gt t t ca	4080
t ct cgt gat a aat cagt cga acaat t aaag acct t acaag ccaagaat ga agaat t aaga	4140
aacact gct g aagaagct ga aggt caat t a gat cgt gct g aaagaagcaa gaagaaagct	4200
gaat t cgat t t agaagaagc cgt caagaat t t ggaagaag aaaccgccaa gaaagt t aaa	4260
gct gaaaaag ccat gaagaa agct gaaact gact at cgt t caaccaa t c t gaat t ggat	4320
gat gccaaaga acgt ct cat c t gaacaat ac gt t caaat ca aacgt ct caa t gaagaact c	4380
t ct gaat t ac gt agt gt ct t ggaagaagct gat gaacgt t gt aact ct gc cat caaagca	4440
aagaaaaccg ct gaat ct gc t t t agaat ca t t gaaagat g aaat t gat gc t gccacaac	4500
gccaaagct a aagct gaaag aaaat ccaa gaat t agaag t t cgt gt cgc t gaat t agaa	4560
gaat cat t gg aagat aaat c t ggt accgt c aat gt t gaat t cat t cgt aa gaaggat gct	4620
gaaat cgat g at t t acgt gc t cgt ct cgac agagaaact g aaagt cgt at caaat ct gat	4680
gaagat aaga agaacact cg t aaacaat t t gct gat t t ag aagct aaggt t gaagaagct	4740
caacgt gaag t t gt caccat cgat agat t a aagaagaac t cgaat ct ga t at cat cgat	4800
t t at caact c aat t ggat ac t gaaaccaa t ct cgt at ca agat t gaaaa gagcaagaag	4860
aaact cgaac aaact ct cgc t gaaagaaga gccgct gaag aaggt t cat c caaagct gct	4920
gat gaagaaa t t cgt aaaca agt ct ggcaa gaggt t gat g agt t acgt gc t caat t agat	4980
agt gaacgt g ct gct ct caa t gct t ct gaa aagaagat ca aat ct t t ggt cgccgaagt c	5040
gat gaagt ca aggaacaat t agaagat gaa at cct cgcca aagacaaat t agt caaagcc	5100
aaacgt gccc t cgaagt t ga at t agaggaa gt cagagacc aat t agaaga ggaagaagat	5160
t ct cgt t cag aat t agaaga cagcaaact cgt ct cact a ct gaagt cga agat at caag	5220
aagaaat acg at gct gaagt cgaacaaaac accaaat t ag at gaagccaa gaagaaact c	5280
act gat gat g t t gat act ct caagaaacaa t t ggaagat g aaaagaagaa at t gaacgaa	5340
t ct gaacgt g ccaagaaacg t t t agaat ct gaaaat gaag at t t cct t gc caaact t gat	5400

N3027PCT\_sequ. list . . txt

gct gaagt t a agaat cgt t c acgt gct gaa aaggat cgt a agaaat acga aaaggat ct c 5460  
aaggat acca aat acaaat t aaacgacgaa gct gccacca agact caaac cgaaat t ggt 5520  
gccgccaaac t cgaagat ca aat cgat gaa t t acgt t cca aact t gaaca agaacaagcc 5580  
aaagccact c aagccgat aa gagt aagaag act t t ggaag gt gaaat t ga caact t acgt 5640  
gct caaat cg aagat gaagg t aagat caag at gagat t ag aaaaagaaaa acgt gct ct c 5700  
gaaggt gaat t agaagaat t aagagaaacc gt t gaagaag ct gaagact c t aaat ct gaa 5760  
gct gaacaat ccaaactgt t t agt cgaat t a gaat t agaag at gct cgt cg t aacct ccaa 5820  
aaagaaat cg at gccaaaga aat cgct gaa gat gccaaat ct aacct cca acgt gaaat c 5880  
gt cgaagcca aaggt cgt ct cgaagaagaa t ccat cgct c gt accaact c t gat cgt t ca 5940  
agaaagagac t cgaagct ga aat t gat gcc ct cact gct c aagt t gat gc t gaacaaaaa 6000  
gccagaat c aacaaat caa agaaaacaag aagat cgaaa ccgaact caa agaat acaga 6060  
aagaaat t cg gcgaat caga aaagaccaag accaaagaat t cct cgt t gt cgaaaaact c 6120  
gaaacagatt t acaagagagc caagaaagaa gct gct gat g aacaacaaca acgt ct t act 6180  
gt t gaaaacg at ct ccgt aa acacct cagt gaaat ct cat t act caaaga t gccat t gat 6240  
aagt t acaac gt gat cacga t aagaccaa cgt gaat t gg aaacagaaac t gccagcaaa 6300  
at cgaaat gc aaagaaagat ggccgat t t c t t t ggt ggt t t caaagct t a a 6351

<210> 2  
<211> 2116  
<212> PRT  
<213> Dictyostelium discoideum

<220>  
<221> MSC\_FEATURE  
<222> (1)..(2116)  
<223> Myosin-2

<400> 2

Met Asn Pro Ile His Asp Arg Thr Ser Asp Tyr His Lys Tyr Leu Lys  
1 5 10 15

Val Lys Gln Gly Asp Ser Asp Leu Phe Lys Leu Thr Val Ser Asp Lys  
20 25 30

Arg Tyr Ile Trp Tyr Asn Pro Asp Pro Lys Glu Arg Asp Ser Tyr Glu  
35 40 45

Cys Gly Glu Ile Val Ser Glu Thr Ser Asp Ser Phe Thr Phe Lys Thr  
50 55 60

Val Asp Gly Gln Asp Arg Gln Val Lys Lys Asp Asp Ala Asn Gln Arg  
65 70 75 80

Asn Pro Ile Lys Phe Asp Gly Val Glu Asp Met Ser Glu Leu Ser Tyr  
85 90 95

N3027PCT\_sequ.list.txt

Leu Asn Glu Pro Ala Val Phe His Asn Leu Arg Val Arg Tyr Asn Gln  
 100 105 110  
 Asp Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Leu Val Ala Val Asn Pro  
 115 120 125  
 Phe Lys Arg Ile Pro Ile Tyr Thr Gln Glu Met Val Asp Ile Phe Lys  
 130 135 140  
 Gly Arg Arg Arg Asn Glu Val Ala Pro His Ile Phe Ala Ile Ser Asp  
 145 150 155 160  
 Val Ala Tyr Arg Ser Met Leu Asp Asp Arg Gln Asn Gln Ser Leu Leu  
 165 170 175  
 Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val  
 180 185 190  
 Ile Gln Tyr Leu Ala Ser Val Ala Gly Arg Asn Gln Ala Asn Gly Ser  
 195 200 205  
 Gly Val Leu Glu Gln Gln Ile Leu Gln Ala Asn Pro Ile Leu Glu Ala  
 210 215 220  
 Phe Gly Asn Ala Lys Thr Thr Arg Asn Asn Asn Ser Ser Arg Phe Gly  
 225 230 235 240  
 Lys Phe Ile Glu Ile Gln Phe Asn Asn Ala Gly Phe Ile Ser Gly Ala  
 245 250 255  
 Ser Ile Gln Ser Tyr Leu Leu Glu Lys Ser Arg Val Val Phe Gln Ser  
 260 265 270  
 Glu Thr Glu Arg Asn Tyr His Ile Phe Tyr Gln Leu Leu Ala Gly Ala  
 275 280 285  
 Thr Ala Glu Glu Lys Lys Ala Leu His Leu Ala Gly Pro Glu Ser Phe  
 290 295 300  
 Asn Tyr Leu Asn Gln Ser Gly Tyr Val Asp Ile Lys Gly Val Ser Asp  
 305 310 315 320  
 Ser Glu Glu Phe Lys Ile Thr Arg Gln Ala Met Asp Ile Val Gly Phe  
 325 330 335  
 Ser Gln Glu Glu Gln Met Ser Ile Phe Lys Ile Ile Ala Gly Ile Leu  
 340 345 350  
 His Leu Gly Asn Ile Lys Phe Glu Lys Gly Ala Gly Glu Gly Ala Val  
 355 360 365

N3027PCT\_sequ.list.txt

Leu Lys Asp Lys Thr Ala Leu Asn Ala Ala Ser Thr Val Phe Gly Val  
 370 375 380  
 Asn Pro Ser Val Leu Glu Lys Ala Leu Met Glu Pro Arg Ile Leu Ala  
 385 390 395 400  
 Gly Arg Asp Leu Val Ala Gln His Leu Asn Val Glu Lys Ser Ser Ser  
 405 410 415  
 Ser Arg Asp Ala Leu Val Lys Ala Leu Tyr Gly Arg Leu Phe Leu Trp  
 420 425 430  
 Leu Val Lys Lys Ile Asn Asn Val Leu Cys Gln Glu Arg Lys Ala Tyr  
 435 440 445  
 Phe Ile Gly Val Leu Asp Ile Ser Gly Phe Glu Ile Phe Lys Val Asn  
 450 455 460  
 Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn Glu Lys Leu Gln Gln  
 465 470 475 480  
 Phe Phe Asn His His Met Phe Lys Leu Glu Gln Glu Glu Tyr Leu Lys  
 485 490 495  
 Glu Lys Ile Asn Trp Thr Phe Ile Asp Phe Gly Leu Asp Ser Gln Ala  
 500 505 510  
 Thr Ile Asp Leu Ile Asp Gly Arg Gln Pro Pro Gly Ile Leu Ala Leu  
 515 520 525  
 Leu Asp Glu Gln Ser Val Phe Pro Asn Ala Thr Asp Asn Thr Leu Ile  
 530 535 540  
 Thr Lys Leu His Ser His Phe Ser Lys Lys Asn Ala Lys Tyr Glu Glu  
 545 550 555 560  
 Pro Arg Phe Ser Lys Thr Glu Phe Gly Val Thr His Tyr Ala Gly Gln  
 565 570 575  
 Val Met Tyr Glu Ile Gln Asp Trp Leu Glu Lys Asn Lys Asp Pro Leu  
 580 585 590  
 Gln Gln Asp Leu Glu Leu Cys Phe Lys Asp Ser Ser Asp Asn Val Val  
 595 600 605  
 Thr Lys Leu Phe Asn Asp Pro Asn Ile Ala Ser Arg Ala Lys Lys Gly  
 610 615 620  
 Ala Asn Phe Ile Thr Val Ala Ala Gln Tyr Lys Glu Gln Leu Ala Ser  
 625 630 635 640

N3027PCT\_sequ.list.txt

Leu Met Ala Thr Leu 645 Glu Thr Thr Asn 650 Pro His Phe Val Arg Cys 655 Ile

Ile Pro Asn 660 Asn Lys Gln Leu Pro Ala 665 Lys Leu Glu Asp Lys 670 Val Val

Leu Asp Gln 675 Leu Arg Cys Asn 680 Gly Val Leu Glu Gly Ile 685 Arg Ile Thr

Arg Lys 690 Gly Phe Pro Asn 695 Arg Ile Ile Tyr Ala 700 Asp Phe Val Lys Arg

Tyr 705 Tyr Leu Leu Ala 710 Pro Asn Val Pro Arg Asp 715 Ala Glu Asp Ser Gln 720

Lys Ala Thr Asp 725 Ala Val Leu Lys His 730 Leu Asn Ile Asp Pro Glu 735 Gln

Tyr Arg Phe Gly 740 Ile Thr Lys Ile Phe 745 Phe Arg Ala Gly Gln 750 Leu Ala

Arg Ile Glu 755 Glu Ala Arg Glu Gln 760 Arg Ile Ser Glu 765 Ile Ile Lys Ala

Ile Gln 770 Ala Ala Thr Arg Gly 775 Trp Ile Ala Arg Lys 780 Val Tyr Lys Gln

Ala 785 Arg Glu His Thr Val 790 Ala Ala Arg Ile Ile 795 Gln Gln Asn Leu Arg 800

Ala Tyr Ile Asp 805 Phe Lys Ser Trp Pro Trp 810 Trp Lys Leu Phe Ser 815 Lys

Ala Arg Pro 820 Leu Leu Lys Arg Arg Asn 825 Phe Glu Lys Glu 830 Ile Lys Glu

Lys Glu 835 Arg Glu Ile Leu Glu 840 Leu Lys Ser Asn Leu Thr 845 Asp Ser Thr

Thr Gln 850 Lys Asp Lys Leu Glu 855 Lys Ser Leu Lys Asp 860 Thr Glu Ser Asn

Val 865 Leu Asp Leu Gln Arg 870 Gln Leu Lys Ala Glu 875 Lys Glu Thr Leu Lys 880

Ala Met Tyr Asp 885 Ser Lys Asp Ala Leu Glu 890 Ala Gln Lys Arg Glu 895 Leu

Glu Ile Arg 900 Val Glu Asp Met Glu 905 Ser Glu Leu Asp Glu 910 Lys Lys Leu

Ala Leu Glu Asn Leu Gln Asn Gln Lys Arg Ser Val Glu Glu Lys Val

915

Arg Asp Leu Glu Glu Glu Leu Gln Glu Glu Gln Lys Leu Arg Asn Thr  
930 935 940

Leu Glu Lys Leu Lys Lys Lys Tyr Glu Glu Glu Leu Glu Glu Met Lys  
945 950 955 960

Arg Val Asn Asp Gly Gln Ser Asp Thr Ile Ser Arg Leu Glu Lys Ile  
965 970 975

Lys Asp Glu Leu Gln Lys Glu Val Glu Glu Leu Thr Glu Ser Phe Ser  
980 985 990

Glu Glu Ser Lys Asp Lys Gly Val Leu Glu Lys Thr Arg Val Arg Leu  
995 1000 1005

Gln Ser Glu Leu Asp Asp Leu Thr Val Arg Leu Asp Ser Glu Thr  
1010 1015 1020

Lys Asp Lys Ser Glu Leu Leu Arg Gln Lys Lys Lys Leu Glu Glu  
1025 1030 1035

Glu Leu Lys Gln Val Gln Glu Ala Leu Ala Ala Glu Thr Ala Ala  
1040 1045 1050

Lys Leu Ala Gln Glu Ala Ala Asn Lys Lys Leu Gln Gly Glu Tyr  
1055 1060 1065

Thr Glu Leu Asn Glu Lys Phe Asn Ser Glu Val Thr Ala Arg Ser  
1070 1075 1080

Asn Val Glu Lys Ser Lys Lys Thr Leu Glu Ser Gln Leu Val Ala  
1085 1090 1095

Val Asn Asn Glu Leu Asp Glu Glu Lys Lys Asn Arg Asp Ala Leu  
1100 1105 1110

Glu Lys Lys Lys Lys Ala Leu Asp Ala Met Leu Glu Glu Met Lys  
1115 1120 1125

Asp Gln Leu Glu Ser Thr Gly Gly Glu Lys Lys Ser Leu Tyr Asp  
1130 1135 1140

Leu Lys Val Lys Gln Glu Ser Asp Met Glu Ala Leu Arg Asn Gln  
1145 1150 1155

Ile Ser Glu Leu Gln Ser Thr Ile Ala Lys Leu Glu Lys Ile Lys  
1160 1165 1170

Ser Thr Leu Glu Gly Glu Val Ala Arg Leu Gln Gly Glu Leu Glu  
1175 1180 1185

N3027PCT\_sequ.list.txt

Ala	Glu	Gln	Leu	Ala	Lys	Ser	Asn	Val	Glu	Lys	Gln	Lys	Lys	Lys
	1190					1195					1200			
Val	Glu	Leu	Asp	Leu	Glu	Asp	Lys	Ser	Ala	Gln	Leu	Ala	Glu	Glu
	1205					1210					1215			
Thr	Ala	Ala	Lys	Gln	Ala	Leu	Asp	Lys	Leu	Lys	Lys	Lys	Leu	Glu
	1220					1225					1230			
Gln	Glu	Leu	Ser	Glu	Val	Gln	Thr	Gln	Leu	Ser	Glu	Ala	Asn	Asn
	1235					1240					1245			
Lys	Asn	Val	Asn	Ser	Asp	Ser	Thr	Asn	Lys	His	Leu	Glu	Thr	Ser
	1250					1255					1260			
Phe	Asn	Asn	Leu	Lys	Leu	Glu	Leu	Glu	Ala	Glu	Gln	Lys	Ala	Lys
	1265					1270					1275			
Gln	Ala	Leu	Glu	Lys	Lys	Arg	Leu	Gly	Leu	Glu	Ser	Glu	Leu	Lys
	1280					1285					1290			
His	Val	Asn	Glu	Gln	Leu	Glu	Glu	Glu	Lys	Lys	Gln	Lys	Glu	Ser
	1295					1300					1305			
Asn	Glu	Lys	Arg	Lys	Val	Asp	Leu	Glu	Lys	Glu	Val	Ser	Glu	Leu
	1310					1315					1320			
Lys	Asp	Gln	Ile	Glu	Glu	Glu	Val	Ala	Ser	Lys	Lys	Ala	Val	Thr
	1325					1330					1335			
Glu	Ala	Lys	Asn	Lys	Lys	Glu	Ser	Glu	Leu	Asp	Glu	Ile	Lys	Arg
	1340					1345					1350			
Gln	Tyr	Ala	Asp	Val	Val	Ser	Ser	Arg	Asp	Lys	Ser	Val	Glu	Gln
	1355					1360					1365			
Leu	Lys	Thr	Leu	Gln	Ala	Lys	Asn	Glu	Glu	Leu	Arg	Asn	Thr	Ala
	1370					1375					1380			
Glu	Glu	Ala	Glu	Gly	Gln	Leu	Asp	Arg	Ala	Glu	Arg	Ser	Lys	Lys
	1385					1390					1395			
Lys	Ala	Glu	Phe	Asp	Leu	Glu	Glu	Ala	Val	Lys	Asn	Leu	Glu	Glu
	1400					1405					1410			
Glu	Thr	Ala	Lys	Lys	Val	Lys	Ala	Glu	Lys	Ala	Met	Lys	Lys	Ala
	1415					1420					1425			
Glu	Thr	Asp	Tyr	Arg	Ser	Thr	Lys	Ser	Glu	Leu	Asp	Asp	Ala	Lys
	1430					1435					1440			

N3027PCT\_sequ.list.txt

Asn	Val	Ser	Ser	Glu	Gln	Tyr	Val	Gln	Ile	Lys	Arg	Leu	Asn	Glu
	1445					1450					1455			
Glu	Leu	Ser	Glu	Leu	Arg	Ser	Val	Leu	Glu	Glu	Ala	Asp	Glu	Arg
	1460					1465					1470			
Cys	Asn	Ser	Ala	Ile	Lys	Ala	Lys	Lys	Thr	Ala	Glu	Ser	Ala	Leu
	1475					1480					1485			
Glu	Ser	Leu	Lys	Asp	Glu	Ile	Asp	Ala	Ala	Asn	Asn	Ala	Lys	Ala
	1490					1495					1500			
Lys	Ala	Glu	Arg	Lys	Ser	Lys	Glu	Leu	Glu	Val	Arg	Val	Ala	Glu
	1505					1510					1515			
Leu	Glu	Glu	Ser	Leu	Glu	Asp	Lys	Ser	Gly	Thr	Val	Asn	Val	Glu
	1520					1525					1530			
Phe	Ile	Arg	Lys	Lys	Asp	Ala	Glu	Ile	Asp	Asp	Leu	Arg	Ala	Arg
	1535					1540					1545			
Leu	Asp	Arg	Glu	Thr	Glu	Ser	Arg	Ile	Lys	Ser	Asp	Glu	Asp	Lys
	1550					1555					1560			
Lys	Asn	Thr	Arg	Lys	Gln	Phe	Ala	Asp	Leu	Glu	Ala	Lys	Val	Glu
	1565					1570					1575			
Glu	Ala	Gln	Arg	Glu	Val	Val	Thr	Ile	Asp	Arg	Leu	Lys	Lys	Lys
	1580					1585					1590			
Leu	Glu	Ser	Asp	Ile	Ile	Asp	Leu	Ser	Thr	Gln	Leu	Asp	Thr	Glu
	1595					1600					1605			
Thr	Lys	Ser	Arg	Ile	Lys	Ile	Glu	Lys	Ser	Lys	Lys	Lys	Leu	Glu
	1610					1615					1620			
Gln	Thr	Leu	Ala	Glu	Arg	Arg	Ala	Ala	Glu	Glu	Gly	Ser	Ser	Lys
	1625					1630					1635			
Ala	Ala	Asp	Glu	Glu	Ile	Arg	Lys	Gln	Val	Trp	Gln	Glu	Val	Asp
	1640					1645					1650			
Glu	Leu	Arg	Ala	Gln	Leu	Asp	Ser	Glu	Arg	Ala	Ala	Leu	Asn	Ala
	1655					1660					1665			
Ser	Glu	Lys	Lys	Ile	Lys	Ser	Leu	Val	Ala	Glu	Val	Asp	Glu	Val
	1670					1675					1680			
Lys	Glu	Gln	Leu	Glu	Asp	Glu	Ile	Leu	Ala	Lys	Asp	Lys	Leu	Val
	1685					1690					1695			

Lys Ala Lys Arg Ala Leu Gu Val Gu Leu Gu Gu Val Arg Asp  
 1700 1705 1710  
 Gn Leu Gu Gu Gu Gu Asp Ser Arg Ser Gu Leu Gu Asp Ser  
 1715 1720 1725  
 Lys Arg Arg Leu Thr Thr Gu Val Gu Asp Ile Lys Lys Lys Tyr  
 1730 1735 1740  
 Asp Ala Gu Val Gu Gn Asn Thr Lys Leu Asp Gu Ala Lys Lys  
 1745 1750 1755  
 Lys Leu Thr Asp Asp Val Asp Thr Leu Lys Lys Gn Leu Gu Asp  
 1760 1765 1770  
 Gu Lys Lys Lys Leu Asn Gu Ser Gu Arg Ala Lys Lys Arg Leu  
 1775 1780 1785  
 Gu Ser Gu Asn Gu Asp Phe Leu Ala Lys Leu Asp Ala Gu Val  
 1790 1795 1800  
 Lys Asn Arg Ser Arg Ala Gu Lys Asp Arg Lys Lys Tyr Gu Lys  
 1805 1810 1815  
 Asp Leu Lys Asp Thr Lys Tyr Lys Leu Asn Asp Gu Ala Ala Thr  
 1820 1825 1830  
 Lys Thr Gn Thr Gu Ile Gy Ala Ala Lys Leu Gu Asp Gn Ile  
 1835 1840 1845  
 Asp Gu Leu Arg Ser Lys Leu Gu Gn Gu Gn Ala Lys Ala Thr  
 1850 1855 1860  
 Gn Ala Asp Lys Ser Lys Lys Thr Leu Gu Gy Gu Ile Asp Asn  
 1865 1870 1875  
 Leu Arg Ala Gn Ile Gu Asp Gu Gy Lys Ile Lys Met Arg Leu  
 1880 1885 1890  
 Gu Lys Gu Lys Arg Ala Leu Gu Gy Gu Leu Gu Gu Leu Arg  
 1895 1900 1905  
 Gu Thr Val Gu Gu Ala Gu Asp Ser Lys Ser Gu Ala Gu Gn  
 1910 1915 1920  
 Ser Lys Arg Leu Val Gu Leu Gu Leu Gu Asp Ala Arg Arg Asn  
 1925 1930 1935  
 Leu Gn Lys Gu Ile Asp Ala Lys Gu Ile Ala Gu Asp Ala Lys  
 1940 1945 1950  
 Ser Asn Leu Gn Arg Gu Ile Val Gu Ala Lys Gy Arg Leu Gu

1955

1960

1965

G u G u Ser I l e A l a Arg Thr Asn Ser Asp Arg Ser Arg Lys Arg  
 1970 1975 1980  
 Leu G u A l a G u I l e Asp A l a Leu Thr A l a G n Val Asp A l a G u  
 1985 1990 1995  
 G n Lys A l a Lys Asn G n G n I l e Lys G u Asn Lys Lys I l e G u  
 2000 2005 2010  
 Thr G u Leu Lys G u Tyr Arg Lys Lys Phe G y G u Ser G u Lys  
 2015 2020 2025  
 Thr Lys Thr Lys G u Phe Leu Val Val G u Lys Leu G u Thr Asp  
 2030 2035 2040  
 Tyr Lys Arg A l a Lys Lys G u A l a A l a Asp G u G n G n G n Arg  
 2045 2050 2055  
 Leu Thr Val G u Asn Asp Leu Arg Lys H i s Leu Ser G u I l e Ser  
 2060 2065 2070  
 Leu Leu Lys Asp A l a I l e Asp Lys Leu G n Arg Asp H i s Asp Lys  
 2075 2080 2085  
 Thr Lys Arg G u Leu G u Thr G u Thr A l a Ser Lys I l e G u Met  
 2090 2095 2100  
 G n Arg Lys Met A l a Asp Phe Phe G y G y Phe Lys A l a  
 2105 2110 2115

<210> 3  
 <211> 3018  
 <212> DNA  
 <213> Dictyostelium discoideum

<220>  
 <221> misc\_feature  
 <222> (1)..(3018)  
 <223> Myosin-1E

<400> 3  
 atgattccaa agacaaaagc agaagggtgta ccagattttg ttttgttaaa tcaaatcaca 60  
 gaaaatgcat tcatagagaa ttttaactatg agacataaat cagacaatat ctacacatat 120  
 attggatgat gtagtaatctc aaccaatcca ttcaaaaatc tttaatctat taaagaaagt 180  
 gatattaaag catacaatgg tagatataaa tatgaaatgc caccacatat ttatgcactt 240  
 gcaaatgatg cataccgttc aatgagacaa agtcaagaga atcaatgtgt tattatttca 300  
 ggtgaatcag gtgctggtaa aactgaagca agtaaaaga ttatgcaatt tttaacattt 360  
 gttagtagta atcaaagtc aaatggtgaa agaatttcaa agatgttatt agattccaat 420

N3027PCT\_sequ. list.txt

ccattattgg aagcatttgg t aatgcaaaa actcttagaa atgat aattc atcacgtttt	480
ggtaaatata tggaaatgca attcaatgca gttggttcac caattggtgg taaaattaca	540
aatatattct tggaaaaatc aagagttgtt ggtagaactc aaggtgaaag aagttttcat	600
attttttatc aaatgttaa aggtttatca caatcaaat taaatgaact tggatt aaca	660
ccaaatgcac cagcatatga atattttaaa aagagtggtt gttttgatgt tccaactatt	720
gatgatagt ggtgaatttaa aattattgta aaagcaatgg aaacattagg attaaaagaa	780
agtgacaaaa attcaatttg gagaatttta gcagcaattt tacatattgg taatattaca	840
tttgcagaag cagcagaaca aagaactggt actacaacag tgaaagtatc agat actaaa	900
tcat tggcag cagcagcatc atgtttaaag acagatcaac agtcattatc gat tgcatt a	960
tgttatcgtt caattagtac aggtgttggg aaacgttgtt cagttatttc agt accaatg	1020
gattgt aatc aagcagccta ctctaggat gcacttgcaa aggcattgta tgaacgttta	1080
ttcaattggt tagtcagcaa aatcaat acc attatcaatt gtacaacaga gaagggacca	1140
gtgat tggta tttcttgat at ctatggtttt gaggtttttc aaaat aatag tttcgaacaa	1200
ttgaattata atttctgtaa tgagaaatta caacaactat tcat agagtt gacattgaag	1260
tctgagcaag aggagtacgt tagggagggt atcgagt gga agaataatcga atactttaat	1320
aat aaaccaaa tttgtgagtt aattgaaaag aaaccaattg gtttgatttc gttattggat	1380
gaggcatgtt tgattgcaa gagcactgat caaacttttt tagattcaat ttgt aaacaa	1440
tttgaaaaga atccacattt gcaatcgtat gttgttagta aggatagatc gat tggggat	1500
acatgtttcc gtttgaagca ttatgctggc gatgt aactt atgacgttag aggtttcctc	1560
gat aagaata aggat accct attcggtgat ttaataatcaa gtatgcaaag tagttcagat	1620
ccattggttc aaggcttatt cccaccaact agaccagagg atagt aagaa gagaccagag	1680
actgccggtt cccaatttag aaatgcaatg aatgctctca t cactacatt gttggcttgt	1740
tcaccacatt acgttcgttg tattaaatca aatgat aata aacaagctgg tgt aattgat	1800
gaggatcgtg tacgtcatca agttcgttat ct tggtttac tttgaaaatgt tagagttaga	1860
agagcaggtt tgcaggtag aattgaat at accagattct acaatcgtta taaaatgctt	1920
tgt aaaaaga catggccatc atttaatggc acagcaaac aagccactga attaatcctc	1980
caacaacata atatcgataa agaggaaatt cgtatgggt a aaaccaaagt attcatccgt	2040
aatccaacca ctctattcta ttttgaagag aagagggagc tttgaaatgcc aagaattgta	2100
acatt aattc aaaagacatg gagaggttat agagcacgtt ccaaatggaa tcaaagaaaa	2160
gctgccatt a aaatccagtt attctatcgt agctatcgtt at aagaaatg gttcagagag	2220
ttacatcgtg ctttt aaaga tgtcgctcgt gatccacaat ggggt aaaca agtattttgg	2280
cccaaacatc catccatctt ggatagagct gtccaattaa ct caaaaat tcacaattgt	2340
tggagagcag agaaaatgat tctttctttg ggtgccggtc aaaatcatat gagacaaaag	2400
gttatggctt acgatatttt ccatggtaaa aagaaatggg acttccgtcg tcat ttcgat	2460
gctgat tatt tggagaaacc atccaatcca aatcaacaaa aat acgtatt ggccatgcaa	2520

N3027PCT\_sequ.list.txt

```

aatcttttct caacttatgg tgacacagag gtactctttg ccgattacgt tatcaaagtc 2580
aatccaaagg gtgtgccaca acgtcgtggg atcgttgtca ctggtaaaaa catctataaa 2640
cacgatccaa agaattacaa agtaagaaaa tggggactc cattgggtga tgtaaactca 2700
atctcaattt caccaatggc tgatactttc ttgggtttac attgtaaagc tccacaaaga 2760
gatttcgtat tggatttagg ttgtaatggg tatgaagctg tatctgaaat tacaactgta 2820
atcgttcaac aagctttaa attaaactgg gtcaaattat ctgttcaatt cactagttca 2880
atcacttata ataatgctcg tccaaaagg tctgatacaa ttttaacttt tgctccaatt 2940
aatatgatc caaaattaat tgggttctcaa tttaaaaaag gtaaaggtaa ccaagcaaca 3000
atccaattta aagattaa 3018

```

```

<210> 4
<211> 1005
<212> PRT
<213> Dictyostelium discoideum

```

```

<220>
<221> MSC_FEATURE
<222> (1)..(1005)
<223> Myosin-1E

```

<400> 4

```

Met Ile Pro Lys Thr Lys Ala Glu Gly Val Pro Asp Phe Val Leu Leu
1 5 10 15

```

```

Asn Gln Ile Thr Glu Asn Ala Phe Ile Glu Asn Leu Thr Met Arg His
20 25 30

```

```

Lys Ser Asp Asn Ile Tyr Thr Tyr Ile Gly Asp Val Val Ile Ser Thr
35 40 45

```

```

Asn Pro Phe Lys Asn Leu Asn Ile Tyr Lys Glu Ser Asp Ile Lys Ala
50 55 60

```

```

Tyr Asn Gly Arg Tyr Lys Tyr Glu Met Pro Pro His Ile Tyr Ala Leu
65 70 75 80

```

```

Ala Asn Asp Ala Tyr Arg Ser Met Arg Gln Ser Gln Glu Asn Gln Gys
85 90 95

```

```

Val Ile Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Ser Lys
100 105 110

```

```

Lys Ile Met Gln Phe Leu Thr Phe Val Ser Ser Asn Gln Ser Pro Asn
115 120 125

```

```

Gly Glu Arg Ile Ser Lys Met Leu Leu Asp Ser Asn Pro Leu Leu Glu
130 135 140

```

N3027PCT\_sequ.list.txt

Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe  
145 150 155 160

Gly Lys Tyr Met Glu Met Gln Phe Asn Ala Val Gly Ser Pro Ile Gly  
165 170 175

Gly Lys Ile Thr Asn Tyr Leu Leu Glu Lys Ser Arg Val Val Gly Arg  
180 185 190

Thr Gln Gly Glu Arg Ser Phe His Ile Phe Tyr Gln Met Leu Lys Gly  
195 200 205

Leu Ser Gln Ser Lys Leu Asn Glu Leu Gly Leu Thr Pro Asn Ala Pro  
210 215 220

Ala Tyr Glu Tyr Leu Lys Lys Ser Gly Cys Phe Asp Val Ser Thr Ile  
225 230 235 240

Asp Asp Ser Gly Glu Phe Lys Ile Ile Val Lys Ala Met Glu Thr Leu  
245 250 255

Gly Leu Lys Glu Ser Asp Gln Asn Ser Ile Trp Arg Ile Leu Ala Ala  
260 265 270

Ile Leu His Ile Gly Asn Ile Thr Phe Ala Glu Ala Ala Glu Gln Arg  
275 280 285

Thr Gly Thr Thr Thr Val Lys Val Ser Asp Thr Lys Ser Leu Ala Ala  
290 295 300

Ala Ala Ser Cys Leu Lys Thr Asp Gln Gln Ser Leu Ser Ile Ala Leu  
305 310 315 320

Cys Tyr Arg Ser Ile Ser Thr Gly Val Gly Lys Arg Cys Ser Val Ile  
325 330 335

Ser Val Pro Met Asp Cys Asn Gln Ala Ala Tyr Ser Arg Asp Ala Leu  
340 345 350

Ala Lys Ala Leu Tyr Glu Arg Leu Phe Asn Trp Leu Val Ser Lys Ile  
355 360 365

Asn Thr Ile Ile Asn Cys Thr Thr Glu Lys Gly Pro Val Ile Gly Ile  
370 375 380

Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln Asn Asn Ser Phe Glu Gln  
385 390 395 400

Leu Asn Ile Asn Phe Cys Asn Glu Lys Leu Gln Gln Leu Phe Ile Glu  
405 410 415

Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Val Arg Glu Gly Ile Glu

420

425

430

Trp Lys Asn Ile Glu Tyr Phe Asn Asn Lys Pro Ile Cys Glu Leu Ile  
 435 440 445  
 Glu Lys Lys Pro Ile Gly Leu Ile Ser Leu Leu Asp Glu Ala Cys Leu  
 450 455 460  
 Ile Ala Lys Ser Thr Asp Gln Thr Phe Leu Asp Ser Ile Cys Lys Gln  
 465 470 475 480  
 Phe Glu Lys Asn Pro His Leu Gln Ser Tyr Val Val Ser Lys Asp Arg  
 485 490 495  
 Ser Ile Gly Asp Thr Cys Phe Arg Leu Lys His Tyr Ala Gly Asp Val  
 500 505 510  
 Thr Tyr Asp Val Arg Gly Phe Leu Asp Lys Asn Lys Asp Thr Leu Phe  
 515 520 525  
 Gly Asp Leu Ile Ser Ser Met Gln Ser Ser Ser Asp Pro Leu Val Gln  
 530 535 540  
 Gly Leu Phe Pro Pro Thr Arg Pro Glu Asp Ser Lys Lys Arg Pro Glu  
 545 550 555 560  
 Thr Ala Gly Ser Gln Phe Arg Asn Ala Met Asn Ala Leu Ile Thr Thr  
 565 570 575  
 Leu Leu Ala Cys Ser Pro His Tyr Val Arg Cys Ile Lys Ser Asn Asp  
 580 585 590  
 Asn Lys Gln Ala Gly Val Ile Asp Glu Asp Arg Val Arg His Gln Val  
 595 600 605  
 Arg Tyr Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly Phe  
 610 615 620  
 Ala Gly Arg Ile Glu Tyr Thr Arg Phe Tyr Asn Arg Tyr Lys Met Leu  
 625 630 635 640  
 Cys Lys Lys Thr Trp Pro Ser Phe Asn Gly Thr Ala Lys Gln Ala Thr  
 645 650 655  
 Glu Leu Ile Leu Gln Gln His Asn Ile Asp Lys Glu Glu Ile Arg Met  
 660 665 670  
 Gly Lys Thr Lys Val Phe Ile Arg Asn Pro Thr Thr Leu Phe Tyr Phe  
 675 680 685  
 Glu Glu Lys Arg Glu Leu Glu Met Pro Arg Ile Val Thr Leu Ile Gln  
 690 695 700

N3027PCT\_sequ.list.txt

Lys Thr Trp Arg Gly Tyr Arg Ala Arg Ser Lys Trp Asn Gln Arg Lys  
 705 710 715 720  
 Ala Ala Ile Lys Ile Gln Leu Phe Tyr Arg Ser Tyr Arg Tyr Lys Lys  
 725 730 735  
 Trp Phe Arg Glu Leu His Arg Ala Phe Lys Asp Val Ala Arg Asp Pro  
 740 745 750  
 Gln Trp Gly Lys Gln Val Phe Trp Pro Lys His Pro Ser Ile Leu Asp  
 755 760 765  
 Arg Ala Val Gln Leu Thr His Lys Ile His Asn Cys Trp Arg Ala Glu  
 770 775 780  
 Lys Met Ile Leu Ser Leu Gly Ala Gly Gln Asn His Met Arg Gln Lys  
 785 790 795 800  
 Val Met Ala Tyr Asp Ile Phe His Gly Lys Lys Lys Trp Asp Phe Arg  
 805 810 815  
 Arg His Phe Asp Ala Asp Tyr Leu Glu Lys Pro Ser Asn Pro Asn Gln  
 820 825 830  
 Gln Lys Tyr Val Leu Ala Met Gln Asn Leu Phe Ser Thr Tyr Gly Asp  
 835 840 845  
 Thr Glu Val Leu Phe Ala Asp Tyr Val Ile Lys Val Asn Pro Lys Gly  
 850 855 860  
 Val Pro Gln Arg Arg Gly Ile Val Val Thr Gly Thr Asn Ile Tyr Lys  
 865 870 875 880  
 His Asp Pro Lys Asn Tyr Lys Val Lys Lys Trp Gly Thr Pro Leu Val  
 885 890 895  
 Asp Val Thr Ser Ile Ser Ile Ser Pro Met Ala Asp Thr Phe Leu Val  
 900 905 910  
 Leu His Cys Lys Ala Pro Gln Arg Asp Phe Val Leu Asp Leu Gly Cys  
 915 920 925  
 Asn Gly Tyr Glu Ala Val Ser Glu Ile Thr Thr Val Ile Val Gln Gln  
 930 935 940  
 Val Leu Lys Leu Thr Gly Val Lys Leu Ser Val Gln Phe Thr Ser Ser  
 945 950 955 960  
 Ile Thr Tyr Asn Asn Ala Arg Pro Lys Gly Ser Asp Thr Ile Leu Thr  
 965 970 975

N3027PCT\_sequ.list.txt

Phe Ala Pro Ile Asn Asn Asp Pro Lys Leu Ile Gly Ser Gln Phe Lys  
980 985 990

Lys Gly Lys Gly Asn Gln Ala Thr Ile Gln Phe Lys Asp  
995 1000 1005

<210> 5  
<211> 6925  
<212> DNA  
<213> Gallus gallus

<220>  
<221> mi sc\_feat ure  
<222> (1)..(6925)  
<223> myosi n VA (heavy chain 12, myosi n) (MYO5A)

```

<400> 5
ccgccaggta gcagcaat at ggcgcgccgc gccgcgcct gagcat ct t c ccgccgccgc      60
cgccccgccg cccgccgcag cgcggccgcg ccccgcgcca tggccgcct c cgagct gt ac      120
accaagt at g ccagggt t t g gat ccct gac ccagaggagg t ct ggaagt c agcagaact t      180
ct t aaagat t at aaacct gg agat aaagt t t t gcagct t c gact t gaaga gggcaaggac      240
ct agaat at t gcct cgaccc caagact aag gaact ccccc cct t gcgaaa ccct gacat c      300
ct t gt t ggt g aaaat gacct cact gcgct c agt t at ct cc at gaacct gc t gt gct acac      360
aacct caaag t t cgat t t at agact ct aaa ct cat t t at a cct at t gt gg t at cgt ct t a      420
gt ggcaat aa accct t at ga acagct gcct at ct at ggcg aagat at cat caat gcgt ac      480
agt ggccaaa at at ggggga t at ggat cca cat at ct t t g cagt ggcaga agaggcat ac      540
aagcagat gg ccagagat ga gcgaaat cag t caat cat t g t aagt ggaga at ct ggggca      600
ggaaaagacgg t t t ct gccaa gt at gccat g aggt act t t g ccacggg cag t ggat ct gcc      660
agt gaagcca at gt t gagga gaaagt ct t g gct t caaacc ccat aat gga gt ccat t gga      720
aat gccaaaa caacgaggaa t gacaacagc agt cgct t t g ggaaat acat t gaaat t ggt      780
t t t gacaaga ggt at cgaat cat t ggt gct aacat gagaa ct t at ct ct t ggagaaat ca      840
agagt ggt at t t caggcaga agaggagagg aat t accaca t ct t t t acca act ct gt gcc      900
t ct gcagcat t acct gaat t t aaaact ct a cgat t agggga at gcaaat t a ct t t cat t at      960
acaaagcaag gt ggaagccc t gt gat t gat ggcat t gat g at gct aagga aat ggt aaac      1020
accagacaag cct gcact t t gct agggat t agt gat t cct accagat ggg aat t t t ccga      1080
at cct t gct g gcat cct t ca ct t gggcaac gt ggagt t t g cat ct cggga t t ct gacagc      1140
t gcgccat t c ct cccaaaca t gat cccct c accat ct t ct gt gacct cat gggcgt ggac      1200
t at gaagaga t ggct cact g gct t t gccat aggaagct cg caact gccac t gaaacct ac      1260
at caagccaa t t t ct aaact t cat gccat c aat gccagag at gcact t gc caaacat at c      1320
t at gct aat c t ct t t aact g gat t gt agat cat gt gaaca aagccct t ca t t ct act gt a      1380
aagcaacat t ct t t cat t gg agt act ggac at t t at ggat t t gagacat t t gaaat caac      1440

```

N3027PCT\_sequ. list.txt

agct t cgaac	agt t ct gt at	caact at gcc	aat gagaac	t gcagcagca	gt t caat at g	1500
cat gt gt t t a	agct ggaaca	agaagaat ac	at gaaagaac	aaat accat g	gacct t gat t	1560
gat t t ct at g	acaat cagcc	t t gcat caac	ct cat agaag	ccaaaat ggg	agt t ct ggat	1620
ct gt t agat g	aggaat gcaa	gat gccaaaa	ggct cggat g	acact t gggc	ccaaaaact g	1680
t acaat act c	at t t gaat aa	at gt gccct c	t t t gaaaaac	cacgt t t at c	caat aaggct	1740
t t t at cat ca	aacact t t gc	t gacaagg t g	gaat at cagt	gt gaaggct t	t ct ggaaaag	1800
aat aaggat a	cagt t t at ga	agagcaaat t	aagg t cct aa	aat caagt aa	gaagt t t aag	1860
ct gct accag	aat t at t cca	ggat gaggag	aaggccat ca	gt cccacgt c	agccaccct	1920
t caggccgt g	t gccat t gt c	t cgaact cct	gt aaaaccag	ccaaggccag	gccaggt caa	1980
act agcaagg	agcat aagaa	aact gt gggg	cat cagt t t c	gaaact ct ct	t cat ct gct g	2040
at ggaaaccc	t gaacgccac	aact ccacac	t at gt gcgct	gt at t aagcc	t aacgact t c	2100
aagt t t ccat	t cacat t t ga	cgaaaagcga	gcagt gcagc	agct gagagc	t t gt ggt gt c	2160
ct ggagacca	t ccgaat cag	t gcagct ggt	t t cccct cca	ggg ggacgt a	ccaagagt t c	2220
t t cagccgt t	accgt gt t ct	cat gaagcag	aaagat gt cc	t t agt gaccg	aaaacagaca	2280
t gt aaaaat g	t cct ggagaa	gct gat t ct g	gacaaggat a	agt accagt t	t ggt aagaca	2340
aaaat at t t t	t ccgggct gg	t caagt agcc	t at ct t gaaa	aaat aagggc	agat aagt t g	2400
agagct gcct	gt at ccgcat	ccaaaagaca	at ccgaggct	ggct gat gag	aaagaagt ac	2460
at gcgt at ga	ggagggct gc	cat caccat t	cagagat at g	t cagagggca	ccaagcacga	2520
t gct at gcca	cat t cct gcg	gagaacacgg	gct gccat ca	t t at t cagaa	gt t ccagcgt	2580
at gt at gt gg	t ccgcaaaag	at accagt gc	at gcgagat g	ct act at t gc	t ct t caagct	2640
ct ct t aagag	gt t acct ggt	caggaacaag	t accaaat ga	t gct t cgaga	gcacaagt ct	2700
at t at t at t c	agaaacat gt	aagaggct gg	ct ggct cgag	t gcact at ca	t aggacct t g	2760
aaggcaat t g	t t t act t gca	at gct gt t ac	cggcgcat ga	t ggccaagag	ggagct gaag	2820
aagct gaaga	t agaggct cg	gt ct gt ggaa	cgct acaaga	agct t cacat	t ggct t ggag	2880
aacaagat ca	t gcagct gca	gcggaaaat t	gat gaacaga	acaaagagt a	caaat ct ct g	2940
ct ggagaaga	t gaat aacct	ggagat caca	t acagt acag	agacagagaa	gct t cggagt	3000
gat gt ggaga	ggct t cggat	gagt gaggag	gaggct aaga	at gcaaccaa	ccgt gt t ct c	3060
agcct t cagg	aagagat t gc	caagct ccgg	aaggagct gc	accagact ca	gact gagaag	3120
aagacaat t g	aggaat gggc	agacaaat ac	aaacat gaaa	ct gagcagct	ggg gt cgga	3180
ct gaaagagc	agaacacat t	act gaaaaca	gaaaaggagg	agct gaaccg	ccgt at ccat	3240
gaccaagcaa	aggagat aac	agagacaat g	gagaagaagc	t agt ggagga	aacaaagcag	3300
t t ggagct ag	acct gaacga	t gagagg t a	cggt at caga	acct gct gaa	t gagt t cagc	3360
cgct t ggagg	agcgg t at ga	t gat ct caag	gat gaaat ga	act t aat ggt	gagcat cccc	3420
aagcct ggac	acaaaagaac	ggat t caact	cacagt agca	at gaat ct ga	at at act t t t	3480
agct ct gaga	t cacagaagc	agaagact t a	ccact gagga	t ggaggagcc	aagt gagaaa	3540

N3027PCT\_sequ. list . . txt

aaggcaccat	tggacatgtc	tctgttcctc	aagctgcaga	aacgggttac	agagctggag	3600
caagaaaagc	aatccctgca	ggatgaactg	gacagaaagg	aagaacaggc	tcttcgtgcc	3660
aaagct aagg	aggaggaaag	gcctccaat a	agaggtgcag	agt tggagt a	tgagt cgct c	3720
aagcgt caag	agct tgaat c	tgagaat aaa	aaact gaaga	atgagt t gaa	cgagct gcag	3780
aaggccct ca	cagaaacacg	agct ccagag	gt aact gct c	ct ggt gct cc	agcat acaga	3840
gt cct cct gg	atcagctgac	ttcagt aagc	gaagaact gg	aagt acgcaa	ggaagaagt g	3900
ct t at cct ga	ggt ct cagt t	ggt tagccag	aaagaggct a	ttcaacccaa	ggaggacaag	3960
aacaccat ga	cagat t ct ac	aat cct ct t g	gaggat gt gc	agaagat gaa	agacaaaggg	4020
gaaat agcac	aggcgt at at	tggact gaag	gaaaccaaca	ggct gct gga	gt ct cagct g	4080
cagt cgcaga	agaagagcca	cgagaat gag	ct ggagt cac	tgcgagggt ga	gat ccaaagt	4140
ct gaaggaag	aaaacaat cg	ccagcagcag	ct ct tggcac	agaat ct gca	gct gcccccg	4200
gaggccccga	ttgaagccag	tctgcagcat	gagat caccc	ggct gacaaa	cgagaact t g	4260
gat t t aat gg	aacaact t ga	aaagcaagac	aaaact gt t c	gcaaat t aaa	gaagcaat t g	4320
aaggt at t t g	ct aagaagat	t ggt gaact t	gaagt ggggt c	agat ggagaa	cat at cacct	4380
ggacaaat ca	ttgat gaacc	t at t cgt cca	gt t aacat t c	cacggaagga	aaaggact t c	4440
caggggat gt	tggagt at aa	gaaagaggat	gaacaaaagc	t agt caagaa	t ct t at at t a	4500
gagct gaaac	cacgcgggggt	agcagt caac	ct gat t ccag	gact accagc	at at at t t t g	4560
ttcat gt gt g	tacgccacgc	agat t acct t	aacgat gacc	agaaagt gcg	ttcat t gt t g	4620
acct ccact a	tcaat ggcat	caaaaaagt g	ct gaagaaaa	gaggt gat ga	ct t cgaaacg	4680
gt gt ct t t ct	ggct gt ccaa	cacct gccgg	tttt t gcact	gt t t gaagca	gt acagcgga	4740
gaagaggggt	ttat gaagca	t aat acacct	cgt cagaat g	agcact gcct	cact aat t t t	4800
gact t agct g	aat acagaca	agt cct gagt	gact t ggct a	ttcagat ct a	ccagcaact g	4860
gt ccgcgt gt	tggagaacat	tctgcaaccc	at gat t gt t t	ct ggaat gct	ggagcacgag	4920
act at ccagg	gt gt ct cagg	ggt gaaacca	acagggct gc	ggaagagAAC	at ccagcat t	4980
gct gat gaag	gaacct acac	ttt ggact cc	at t at t cgac	agt t gaact c	ttt ccat t cc	5040
gt gat gt gt c	agcat ggaat	ggat ccagag	ct gat caaac	aggt t gt caa	gcagat gt t c	5100
t acat cat t g	gggct gt aac	act t aat aat	ct t ct cct gc	gcaaggacat	gt gt t cat gg	5160
agcaaaggaa	tgcagat aag	gt acaat gt g	agt caact t g	aagaat ggct	acgt gat aaa	5220
aat ct aat ga	acagt ggggc	caaagaaaca	ct ggagcccc	t cat acaggc	t gcacagt t g	5280
ttgcaagt ga	aaaagaaaac	agat gaagat	gcagaagcca	ttt gt t caat	gt gcaat gca	5340
ct gact act g	cccagat t gt	gaaagt act g	aat t t gt at a	ct ccagt t aa	t gaat t t gaa	5400
gagagagt ct	t ggt at cgt t	t at acgt aca	at acagct gc	gt ct gcgaga	caggaaggac	5460
t ct cct caac	t gct cat gga	t gct aaacac	at ct t t cct g	ttact t t t cc	at t t aat cca	5520
t cct ccct gg	cat t agaaac	cat ccagat c	ccagccagt t	t ggggct ggg	ttt cat at ca	5580

cgt gt ct gat	cct aaggct g	t t ct gt cagt	gct agat gga	gaat t gt t t g	cct gat at ca	5640
t t acccat t a	aaacat agt g	agccact gaa	aacacat t t t	t gaacaaaca	gt ct ccgt at	5700
gct cagat t t	gt t gt aaaag	t agct gggaa	act acacaac	agcaccacag	at t gaaggct	5760
gat agaaaga	t gt gcat t t g	t gt t cagt ca	t t gcact t ac	gaggacat t a	ct gat t cat a	5820
cgt t t ccaga	gat ggaaat t	gggt t t ggac	aaaaat t gt g	t ct t cagct g	t t t agagacg	5880
t t t t t agat c	t t t agt aaca	t at t t aaat a	gt gt aaat t a	aact ccat gt	at aacct t ct	5940
cat gggcagg	gaccaat ggg	gacagt ccca	gt ccccat	ggaagacgt a	aaagt aaggc	6000
at t t t gt agt	agaat at gca	gt t act t ggg	agcct gt t ac	t t t t aat t t g	t aaaaact gg	6060
aat ggagaag	caaaaact t g	caat at at aa	cat gat t t ct	t aaaccact t	cct t act t at	6120
gt cggt t t ga	cat aaat t ct	agt gat aagt	ct t at agct t	act gt at gct	at aacat agg	6180
t gt t cat t t g	t t agt aat gt	gg t t t accaa	gcat at t aaa	t t gct gct gc	at at t gt gt t	6240
ct t t t aaat g	t at gacagt a	t cat gct agg	cact aaaaat	aagat gct t c	at t t t t ggt t	6300
gt caacct t a	t t t acagt cc	aat gcagt ct	gt t at t ct aa	ct ggat t t t t	gcagat gt t a	6360
t ccaat at ca	cct gt aaagg	aaaat ggt aa	ct aagcacaa	gt agcacact	ggaaat t at g	6420
t gt t t aggg t	t at t t t gt t t	t gt t t t gcct	t t t t t t t t t	aagt agt t at	ct aaaaat ac	6480
agaat ct cga	agcagat gat	cagaaat gag	t cacaat t t t	t gt at t t at t	t agat t t t gt	6540
agcat gt ccg	at gt t t t t ct	t t gt t t gt ag	accccaggga	t gacagt gt g	t at t t t cagt	6600
at aacagat t	t t gt t gacac	at ct aaaaaa	aaaaaaaaaa	agaaat ct t a	agaat at gt a	6660
t at at gt t t t	cct t cct t ca	t at t t gt at t	t gagaggaaa	agct aacaga	aaact t cagc	6720
agt agt gcag	ggct cat t cc	t t gaaagg t	ggccaacaca	aacgcaaagt	aagt t ct gag	6780
t gt gat gct g	t cat t gact g	ccat t ggt gc	t gact t aat g	gt t ggagat c	t ggagt gcgt	6840
aat gacaaat	ggagt t act t	t ggct at t gc	acat ccagt t	gggagggt t t	t ct gt ct cac	6900
act cct t gga	t gt gt t aaag	aat t c				6925

<210>	6
<211>	1830
<212>	PRT
<213>	Gal l us gal l us

```
<220>
<221> M SC_FEATURE
<222> (1)..(1830)
<223> myosin VA (heavy chain 12, myosin) (MYO5A)
```

<400> 6

Met Ala Ala Ser Gu Leu Tyr Thr Lys Tyr Ala Arg Val Trp Ile Pro  
1 5 10 15

Asp Pro Gu Gu Val Trp Lys Ser Ala Gu Leu Leu Lys Asp Tyr Lys  
20 25 30

Pro Gly Asp Lys Val Leu Gln Leu Arg Leu Glu Glu Gly Lys Asp Leu

G u Tyr Oys Leu Asp Pro Lys Thr Lys G u Leu Pro Pro Leu Arg Asn  
 50 55 60  
 Pro Asp Ile Leu Val Gly G u Asn Asp Leu Thr Ala Leu Ser Tyr Leu  
 65 70 75 80  
 His G u Pro Ala Val Leu His Asn Leu Lys Val Arg Phe Ile Asp Ser  
 85 90 95  
 Lys Leu Ile Tyr Thr Tyr Oys Gly Ile Val Leu Val Ala Ile Asn Pro  
 100 105 110  
 Tyr G u G n Leu Pro Ile Tyr Gly G u Asp Ile Ile Asn Ala Tyr Ser  
 115 120 125  
 Gly G n Asn Met Gly Asp Met Asp Pro His Ile Phe Ala Val Ala G u  
 130 135 140  
 G u Ala Tyr Lys G n Met Ala Arg Asp G u Arg Asn G n Ser Ile Ile  
 145 150 155 160  
 Val Ser Gly G u Ser Gly Ala Gly Lys Thr Val Ser Ala Lys Tyr Ala  
 165 170 175  
 Met Arg Tyr Phe Ala Thr Val Ser Gly Ser Ala Ser G u Ala Asn Val  
 180 185 190  
 G u G u Lys Val Leu Ala Ser Asn Pro Ile Met G u Ser Ile Gly Asn  
 195 200 205  
 Ala Lys Thr Thr Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Ile  
 210 215 220  
 G u Ile Gly Phe Asp Lys Arg Tyr Arg Ile Ile Gly Ala Asn Met Arg  
 225 230 235 240  
 Thr Tyr Leu Leu G u Lys Ser Arg Val Val Phe G n Ala G u G u G u  
 245 250 255  
 Arg Asn Tyr His Ile Phe Tyr G n Leu Oys Ala Ser Ala Ala Leu Pro  
 260 265 270  
 G u Phe Lys Thr Leu Arg Leu Gly Asn Ala Asn Tyr Phe His Tyr Thr  
 275 280 285  
 Lys G n Gly Gly Ser Pro Val Ile Asp Gly Ile Asp Asp Ala Lys G u  
 290 295 300  
 Met Val Asn Thr Arg G n Ala Oys Thr Leu Leu Gly Ile Ser Asp Ser  
 305 310 315 320

N3027PCT\_sequ.list.txt

Tyr Gln Met Gly Ile Phe Arg Ile Leu Ala Gly Ile Leu His Leu Gly  
 325 330 335  
 Asn Val Glu Phe Ala Ser Arg Asp Ser Asp Ser Cys Ala Ile Pro Pro  
 340 345 350  
 Lys His Asp Pro Leu Thr Ile Phe Cys Asp Leu Met Gly Val Asp Tyr  
 355 360 365  
 Glu Glu Met Ala His Trp Leu Cys His Arg Lys Leu Ala Thr Ala Thr  
 370 375 380  
 Glu Thr Tyr Ile Lys Pro Ile Ser Lys Leu His Ala Ile Asn Ala Arg  
 385 390 395 400  
 Asp Ala Leu Ala Lys His Ile Tyr Ala Asn Leu Phe Asn Trp Ile Val  
 405 410 415  
 Asp His Val Asn Lys Ala Leu His Ser Thr Val Lys Gln His Ser Phe  
 420 425 430  
 Ile Gly Val Leu Asp Ile Tyr Gly Phe Glu Thr Phe Glu Ile Asn Ser  
 435 440 445  
 Phe Glu Gln Phe Cys Ile Asn Tyr Ala Asn Glu Lys Leu Gln Gln Gln  
 450 455 460  
 Phe Asn Met His Val Phe Lys Leu Glu Gln Glu Glu Tyr Met Lys Glu  
 465 470 475 480  
 Gln Ile Pro Trp Thr Leu Ile Asp Phe Tyr Asp Asn Gln Pro Cys Ile  
 485 490 495  
 Asn Leu Ile Glu Ala Lys Met Gly Val Leu Asp Leu Leu Asp Glu Glu  
 500 505 510  
 Cys Lys Met Pro Lys Gly Ser Asp Asp Thr Trp Ala Gln Lys Leu Tyr  
 515 520 525  
 Asn Thr His Leu Asn Lys Cys Ala Leu Phe Glu Lys Pro Arg Leu Ser  
 530 535 540  
 Asn Lys Ala Phe Ile Ile Lys His Phe Ala Asp Lys Val Glu Tyr Gln  
 545 550 555 560  
 Cys Glu Gly Phe Leu Glu Lys Asn Lys Asp Thr Val Tyr Glu Glu Gln  
 565 570 575  
 Ile Lys Val Leu Lys Ser Ser Lys Lys Phe Lys Leu Leu Pro Glu Leu  
 580 585 590

N3027PCT\_sequ.list.txt

Phe Gln Asp Glu Glu Lys Ala Ile Ser Pro Thr Ser Ala Thr Pro Ser  
 595 600 605  
 Gly Arg Val Pro Leu Ser Arg Thr Pro Val Lys Pro Ala Lys Ala Arg  
 610 615 620  
 Pro Gly Gln Thr Ser Lys Glu His Lys Lys Thr Val Gly His Gln Phe  
 625 630 635 640  
 Arg Asn Ser Leu His Leu Leu Met Glu Thr Leu Asn Ala Thr Thr Pro  
 645 650 655  
 His Tyr Val Arg Cys Ile Lys Pro Asn Asp Phe Lys Phe Pro Phe Thr  
 660 665 670  
 Phe Asp Glu Lys Arg Ala Val Gln Gln Leu Arg Ala Cys Gly Val Leu  
 675 680 685  
 Glu Thr Ile Arg Ile Ser Ala Ala Gly Phe Pro Ser Arg Trp Thr Tyr  
 690 695 700  
 Gln Glu Phe Phe Ser Arg Tyr Arg Val Leu Met Lys Gln Lys Asp Val  
 705 710 715 720  
 Leu Ser Asp Arg Lys Gln Thr Cys Lys Asn Val Leu Glu Lys Leu Ile  
 725 730 735  
 Leu Asp Lys Asp Lys Tyr Gln Phe Gly Lys Thr Lys Ile Phe Phe Arg  
 740 745 750  
 Ala Gly Gln Val Ala Tyr Leu Glu Lys Ile Arg Ala Asp Lys Leu Arg  
 755 760 765  
 Ala Ala Cys Ile Arg Ile Gln Lys Thr Ile Arg Gly Trp Leu Met Arg  
 770 775 780  
 Lys Lys Tyr Met Arg Met Arg Arg Ala Ala Ile Thr Ile Gln Arg Tyr  
 785 790 795 800  
 Val Arg Gly His Gln Ala Arg Cys Tyr Ala Thr Phe Leu Arg Arg Thr  
 805 810 815  
 Arg Ala Ala Ile Ile Ile Gln Lys Phe Gln Arg Met Tyr Val Val Arg  
 820 825 830  
 Lys Arg Tyr Gln Cys Met Arg Asp Ala Thr Ile Ala Leu Gln Ala Leu  
 835 840 845  
 Leu Arg Gly Tyr Leu Val Arg Asn Lys Tyr Gln Met Met Leu Arg Glu  
 850 855 860

N3027PCT\_sequ.list.txt

His Lys Ser Ile Ile Ile Gln Lys His Val Arg Gly Trp Leu Ala Arg  
 865 870 875 880  
 Val His Tyr His Arg Thr Leu Lys Ala Ile Val Tyr Leu Gln Cys Cys  
 885 890 895  
 Tyr Arg Arg Met Met Ala Lys Arg Glu Leu Lys Lys Leu Lys Ile Glu  
 900 905 910  
 Ala Arg Ser Val Glu Arg Tyr Lys Lys Leu His Ile Gly Leu Glu Asn  
 915 920 925  
 Lys Ile Met Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys Glu Tyr  
 930 935 940  
 Lys Ser Leu Leu Glu Lys Met Asn Asn Leu Glu Ile Thr Tyr Ser Thr  
 945 950 955 960  
 Glu Thr Glu Lys Leu Arg Ser Asp Val Glu Arg Leu Arg Met Ser Glu  
 965 970 975  
 Glu Glu Ala Lys Asn Ala Thr Asn Arg Val Leu Ser Leu Gln Glu Glu  
 980 985 990  
 Ile Ala Lys Leu Arg Lys Glu Leu His Gln Thr Gln Thr Glu Lys Lys  
 995 1000 1005  
 Thr Ile Glu Glu Trp Ala Asp Lys Tyr Lys His Glu Thr Glu Gln  
 1010 1015 1020  
 Leu Val Ser Glu Leu Lys Glu Gln Asn Thr Leu Leu Lys Thr Glu  
 1025 1030 1035  
 Lys Glu Glu Leu Asn Arg Arg Ile His Asp Gln Ala Lys Glu Ile  
 1040 1045 1050  
 Thr Glu Thr Met Glu Lys Lys Leu Val Glu Glu Thr Lys Gln Leu  
 1055 1060 1065  
 Glu Leu Asp Leu Asn Asp Glu Arg Leu Arg Tyr Gln Asn Leu Leu  
 1070 1075 1080  
 Asn Glu Phe Ser Arg Leu Glu Glu Arg Tyr Asp Asp Leu Lys Asp  
 1085 1090 1095  
 Glu Met Asn Leu Met Val Ser Ile Pro Lys Pro Gly His Lys Arg  
 1100 1105 1110  
 Thr Asp Ser Thr His Ser Ser Asn Glu Ser Glu Tyr Thr Phe Ser  
 1115 1120 1125  
 Ser Glu Ile Thr Glu Ala Glu Asp Leu Pro Leu Arg Met Glu Gln

1130														
G u	Pro	Ser	G u	Lys	Lys	Al a	Pro	Leu	Asp	Met	Ser	Leu	Phe	Leu
1145						1150					1155			
Lys	Leu	G n	Lys	Arg	Val	Thr	G u	Leu	G u	G n	G u	Lys	G n	Ser
1160						1165					1170			
Leu	G n	Asp	G u	Leu	Asp	Arg	Lys	G u	G u	G n	Al a	Leu	Arg	Al a
1175						1180					1185			
Lys	Al a	Lys	G u	G u	G u	Arg	Pro	Pro	I le	Arg	G ly	Al a	G u	Leu
1190						1195					1200			
G u	Tyr	G u	Ser	Leu	Lys	Arg	G n	G u	Leu	G u	Ser	G u	Asn	Lys
1205						1210					1215			
Lys	Leu	Lys	Asn	G u	Leu	Asn	G u	Leu	G n	Lys	Al a	Leu	Thr	G u
1220						1225					1230			
Thr	Arg	Al a	Pro	G u	Val	Thr	Al a	Pro	G ly	Al a	Pro	Al a	Tyr	Arg
1235						1240					1245			
Val	Leu	Leu	Asp	G n	Leu	Thr	Ser	Val	Ser	G u	G u	Leu	G u	Val
1250						1255					1260			
Arg	Lys	G u	G u	Val	Leu	I le	Leu	Arg	Ser	G n	Leu	Val	Ser	G n
1265						1270					1275			
Lys	G u	Al a	I le	G n	Pro	Lys	G u	Asp	Lys	Asn	Thr	Met	Thr	Asp
1280						1285					1290			
Ser	Thr	I le	Leu	Leu	G u	Asp	Val	G n	Lys	Met	Lys	Asp	Lys	G ly
1295						1300					1305			
G u	I le	Al a	G n	Al a	Tyr	I le	G ly	Leu	Lys	G u	Thr	Asn	Arg	Leu
1310						1315					1320			
Leu	G u	Ser	G n	Leu	G n	Ser	G n	Lys	Lys	Ser	His	G u	Asn	G u
1325						1330					1335			
Leu	G u	Ser	Leu	Arg	G y	G u	I le	G n	Ser	Leu	Lys	G u	G u	Asn
1340						1345					1350			
Asn	Arg	G n	G n	G n	Leu	Leu	Al a	G n	Asn	Leu	G n	Leu	Pro	Pro
1355						1360					1365			
G u	Al a	Arg	I le	G u	Al a	Ser	Leu	G n	His	G u	I le	Thr	Arg	Leu
1370						1375					1380			
Thr	Asn	G u	Asn	Leu	Asp	Leu	Met	G u	G n	Leu	G u	Lys	G n	Asp
1385						1390					1395			

N3027PCT\_sequ.list.txt

Lys	Thr	Val	Arg	Lys	Leu	Lys	Lys	Gln	Leu	Lys	Val	Phe	Ala	Lys
	1400					1405					1410			
Lys	Ile	Gly	Glu	Leu	Glu	Val	Gly	Gln	Met	Glu	Asn	Ile	Ser	Pro
	1415					1420					1425			
Gly	Gln	Ile	Ile	Asp	Glu	Pro	Ile	Arg	Pro	Val	Asn	Ile	Pro	Arg
	1430					1435					1440			
Lys	Glu	Lys	Asp	Phe	Gln	Gly	Met	Leu	Glu	Tyr	Lys	Lys	Glu	Asp
	1445					1450					1455			
Glu	Gln	Lys	Leu	Val	Lys	Asn	Leu	Ile	Leu	Glu	Leu	Lys	Pro	Arg
	1460					1465					1470			
Gly	Val	Ala	Val	Asn	Leu	Ile	Pro	Gly	Leu	Pro	Ala	Tyr	Ile	Leu
	1475					1480					1485			
Phe	Met	Cys	Val	Arg	His	Ala	Asp	Tyr	Leu	Asn	Asp	Asp	Gln	Lys
	1490					1495					1500			
Val	Arg	Ser	Leu	Leu	Thr	Ser	Thr	Ile	Asn	Gly	Ile	Lys	Lys	Val
	1505					1510					1515			
Leu	Lys	Lys	Arg	Gly	Asp	Asp	Phe	Glu	Thr	Val	Ser	Phe	Trp	Leu
	1520					1525					1530			
Ser	Asn	Thr	Cys	Arg	Phe	Leu	His	Cys	Leu	Lys	Gln	Tyr	Ser	Gly
	1535					1540					1545			
Glu	Glu	Gly	Phe	Met	Lys	His	Asn	Thr	Pro	Arg	Gln	Asn	Glu	His
	1550					1555					1560			
Cys	Leu	Thr	Asn	Phe	Asp	Leu	Ala	Glu	Tyr	Arg	Gln	Val	Leu	Ser
	1565					1570					1575			
Asp	Leu	Ala	Ile	Gln	Ile	Tyr	Gln	Gln	Leu	Val	Arg	Val	Leu	Glu
	1580					1585					1590			
Asn	Ile	Leu	Gln	Pro	Met	Ile	Val	Ser	Gly	Met	Leu	Glu	His	Glu
	1595					1600					1605			
Thr	Ile	Gln	Gly	Val	Ser	Gly	Val	Lys	Pro	Thr	Gly	Leu	Arg	Lys
	1610					1615					1620			
Arg	Thr	Ser	Ser	Ile	Ala	Asp	Glu	Gly	Thr	Tyr	Thr	Leu	Asp	Ser
	1625					1630					1635			
Ile	Ile	Arg	Gln	Leu	Asn	Ser	Phe	His	Ser	Val	Met	Cys	Gln	His
	1640					1645					1650			

N3027PCT\_sequ.list.txt

Gly Met Asp Pro Glu Leu Ile Lys Gln Val Val Lys Gln Met Phe  
1655 1660 1665

Tyr Ile Ile Gly Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys  
1670 1675 1680

Asp Met Cys Ser Trp Ser Lys Gly Met Gln Ile Arg Tyr Asn Val  
1685 1690 1695

Ser Gln Leu Glu Glu Trp Leu Arg Asp Lys Asn Leu Met Asn Ser  
1700 1705 1710

Gly Ala Lys Glu Thr Leu Glu Pro Leu Ile Gln Ala Ala Gln Leu  
1715 1720 1725

Leu Gln Val Lys Lys Lys Thr Asp Glu Asp Ala Glu Ala Ile Cys  
1730 1735 1740

Ser Met Cys Asn Ala Leu Thr Thr Ala Gln Ile Val Lys Val Leu  
1745 1750 1755

Asn Leu Tyr Thr Pro Val Asn Glu Phe Glu Glu Arg Val Leu Val  
1760 1765 1770

Ser Phe Ile Arg Thr Ile Gln Leu Arg Leu Arg Asp Arg Lys Asp  
1775 1780 1785

Ser Pro Gln Leu Leu Met Asp Ala Lys His Ile Phe Pro Val Thr  
1790 1795 1800

Phe Pro Phe Asn Pro Ser Ser Leu Ala Leu Glu Thr Ile Gln Ile  
1805 1810 1815

Pro Ala Ser Leu Gly Leu Gly Phe Ile Ser Arg Val  
1820 1825 1830

<210> 7  
<211> 6401  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(6401)  
<223> myosin heavy chain 12

<400> 7  
aat acacccc gggcaggtgg agcgctcgcg gctgctcgcg gcgagcccgg gagt gat ggc 60  
gaggcccctg cgggcgccca ggcctgagg cgccccgccc cgccccgccc cgcgcgggccc 120  
tccccgccc ggcctgccct gccctgctcc ctgccggcgg ctgcgggcgc tt cct agt cc 180  
gctcgggcgg ccgcccaggc gaggtgcggc ctccgcacag gccggggggc gt aggcgcgc 240

N3027PCT\_sequ. list . . txt

ggggcccgcc	at ggct gcgt	cggagct cta	cacaaagt t t	gccagggt t t	ggat acct ga	300
t ccagaggaa	gt ct ggaagt	cagcagagct	gct caaagat	t at aagccag	gagat aaagt	360
cct cct gct t	cacct cgagg	aaggaaagga	t t t ggaat ac	cat ct agat c	caaagaccaa	420
ggagct gcct	cact t acgaa	at cct gacat	act t gt t ggt	gaaaat gacc	t cacagccct	480
cagct at ct t	cat gagcct g	ct gt gct cca	t aat ct caga	gt ccgct t t a	t t gat t ccaa	540
act t at t t at	acgt at t gt g	gt at agt cct	agt agct at a	aat ccct at g	aacagct gcc	600
t at t t at gga	gaagat at t a	t t aat gcat a	cagt ggt cag	aacat gggg t	at at ggat cc	660
acat at ct t t	gcagt agct g	aagaagct t a	caagcaaat g	gccagagat g	aacgaaat ca	720
gt ccat cat c	gt aagt ggag	agt ct ggggc	aggaaaaaca	gt ct cagct a	agt at gccat	780
gcgat act t t	gcaact gt ga	gt ggt t ct gc	cagt gaggcc	aat gt ggagg	aaaaggt ct t	840
gacct ccaac	cccat cat gg	agt ccat t gg	aaat gct aaa	acaaccagga	at gat aat ag	900
cagccgt t t t	gggaagt at a	t t gagat t gg	t t t t gat aag	agat at cgaa	t cat t ggt gc	960
caat at gaga	act t at ct t t	t agagaaat c	cagagt ggt a	t t ccaggcag	aagaggagag	1020
aaact at cat	at ct t ct at c	agct t t gt gc	ct cagcaaag	t t acct gaat	t t aaaat gct	1080
acgat t agga	aat gcagat a	act t t aat t a	cacaaaacaa	ggaggcagt c	ct gt gat t ga	1140
aggagt ggat	gat gcaaagg	agat ggcaca	t act aggag	gcct gcact t	t gct aggaat	1200
t agt gaat ct	cat caaat gg	gaat t t t ccg	aat act t gct	ggcat cct t c	act t aggcaa	1260
t gt t ggat t t	acat cccgag	at gcagacag	ct gcacaat a	cct cccaagc	at gaacct ct	1320
ct gcct ct t c	t gt gacct ca	t gggg t gga	ct at gaggag	at gt gt cact	ggct ct gcca	1380
t cgaaaact g	gct act gcca	cagagacat a	cat caagccc	at ct ccaagc	t gcaggccac	1440
gaat gcccgc	gat gct t t gg	ccaaacacat	ct at gccaaag	ct ct t t aact	ggat t gt aga	1500
t aat gt caat	caggct ct cc	at t ct gct gt	caaacagcac	t ct t t t at t g	gt gt gct aga	1560
cat t t acgga	t t t gaaacat	t t gagat aaa	t agt t t t gaa	cagt t t t gca	t aaat t at gc	1620
aaat gaaaaa	ct acagcaac	aat t caat at	gcat gt ct t c	aaat t ggagc	aagaagaat a	1680
t at gaaggaa	caaat t ccat	ggacact cat	agat t t t t at	gat aat cagc	ct t gt at t aa	1740
t ct t at agaa	t caaaaact ag	gcat t ct aga	t t t act ggat	gaggaat gca	agat gcct aa	1800
aggcacagat	gacacct ggg	cccaaaaat t	gt acaacaca	cat t t gaaca	aat gt gcact	1860
ct t t gaaaag	cct cgt ct at	caaacaaagc	t t t cat cat c	caacat t t t g	ct gacaaagt	1920
ggaat accag	t gt gaaggat	t t ct cgaaaa	gaat aaagac	accgt t t t t g	aagaacaaat	1980
t aaagt t ct t	aaat caagca	agt t t aagat	gct accagaa	ct at t t caag	at gat gagaa	2040
ggccat cagt	ccaact t cag	ccacct cct c	agggcgcaca	cccct cacac	gaact cct gc	2100
aaagcccacc	aaaggcagac	caggccaaat	ggccaaagag	cacaagaaaa	cagt ggggca	2160
t cagt t caga	aact ccct gc	acct gct t at	ggagacact c	aat gccact a	cccct cact a	2220
t gt gcgt gt	at caagcct a	at gact t caa	gct cccat t c	acgt t t gat g	agaagagggc	2280
agt gcagcag	ct gagagcat	gt ggt gt cct	ggaaaccat c	cgaat cagt g	cggccggt t t	2340

N3027PCT\_sequ. list . . txt

cccct cacgg tggactt acc aagaat t t t t cagccgct ac cgt gt cct aa t gaagcagaa	2400
agat gt gct g agt gacagaa agcaaacat g caagaat gt g t t agagaaac t gat act gga	2460
caaggacaaa t accagt t t g gt aagacaaa gat ct t t t t c cgt gccggt c aagt ggcct a	2520
t ct agaaaaa t t gagagct g acaaact gag agct gcct gc at ccgcat cc agaagacat	2580
ccgaggggt gg ct gct gagaa agaagt acct acgcat gcgg aaggcagcca t caccat gca	2640
gagat acgt g cggggct acc aggcccgat g ct at gct aag t t t ct gcgca gaaccaaggc	2700
agcaacat c at t caaaagt act ggcgcat gt at gt ggt c cgcaggaggt acaagat t ag	2760
acgagct gcc act at t gt t c t t cagt ct t a ct t gcgaggc t t ct t ggcca gaaat aggt a	2820
t cgcaagat a ct ccgt gggc acaaagcagt cat cat t cag aagcgagt cc ggggct ggct	2880
ggccccgcaca cact acaaga ggagcat gca t gccat cat c t acct t cagt gct gct t cag	2940
gcggat gat g gccaaagcgt g agct aaagaa gct caaaat c gaggct cgct cagt ggagcg	3000
ct at aagaag ct gcgcat cg gcat ggagaa caagat cat g cagct gcagc gcaaagt t ga	3060
t gagcagaac aaagact aca aat gcct t gt ggagaaact a accaat ct gg aaggaat at a	3120
caact ct gag act gagaaac t acgaagt ga ct t agaacgt ct t caact aa gt gaagagga	3180
agcgaaagt t gccact gggc ggggt cct t ag t ct gcaggag gaaat t gcca agct ccggaa	3240
agacct ggag caaact cgt t cagagaaaaa at gcat t gag gaacat gcag at cgat acaa	3300
acaagaaaca gagcagct gg t at caaat ct gaaggaagaa aat act t t gc t gaagcaaga	3360
aaaagaagcc ct caat cacc gcat cgt gca gcaggct aag gagat gacag aaact at gga	3420
gaagaagt t a gt agaagaaa cgaaacaact ggaact cgac ct t aat gat g aaaggct gag	3480
at at cagaac ct t ct gaat g agt t cagt cg cct ggaagaa agat at gat g acct caagga	3540
agagat gacc ct t at ggt gc at gt gcct aa gcct ggacac aagagaacag act ccaccca	3600
cagcagcaac gagt ct gaat at at ct t t ag ct ct gaaat t gcagaaat gg aagacat t cc	3660
at caaggaca gaggaaccaa gt gagaagaa ggt acct ct g gacat gt cat t gt t cct t aa	3720
gct ccagaag cgggt cacag agct ggagca ggagaagcag gt gat gcagg at gagct gga	3780
ccgcaaggag gagcaggt gc t ccgcagcaa ggccaaggaa gaagaaagac caaaaat t ag	3840
aggt gcagaa ct ggaat at g agt cact caa gcgt caagaa ct agaat cag aaaacaaaaa	3900
act gaagaat gagct aaat g agt t gcgcaa ggccct cagt gagaaaagt g ccccagaggt	3960
gaccgccccca ggt gcacct g cct accgt gt cct cat ggag cagct gacct ct gt gagcga	4020
ggagct t gat gt ccgcaagg aggaagt cct cat ct t aagg t ct caact gg t gagccagaa	4080
agaggccat c caacccaagg at gacaagaa t acaat gaca gat t ccacaa t act t t t gga	4140
agat gt acaa aaaat gaaag at aaagggt ga aat agcacia gcat acat t g gt t t gaaaga	4200
aacaaat aga t cat ct gct c t ggat t acca t gagt t gaat gaggat ggag agct gt ggct	4260
gggt t t at gaa ggggt t aaaac aagccaat ag gct cct ggaa t cccagct gc agt cacagaa	4320
gaggagccat gagaat gagg ccgaggccct ccgt ggggag at ccagagcc t gaaggagga	4380

N3027PCT\_sequ. list .txt

gaacaaccga	cagcagcagc	t gct ggccca	gaacct gcag	ct gccccag	aggcccgcat	4440
t gaggccagc	ct gcagcacg	agat caccgc	gct gaccaac	gaaaact t gg	at t t gat gga	4500
acaact t gaa	aaacaggat a	agacggt ccg	t aaact gaaa	aaacaact ga	aagt at t t gc	4560
caaaaaaat t	ggcgaact ag	aagt gggcca	gat ggagaac	at at ccccag	gacagat cat	4620
t gat gaaccc	at ccgaccag	t caacat t cc	caggaaagaa	aaggat t t cc	aagggat gct	4680
ggaat acaag	aaggaggat g	agcaaaaact	t gt t aagaac	ct gat t ct gg	aact gaagcc	4740
acgt ggt gt a	gcagt caat t	t gat t ccagg	at t accggca	t at at cct gt	t cat gt gt gt	4800
t cgacat gct	gact acct ga	at gat gat ca	gaaagt aagg	t cgt t gct aa	cat caacaat	4860
t aacagcat c	aaaaaagt at	t gaagaaaag	aggt gat gat	t t t gaaaccg	t ct cct t ct g	4920
gct ct ct aac	acat gccgat	t t t t gcact g	ct t gaaacag	t acagt ggag	aagagggct t	4980
t at gaagcac	aacacat ct c	gccagaat ga	acact gcct c	accaat t t t g	acct ggct ga	5040
gt at cggcag	gt gct gagt g	act t ggccat	t cagat ct ac	cagcagct cg	t gcgggt gt t	5100
agagaacat c	ct t cagccaa	t gat t gt ct c	aggcat gct g	gaacat gaaa	cgat t caggg	5160
cgt gt ct ggg	gt gaagccca	cagggt t gag	aaagcgaacc	t ccagt at cg	ccgat gaggg	5220
cacct acaca	ct ggact cca	t cct ccggca	gct caact cc	t t ccact cgg	t cat gt gt ca	5280
gcat ggcat g	gaccct gaac	t gat caagca	ggg ggt caag	cagat gt t ct	acat cat agg	5340
ggccat cacc	ct gaacaacc	t t ct cct gcg	gaaggacat g	t gct cct gga	gt aaaggcat	5400
gcagat cagg	t acaat gt ca	gt caact gga	agaat ggct g	cgt gacaaga	at ct gat gaa	5460
t agt ggggct	aaagaaaccc	t ggaacct ct	cat t caggct	gct caact t t	t gcaagt gaa	5520
aaagaaaaca	gat gat gat g	cagaagccat	t t gt t ct at g	t gcaat gct t	t aact act gc	5580
ccagat t gt g	aaagt gt t ga	at t t gt at ac	t ccagt t aat	gagt t t gaag	aaagagt ct c	5640
t gt gt cgt t c	at t cgt act a	t acagat gcg	t t t acgagac	aggaaagact	ct ccccagct	5700
gct cat ggat	gct aaacaca	t ct t t cct gt	cacct t t cct	t t caacccat	ct t ccct cgc	5760
act agaaacc	at ccagat t c	cagccagcct	cggcct gggc	t t t at t t cac	gggt ct gaaa	5820
gt gat gt cca	ggcaaaaat t	gacaat acat	t t ct t gcccg	aaat aagaac	ccat t at t t c	5880
cagt gagt t a	ct gaaaat ac	at t t t t aaag	agaaagt act	gat t at ct cc	caaat gagaa	5940
gt cat t aact	ggaaat ct cc	ct agaat act	t t cat cact t	t ggaaacaaa	gat aggct ct	6000
t t cgt gct gt	gt t at ct t t a	t agcaacact	cat cct t aac	caact aggt a	ccgt gagt t t	6060
acat acagga	gaat gat gga	aggaaggag	gaaggaaagg	aggagaaaaa	t gt gt ct t ca	6120
gct ggcagca	t t t at t t t aa	at cct t agca	ct gagt t t ga	at ggt at aaa	aagt at aact	6180
t ccat agat g	agct gt t gt t	aggaaggcac	caaagaacct	cct ct gcact	aaacaggaga	6240
at ggaaagaa	aagt ct ccat	t gagt acat a	t cat gt cagt	t t agt aat ca	at t at gt t ga	6300
t at t gt t aaa	ct ggt t caaa	gaaat aaact	ggcaat at gt	aaagt aat t c	ct cat t t gt g	6360
t cact at gat	at agagat at	t aaaggaat g	t t ggt t t gct	a		6401

N3027PCT\_sequ.list.txt

<210> 8  
 <211> 1855  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1855)  
 <223> myosin heavy chain 12

<400> 8

Met Ala Ala Ser Glu Leu Tyr Thr Lys Phe Ala Arg Val Trp Ile Pro  
 1 5 10 15

Asp Pro Glu Glu Val Trp Lys Ser Ala Glu Leu Leu Lys Asp Tyr Lys  
 20 25 30

Pro Gly Asp Lys Val Leu Leu Leu His Leu Glu Glu Gly Lys Asp Leu  
 35 40 45

Glu Tyr His Leu Asp Pro Lys Thr Lys Glu Leu Pro His Leu Arg Asn  
 50 55 60

Pro Asp Ile Leu Val Gly Glu Asn Asp Leu Thr Ala Leu Ser Tyr Leu  
 65 70 75 80

His Glu Pro Ala Val Leu His Asn Leu Arg Val Arg Phe Ile Asp Ser  
 85 90 95

Lys Leu Ile Tyr Thr Tyr Cys Gly Ile Val Leu Val Ala Ile Asn Pro  
 100 105 110

Tyr Glu Gln Leu Pro Ile Tyr Gly Glu Asp Ile Ile Asn Ala Tyr Ser  
 115 120 125

Gly Gln Asn Met Gly Asp Met Asp Pro His Ile Phe Ala Val Ala Glu  
 130 135 140

Glu Ala Tyr Lys Gln Met Ala Arg Asp Glu Arg Asn Gln Ser Ile Ile  
 145 150 155 160

Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Val Ser Ala Lys Tyr Ala  
 165 170 175

Met Arg Tyr Phe Ala Thr Val Ser Gly Ser Ala Ser Glu Ala Asn Val  
 180 185 190

Glu Glu Lys Val Leu Thr Ser Asn Pro Ile Met Glu Ser Ile Gly Asn  
 195 200 205

Ala Lys Thr Thr Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Ile  
 210 215 220

G u I l e G y P h e A s p L y s A r g T y r A r g I l e I l e G y A l a A s n M e t A r g  
 225 230 235 240  
 T h r T y r L e u L e u G u L y s S e r A r g V a l V a l P h e G n A l a G u G u G u  
 245 250 255  
 A r g A s n T y r H i s I l e P h e T y r G n L e u O y s A l a S e r A l a L y s L e u P r o  
 260 265 270  
 G u P h e L y s M e t L e u A r g L e u G y A s n A l a A s p A s n P h e A s n T y r T h r  
 275 280 285  
 L y s G n G y G y S e r P r o V a l I l e G u G y V a l A s p A s p A l a L y s G u  
 290 295 300  
 M e t A l a H i s T h r A r g G n A l a O y s T h r L e u L e u G y I l e S e r G u S e r  
 305 310 315 320  
 H i s G n M e t G y I l e P h e A r g I l e L e u A l a G y I l e L e u H i s L e u G y  
 325 330 335  
 A s n V a l G y P h e T h r S e r A r g A s p A l a A s p S e r O y s T h r I l e P r o P r o  
 340 345 350  
 L y s H i s G u P r o L e u O y s I l e P h e O y s A s p L e u M e t G y V a l A s p T y r  
 355 360 365  
 G u G u M e t O y s H i s T r p L e u O y s H i s A r g L y s L e u A l a T h r A l a T h r  
 370 375 380  
 G u T h r T y r I l e L y s P r o I l e S e r L y s L e u G n A l a T h r A s n A l a A r g  
 385 390 395 400  
 A s p A l a L e u A l a L y s H i s I l e T y r A l a L y s L e u P h e A s n T r p I l e V a l  
 405 410 415  
 A s p A s n V a l A s n G n A l a L e u H i s S e r A l a V a l L y s G n H i s S e r P h e  
 420 425 430  
 I l e G y V a l L e u A s p I l e T y r G y P h e G u T h r P h e G u I l e A s n S e r  
 435 440 445  
 P h e G u G n P h e O y s I l e A s n T y r A l a A s n G u L y s L e u G n G n G n  
 450 455 460  
 P h e A s n M e t H i s V a l P h e L y s L e u G u G n G u G u T y r M e t L y s G u  
 465 470 475 480  
 G n I l e P r o T r p T h r L e u I l e A s p P h e T y r A s p A s n G n P r o O y s I l e  
 485 490 495  
 A s n L e u I l e G u S e r L y s L e u G y I l e L e u A s p L e u L e u A s p G u G u

500

505

510

Cys Lys Met Pro Lys Gly Thr Asp Asp Thr Trp Ala Gln Lys Leu Tyr  
 515 520 525  
 Asn Thr His Leu Asn Lys Cys Ala Leu Phe Glu Lys Pro Arg Leu Ser  
 530 535 540  
 Asn Lys Ala Phe Ile Ile Gln His Phe Ala Asp Lys Val Glu Tyr Gln  
 545 550 555 560  
 Cys Glu Gly Phe Leu Glu Lys Asn Lys Asp Thr Val Phe Glu Glu Gln  
 565 570 575  
 Ile Lys Val Leu Lys Ser Ser Lys Phe Lys Met Leu Pro Glu Leu Phe  
 580 585 590  
 Gln Asp Asp Glu Lys Ala Ile Ser Pro Thr Ser Ala Thr Ser Ser Gly  
 595 600 605  
 Arg Thr Pro Leu Thr Arg Thr Pro Ala Lys Pro Thr Lys Gly Arg Pro  
 610 615 620  
 Gly Gln Met Ala Lys Glu His Lys Lys Thr Val Gly His Gln Phe Arg  
 625 630 635 640  
 Asn Ser Leu His Leu Leu Met Glu Thr Leu Asn Ala Thr Thr Pro His  
 645 650 655  
 Tyr Val Arg Cys Ile Lys Pro Asn Asp Phe Lys Leu Pro Phe Thr Phe  
 660 665 670  
 Asp Glu Lys Arg Ala Val Gln Gln Leu Arg Ala Cys Gly Val Leu Glu  
 675 680 685  
 Thr Ile Arg Ile Ser Ala Ala Gly Phe Pro Ser Arg Trp Thr Tyr Gln  
 690 695 700  
 Glu Phe Phe Ser Arg Tyr Arg Val Leu Met Lys Gln Lys Asp Val Leu  
 705 710 715 720  
 Ser Asp Arg Lys Gln Thr Cys Lys Asn Val Leu Glu Lys Leu Ile Leu  
 725 730 735  
 Asp Lys Asp Lys Tyr Gln Phe Gly Lys Thr Lys Ile Phe Phe Arg Ala  
 740 745 750  
 Gly Gln Val Ala Tyr Leu Glu Lys Leu Arg Ala Asp Lys Leu Arg Ala  
 755 760 765  
 Ala Cys Ile Arg Ile Gln Lys Thr Ile Arg Gly Trp Leu Leu Arg Lys  
 770 775 780

N3027PCT\_sequ.list.txt

Lys Tyr Leu Arg Met Arg Lys Ala Ala Ile Thr Met Gln Arg Tyr Val  
 785 790 795 800  
 Arg Gly Tyr Gln Ala Arg Cys Tyr Ala Lys Phe Leu Arg Arg Thr Lys  
 805 810 815  
 Ala Ala Thr Ile Ile Gln Lys Tyr Trp Arg Met Tyr Val Val Arg Arg  
 820 825 830  
 Arg Tyr Lys Ile Arg Arg Ala Ala Thr Ile Val Leu Gln Ser Tyr Leu  
 835 840 845  
 Arg Gly Phe Leu Ala Arg Asn Arg Tyr Arg Lys Ile Leu Arg Gly His  
 850 855 860  
 Lys Ala Val Ile Ile Gln Lys Arg Val Arg Gly Trp Leu Ala Arg Thr  
 865 870 875 880  
 His Tyr Lys Arg Ser Met His Ala Ile Ile Tyr Leu Gln Cys Cys Phe  
 885 890 895  
 Arg Arg Met Met Ala Lys Arg Glu Leu Lys Lys Leu Lys Ile Glu Ala  
 900 905 910  
 Arg Ser Val Glu Arg Tyr Lys Lys Leu Arg Ile Gly Met Glu Asn Lys  
 915 920 925  
 Ile Met Gln Leu Gln Arg Lys Val Asp Glu Gln Asn Lys Asp Tyr Lys  
 930 935 940  
 Cys Leu Val Glu Lys Leu Thr Asn Leu Glu Gly Ile Tyr Asn Ser Glu  
 945 950 955 960  
 Thr Glu Lys Leu Arg Ser Asp Leu Glu Arg Leu Gln Leu Ser Glu Glu  
 965 970 975  
 Glu Ala Lys Val Ala Thr Gly Arg Val Leu Ser Leu Gln Glu Glu Ile  
 980 985 990  
 Ala Lys Leu Arg Lys Asp Leu Glu Gln Thr Arg Ser Glu Lys Lys Cys  
 995 1000 1005  
 Ile Glu Glu His Ala Asp Arg Tyr Lys Gln Glu Thr Glu Gln Leu  
 1010 1015 1020  
 Val Ser Asn Leu Lys Glu Glu Asn Thr Leu Leu Lys Gln Glu Lys  
 1025 1030 1035  
 Glu Ala Leu Asn His Arg Ile Val Gln Gln Ala Lys Glu Met Thr  
 1040 1045 1050

N3027PCT\_sequ.list.txt

Glu	Thr 1055	Met	Glu	Lys	Lys	Leu 1060	Val	Glu	Glu	Thr	Lys 1065	Gln	Leu	Glu
Leu	Asp 1070	Leu	Asn	Asp	Glu	Arg 1075	Leu	Arg	Tyr	Gln	Asn 1080	Leu	Leu	Asn
Glu	Phe 1085	Ser	Arg	Leu	Glu	Glu 1090	Arg	Tyr	Asp	Asp	Leu 1095	Lys	Glu	Glu
Met	Thr 1100	Leu	Met	Val	His	Val 1105	Pro	Lys	Pro	Gly	His 1110	Lys	Arg	Thr
Asp	Ser 1115	Thr	His	Ser	Ser	Asn 1120	Glu	Ser	Glu	Tyr	Ile 1125	Phe	Ser	Ser
Glu	Ile 1130	Ala	Glu	Met	Glu	Asp 1135	Ile	Pro	Ser	Arg	Thr 1140	Glu	Glu	Pro
Ser	Glu 1145	Lys	Lys	Val	Pro	Leu 1150	Asp	Met	Ser	Leu	Phe 1155	Leu	Lys	Leu
Gln	Lys 1160	Arg	Val	Thr	Glu	Leu 1165	Glu	Gln	Glu	Lys	Gln 1170	Val	Met	Gln
Asp	Glu 1175	Leu	Asp	Arg	Lys	Glu 1180	Glu	Gln	Val	Leu	Arg 1185	Ser	Lys	Ala
Lys	Glu 1190	Glu	Glu	Arg	Pro	Gln 1195	Ile	Arg	Gly	Ala	Glu 1200	Leu	Glu	Tyr
Glu	Ser 1205	Leu	Lys	Arg	Gln	Glu 1210	Leu	Glu	Ser	Glu	Asn 1215	Lys	Lys	Leu
Lys	Asn 1220	Glu	Leu	Asn	Glu	Leu 1225	Arg	Lys	Ala	Leu	Ser 1230	Glu	Lys	Ser
Ala	Pro 1235	Glu	Val	Thr	Ala	Pro 1240	Gly	Ala	Pro	Ala	Tyr 1245	Arg	Val	Leu
Met	Glu 1250	Gln	Leu	Thr	Ser	Val 1255	Ser	Glu	Glu	Leu	Asp 1260	Val	Arg	Lys
Glu	Glu 1265	Val	Leu	Ile	Leu	Arg 1270	Ser	Gln	Leu	Val	Ser 1275	Gln	Lys	Glu
Ala	Ile 1280	Gln	Pro	Lys	Asp	Asp 1285	Lys	Asn	Thr	Met	Thr 1290	Asp	Ser	Thr
Ile	Leu 1295	Leu	Glu	Asp	Val	Gln 1300	Lys	Met	Lys	Asp	Lys 1305	Gly	Glu	Ile

Ala Gln 1310 Ala Tyr Ile Gly Leu 1315 Lys Glu Thr Asn Arg 1320 Ser Ser Ala  
 Leu Asp 1325 Tyr His Glu Leu Asn 1330 Glu Asp Gly Glu Leu 1335 Trp Leu Val  
 Tyr Glu 1340 Gly Leu Lys Gln Ala 1345 Asn Arg Leu Leu Glu 1350 Ser Gln Leu  
 Gln Ser 1355 Gln Lys Arg Ser His 1360 Glu Asn Glu Ala Glu 1365 Ala Leu Arg  
 Gly Glu 1370 Ile Gln Ser Leu Lys 1375 Glu Glu Asn Asn Arg 1380 Gln Gln Gln  
 Leu Leu 1385 Ala Gln Asn Leu Gln 1390 Leu Pro Pro Glu Ala 1395 Arg Ile Glu  
 Ala Ser 1400 Leu Gln His Glu Ile 1405 Thr Arg Leu Thr Asn 1410 Glu Asn Leu  
 Asp Leu 1415 Met Glu Gln Leu Glu 1420 Lys Gln Asp Lys Thr 1425 Val Arg Lys  
 Leu Lys 1430 Lys Gln Leu Lys Val 1435 Phe Ala Lys Lys Ile 1440 Gly Glu Leu  
 Glu Val 1445 Gly Gln Met Glu Asn 1450 Ile Ser Pro Gly Gln 1455 Ile Ile Asp  
 Glu Pro 1460 Ile Arg Pro Val Asn 1465 Ile Pro Arg Lys Glu 1470 Lys Asp Phe  
 Gln Gly 1475 Met Leu Glu Tyr Lys 1480 Lys Glu Asp Glu Gln 1485 Lys Leu Val  
 Lys Asn 1490 Leu Ile Leu Glu Leu 1495 Lys Pro Arg Gly Val 1500 Ala Val Asn  
 Leu Ile 1505 Pro Gly Leu Pro Ala 1510 Tyr Ile Leu Phe Met 1515 Cys Val Arg  
 His Ala 1520 Asp Tyr Leu Asn Asp 1525 Asp Gln Lys Val Arg 1530 Ser Leu Leu  
 Thr Ser 1535 Thr Ile Asn Ser Ile 1540 Lys Lys Val Leu Lys 1545 Lys Arg Gly  
 Asp Asp 1550 Phe Glu Thr Val Ser 1555 Phe Trp Leu Ser Asn 1560 Thr Cys Arg  
 Phe Leu His Cys Leu Lys Gln Tyr Ser Gly Glu Glu Gly Phe Met



N3027PCT\_sequ.list.txt

Ser Ser Leu Ala Leu Glu Thr Ile Glu Ile Pro Ala Ser Leu Gly  
1835 1840 1845

Leu Gly Phe Ile Ser Arg Val  
1850 1855

<210> 9  
<211> 3549  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_ feature  
<222> (1)..(3549)  
<223> brush border myosi n I (BBM)

<400> 9  
t cagggagcc t gggct ggaa gaggcagcaa aagggaaaat cagaagagt g gacact ggca 60  
agaggagggc agcctttttc ccagcttcct tgcaccat gg acagct ccca ttaagccacc 120  
tctccatcct ggggccagga ctcttatgcc ccat t cctgt caaat t gaga tttcatccac 180  
cat t ctccaa ggacagt gaa tttat accct agt t ccagt g t t gggat cag t ggcccct ct 240  
ggacat gcct ct cct ggaag gt t ct gt ggg ggt ggaggat ct t gt cct cc t ggaaccct t 300  
gggaggagg t cact gct ca agaat ct t ca gct t cgct at gaaaacaagg agat t t at ac 360  
ct acat t ggg aat gt ggt ga t ct cagt gaa t ccct at caa cagct t ccca t ct at gggcc 420  
agagt t cat t gccaaat at c aagact at ac tttct at gag ct gaagcccc at at ct acgc 480  
at t ggcaaat gt ggcgt acc agt cact gag ggacagggac cgagaccagt gt at cct cat 540  
cacaggcgag agt ggat cag ggaagact ga ggccagcaag ct ggt gat gt ct t at gt ggc 600  
t gccgt ct gt gggaaaggag agcaggt gaa ct ct gt gaag gagcagct gc t acagt ct aa 660  
cccagt gct g gaggc t t t g gcaat gccaa gaccat t cgc aacaacaat t cct cccgat t 720  
t ggaaaat ac at ggat at t g aat t t gact t caagggat cc cccct cggg g gt gt cat cac 780  
aaact at ct g ct t gagaaat cccgat t agt gaagcagct c aaaggagaaa ggaact t cca 840  
cat ct t ct at cagct gct gg ct ggagcaga t gaacagct g ct gaaggccc t gaagct t ga 900  
gcgggat aca act ggct at g cct at ct gaa t cat gaagt a t ccagagt gg at ggcat gga 960  
cgacgcct cc agct t caggg ct gt acagag t gcaat ggca gt gat t gggg t ct cggagga 1020  
ggagat t cga caagt gct ag aggt gacat c cat ggt gct a aagct gggga acgt gt t ggt 1080  
ggct gat gag t t ccaggcca gt gggat acc agcaagt ggc at ccgt gat g ggagaggt gt 1140  
t cgggagat t ggggagat gg t gggct t gaa t t cagaagaa gt agagagag ct t t gt gct c 1200  
gaggaccat g gaaacagcca aggaaaaggt ggt cact gca ct gaat gt t a t gcaggct ca 1260  
gt at gct cgg gacgccct gg ct aagaacat ct acagccgc ct ct t t gact ggat agt gaa 1320  
t cgaat caat gagagcat ca aggt gggcat cggggaaaag aagaaggt aa t gggagt cct 1380  
t gat at ct ac ggt t t t gaga t at t agagga t aat agct t t gagcaat t t g t gat caact a 1440

N3027PCT\_sequ. list . . txt

ct gcaat gag	aagct gcagc	aggt gt t cat	agagat gacc	ct gaaagaag	agcaagagga	1500
at at aagaga	gaaggcat ac	cgt ggacaaa	ggg ggact ac	t t t gat aat g	gc at cat t t g	1560
t aagct cat t	gagcat aat c	agcgaggt at	cct ggccat g	t t ggat gagg	agt gcct gcg	1620
gcct ggggt g	gt cagt gact	ccact t t cct	agcaaagct g	aaccagct ct	t ct ccaagca	1680
t ggccact ac	gagagcaaag	t caccagaa	t gccagcgt	cagt at gacc	acacat ggg	1740
cct cagct gc	t t ccgcat ct	gccact at gc	gggcaaggt g	acat acaacg	t gaccagct t	1800
t at t gacaag	aat aat gacc	t act ct t ccg	agacct gt t g	caggccat gt	ggaaggccca	1860
gcacccct c	ct t cggcct	t gt t t cct ga	gggcaat cct	aagcaggcat	ct ct caaacg	1920
ccccccgact	gct gggggcc	agt t caagag	t t ct gt ggcc	at cct cat ga	agaat ct gt a	1980
t t ccaagagc	cccaact aca	t caggt gcat	aaagcccaat	gagcat cagc	agcgaggt ca	2040
gt t ct ct t ca	gacct ggt gg	caaccaggc	t cggc acct g	ggact gct gg	agaacgt acg	2100
ggg gcgacgg	gcaggct at g	cccaccgcca	gggt t at ggg	ccct t cct gg	aaaggt accg	2160
at t gct gagc	cggagcacct	ggcct cact g	gaat ggggga	gaccgggaag	gt gt t gagaa	2220
ggg cct gggg	gagct gagca	t gt cct cggg	ggagct ggcc	t t t ggcaaga	caaagat ct t	2280
cat t agaagc	ccaagact c	t t t t ct acct	cgaagaacag	aggcgct ga	gact ccagca	2340
gct ggccaca	ct cat acaga	agat t t accg	aggct ggcgc	t gccgcacc	act accaact	2400
gat gcgaaag	agt cagat cc	t cat ct cct c	t t ggt t t cgg	ggaaacat gc	aaaagaaat g	2460
ct at gggaag	at aaaggcat	ccgt gt t at t	gat ccaggct	t t t gt gagag	ggg ggaaggc	2520
ccgaaagaat	t at cgcaaat	at t t ccggt c	agaggct gcc	ct cacct t gg	cagat t t cat	2580
ct acaagagc	at ggt acaga	aat t cct act	ggggct gaag	aacaat t t gc	cat ccacaaa	2640
cgt ct t agac	aagacat ggc	cagccgcccc	ct acaagt gc	ct cagcacag	caaat cagga	2700
gct gcagcag	ct ct t ct acc	agt ggaagt g	caagaggt t c	cgggat cagc	t gt ccccgaa	2760
gcaggat agag	at cct gaggg	aaaagct ct g	t gccagt gaa	ct gt t caagg	gcaagaaggc	2820
t t cat at ccc	cagagt gt cc	ccat t ccat t	ct gt ggt gac	t acat t gggc	t gcaagggaa	2880
ccccaaagct g	cagaagct ga	aaggcgggga	ggaggggcct	gt t ct gat gg	cagaggccgt	2940
gaagaagggt c	aat cgt ggca	at ggcaagac	t t ct t ct cgg	at t ct cct cc	t gaccaaggg	3000
ccat gt gat t	ct cacagaca	ccaagaagt c	ccaggccaaa	at t gt cat t g	ggct agacaa	3060
t gt ggct ggg	gt gt cagt ca	ccagcct caa	ggat gggct c	t t t agct t gc	at ct gagt ga	3120
gat gt cat cg	gt gggct cca	agggggact t	cct gct ggt c	agcgagcat g	t gat t gaact	3180
gct gaccaa	at gt accggg	ct gt gct gga	t gccacgcag	aggcagct t a	cagt caccgt	3240
gact gagaag	t t ct cagt ga	ggg t caagga	gaacagt gt g	gct gt caagg	t cgt ccaggg	3300
ccct gcagggt	ggg gacaaca	gcaagct acg	ct acaaaaaa	aaggggaggt c	at t gct t gga	3360
ggg gact gt g	cagt gaggag	ggggcaccat	gcagagat gg	cagt t gct t c	ct cct gaacc	3420
agcact aat c	cccct ct gcc	ct cct gt gt g	ggaggat ct c	t aaccct ct	gat cgt ggcg	3480

N3027PCT\_sequ.list.txt

catggccttg gggattaaac tacccttgaa gaggaaaaaa aaaaaaaaaa aaaaaaaaaa 3540

aaaaaaaaa 3549

<210> 10  
<211> 1043  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1043)  
<223> brush border myosin I (BBM)

<400> 10

Met Pro Leu Leu Glu Gly Ser Val Gly Val Glu Asp Leu Val Leu Leu  
1 5 10 15

Glu Pro Leu Val Glu Glu Ser Leu Leu Lys Asn Leu Gln Leu Arg Tyr  
20 25 30

Glu Asn Lys Glu Ile Tyr Thr Tyr Ile Gly Asn Val Val Ile Ser Val  
35 40 45

Asn Pro Tyr Gln Gln Leu Pro Ile Tyr Gly Pro Glu Phe Ile Ala Lys  
50 55 60

Tyr Gln Asp Tyr Thr Phe Tyr Glu Leu Lys Pro His Ile Tyr Ala Leu  
65 70 75 80

Ala Asn Val Ala Tyr Gln Ser Leu Arg Asp Arg Asp Arg Asp Gln Cys  
85 90 95

Ile Leu Ile Thr Gly Glu Ser Gly Ser Gly Lys Thr Glu Ala Ser Lys  
100 105 110

Leu Val Met Ser Tyr Val Ala Ala Val Cys Gly Lys Gly Glu Gln Val  
115 120 125

Asn Ser Val Lys Glu Gln Leu Leu Gln Ser Asn Pro Val Leu Glu Ala  
130 135 140

Phe Gly Asn Ala Lys Thr Ile Arg Asn Asn Asn Ser Ser Arg Phe Gly  
145 150 155 160

Lys Tyr Met Asp Ile Glu Phe Asp Phe Lys Gly Ser Pro Leu Gly Gly  
165 170 175

Val Ile Thr Asn Tyr Leu Leu Glu Lys Ser Arg Leu Val Lys Gln Leu  
180 185 190

Lys Gly Glu Arg Asn Phe His Ile Phe Tyr Gln Leu Leu Ala Gly Ala  
195 200 205

N3027PCT\_sequ.list.txt

Asp Glu Gln Leu Leu Lys Ala Leu Lys Leu Glu Arg Asp Thr Thr Gly  
 210 215 220  
 Tyr Ala Tyr Leu Asn His Glu Val Ser Arg Val Asp Gly Met Asp Asp  
 225 230 235 240  
 Ala Ser Ser Phe Arg Ala Val Gln Ser Ala Met Ala Val Ile Gly Phe  
 245 250 255  
 Ser Glu Glu Glu Ile Arg Gln Val Leu Glu Val Thr Ser Met Val Leu  
 260 265 270  
 Lys Leu Gly Asn Val Leu Val Ala Asp Glu Phe Gln Ala Ser Gly Ile  
 275 280 285  
 Pro Ala Ser Gly Ile Arg Asp Gly Arg Gly Val Arg Glu Ile Gly Glu  
 290 295 300  
 Met Val Gly Leu Asn Ser Glu Glu Val Glu Arg Ala Leu Cys Ser Arg  
 305 310 315 320  
 Thr Met Glu Thr Ala Lys Glu Lys Val Val Thr Ala Leu Asn Val Met  
 325 330 335  
 Gln Ala Gln Tyr Ala Arg Asp Ala Leu Ala Lys Asn Ile Tyr Ser Arg  
 340 345 350  
 Leu Phe Asp Trp Ile Val Asn Arg Ile Asn Glu Ser Ile Lys Val Gly  
 355 360 365  
 Ile Gly Glu Lys Lys Lys Val Met Gly Val Leu Asp Ile Tyr Gly Phe  
 370 375 380  
 Glu Ile Leu Glu Asp Asn Ser Phe Glu Gln Phe Val Ile Asn Tyr Cys  
 385 390 395 400  
 Asn Glu Lys Leu Gln Gln Val Phe Ile Glu Met Thr Leu Lys Glu Glu  
 405 410 415  
 Gln Glu Glu Tyr Lys Arg Glu Gly Ile Pro Trp Thr Lys Val Asp Tyr  
 420 425 430  
 Phe Asp Asn Gly Ile Ile Cys Lys Leu Ile Glu His Asn Gln Arg Gly  
 435 440 445  
 Ile Leu Ala Met Leu Asp Glu Glu Cys Leu Arg Pro Gly Val Val Ser  
 450 455 460  
 Asp Ser Thr Phe Leu Ala Lys Leu Asn Gln Leu Phe Ser Lys His Gly  
 465 470 475 480

His Tyr Glu Ser Lys Val Thr Gln Asn Ala Gln Arg Gln Tyr Asp His  
 485 490 495  
 Thr Met Gly Leu Ser Cys Phe Arg Ile Cys His Tyr Ala Gly Lys Val  
 500 505 510  
 Thr Tyr Asn Val Thr Ser Phe Ile Asp Lys Asn Asn Asp Leu Leu Phe  
 515 520 525  
 Arg Asp Leu Leu Gln Ala Met Trp Lys Ala Gln His Pro Leu Leu Arg  
 530 535 540  
 Ser Leu Phe Pro Glu Gly Asn Pro Lys Gln Ala Ser Leu Lys Arg Pro  
 545 550 555 560  
 Pro Thr Ala Gly Ala Gln Phe Lys Ser Ser Val Ala Ile Leu Met Lys  
 565 570 575  
 Asn Leu Tyr Ser Lys Ser Pro Asn Tyr Ile Arg Cys Ile Lys Pro Asn  
 580 585 590  
 Glu His Gln Gln Arg Gly Gln Phe Ser Ser Asp Leu Val Ala Thr Gln  
 595 600 605  
 Ala Arg Tyr Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly  
 610 615 620  
 Tyr Ala His Arg Gln Gly Tyr Gly Pro Phe Leu Glu Arg Tyr Arg Leu  
 625 630 635 640  
 Leu Ser Arg Ser Thr Trp Pro His Trp Asn Gly Gly Asp Arg Glu Gly  
 645 650 655  
 Val Glu Lys Val Leu Gly Glu Leu Ser Met Ser Ser Gly Glu Leu Ala  
 660 665 670  
 Phe Gly Lys Thr Lys Ile Phe Ile Arg Ser Pro Lys Thr Leu Phe Tyr  
 675 680 685  
 Leu Glu Glu Gln Arg Arg Leu Arg Leu Gln Gln Leu Ala Thr Leu Ile  
 690 695 700  
 Gln Lys Ile Tyr Arg Gly Trp Arg Cys Arg Thr His Tyr Gln Leu Met  
 705 710 715 720  
 Arg Lys Ser Gln Ile Leu Ile Ser Ser Trp Phe Arg Gly Asn Met Gln  
 725 730 735  
 Lys Lys Cys Tyr Gly Lys Ile Lys Ala Ser Val Leu Leu Ile Gln Ala  
 740 745 750  
 Phe Val Arg Gly Trp Lys Ala Arg Lys Asn Tyr Arg Lys Tyr Phe Arg

755

Ser Glu Ala Ala Leu Thr Leu Ala Asp Phe Ile Tyr Lys Ser Met Val  
770 775 780

Gln Lys Phe Leu Leu Gly Leu Lys Asn Asn Leu Pro Ser Thr Asn Val  
785 790 795 800

Leu Asp Lys Thr Trp Pro Ala Ala Pro Tyr Lys Cys Leu Ser Thr Ala  
805 810 815

Asn Gln Glu Leu Gln Gln Leu Phe Tyr Gln Trp Lys Cys Lys Arg Phe  
820 825 830

Arg Asp Gln Leu Ser Pro Lys Gln Val Glu Ile Leu Arg Glu Lys Leu  
835 840 845

Cys Ala Ser Glu Leu Phe Lys Gly Lys Lys Ala Ser Tyr Pro Gln Ser  
850 855 860

Val Pro Ile Pro Phe Cys Gly Asp Tyr Ile Gly Leu Gln Gly Asn Pro  
865 870 875 880

Lys Leu Gln Lys Leu Lys Gly Gly Glu Glu Gly Pro Val Leu Met Ala  
885 890 895

Glu Ala Val Lys Lys Val Asn Arg Gly Asn Gly Lys Thr Ser Ser Arg  
900 905 910

Ile Leu Leu Leu Thr Lys Gly His Val Ile Leu Thr Asp Thr Lys Lys  
915 920 925

Ser Gln Ala Lys Ile Val Ile Gly Leu Asp Asn Val Ala Gly Val Ser  
930 935 940

Val Thr Ser Leu Lys Asp Gly Leu Phe Ser Leu His Leu Ser Glu Met  
945 950 955 960

Ser Ser Val Gly Ser Lys Gly Asp Phe Leu Leu Val Ser Glu His Val  
965 970 975

Ile Glu Leu Leu Thr Lys Met Tyr Arg Ala Val Leu Asp Ala Thr Gln  
980 985 990

Arg Gln Leu Thr Val Thr Val Thr Glu Lys Phe Ser Val Arg Phe Lys  
995 1000 1005

Glu Asn Ser Val Ala Val Lys Val Val Gln Gly Pro Ala Gly Gly  
1010 1015 1020

Asp Asn Ser Lys Leu Arg Tyr Lys Lys Lys Gly Ser His Cys Leu  
1025 1030 1035

N3027PCT\_sequ. list . . txt

G u Val Thr Val G n  
1040

<210> 11  
<211> 6786  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc \_f eat ur e  
<222> (1) . . (6786)  
<223> myosi n heavy chai n (MYH14)

<400> 11  
ct ct t t ct cc ccaggccgaa gcct cgggac ggccct ggaa gccgaccat g gcagccgt ga 60  
ccat gt cggg gcccggggcgg aaggcgcccc ccaggccggg cccagt gccg gaggcggccc 120  
agccgt t cct gt t cacgccc cgcgggccca gcgcgggt gg cgggcct ggc t cgggcacct 180  
ccccgcagggt ggagt ggacg gcccggcgt c t cgt gt gggg gcct t cggag ct t cacgggt 240  
t cgaggcggc ggcgct gcgg gacgaaggcg aggaggaggc ggaggt ggag ct ggcggaga 300  
gcgggaggcg gct gcgact g ccgcgggacc agat ccagcg cat gaaccg cccaagt t ca 360  
gcaaggccga ggacat ggcc gagct gacct gcct caacga ggcct cggg c ct gcacaacc 420  
t ccgggagcg gt act act cc ggcct cat ct acacgt act c cggcct t t t c t gt gt ggt ca 480  
t caaccgta caagcagct t cccat ct aca cagaagccat t gt ggagat g t accggggca 540  
agaagcgcca cgagggt gcc a cccacgt gt acgcagt gac cgagggggcc t at cggagca 600  
t gct gcagga t cgt gaggac cagt ccat t c t ct gcact gg agagt ct gga gct gggaaga 660  
cggaaaacac caagaagg t c at ccagt acc t cgccacgt ggcat cgt ct ccaaagggca 720  
ggaaggagcc ggggt gt cccc ggt gagct gg agcggcagct gct t caggcc aaccccat cc 780  
t agaggcct t t ggcaat gcc aagacagt ga agaat gacaa ct cct cccga t t cggcaaat 840  
t cat ccgcat caact t t gat gt t gccgggt acat cgt ggg cgccaacat t gagacct acc 900  
t gct ggagaa gt cgcgggcc at ccgccagg ccaaggacga gt gcagct t c cacat ct t ct 960  
accagct gct ggggggcgt ggagagcagc t caaagccga cct cct cct c gagccct gct 1020  
cccact accg gt t cct gacc aacggggcgt cat cct ct cc cggccaggag cgggaact ct 1080  
t ccaggagac gct ggagt cg ct gcgggt cc t gggat t cag ccacgaggaa at cat ct cca 1140  
t gct gcggat ggt ct cagca gt t ct ccagt t t ggcaacat t gcct t gaag agagaacgga 1200  
acaccgat ca agccacat g cct gacaaca cagct gcaca gaagct ct gc cgcct ct t gg 1260  
gact ggggggt gacggat t t c t cccgagcct t gct caccct t cgcacaaa gt t ggccgag 1320  
act at gt gca gaaagcccag act aaggaac aggct gact t cgcgct ggag gccct ggcca 1380  
aggccacct a cgagcgcct c t t ccgct ggc t ggt t ct gcg cct caaccgg gcct t ggacc 1440  
gcagcccccg ccaaggcgcc t cct t cct gg gcat cct gga cat cgcgggc t t t gagat ct 1500  
t ccagct gaa ct cct t cgag cagct ct gca t caact acac caacgagaag ct gcagcagc 1560

N3027PCT\_sequ. list . . txt

t c t t c a a c c a	c a c c a t g t t c	g t g c t g g a g c	a g g a g g a g t a	c c a g c g t g a g	g g c a t c c c c t	1620
g g a c c t t c c t	c g a c t t t g g c	c t c g a c c t g c	a g c c c t g c a t	c g a c c t c a t c	g a g c g g c c g g	1680
c c a a c c c c c c	t g g a c t c c t g	g c c c t g c t g g	a t g a g g a g t g	c t g g t t c c c g	a a g g c c a c a g	1740
a c a a g t c g t t	t g t g g a g a a g	g t a g c c c a g g	a g c a g g g c g g	c c a c c c c a a g	t t c c a g c g g c	1800
c g a g g c a c c t	g c g g g a t c a g	g c c g a c t t c a	g t g t t c t c c a	c t a c g c g g g c	a a g g t c g a c t	1860
a c a a g g c c a a	c g a g t g g c t g	a t g a a a a c a	t g g a c c c t c t	g a a t g a c a a c	g t c g c a g c c t	1920
t g c t c c a c c a	g a g c a c a g a c	c g g c t g a c g g	c a g a g a t c t g	g a a a g a c g t g	g a g g g c a t c g	1980
t g g g g c t g g a	a c a g g t g a g c	a g c c t g g g c g	a c g g c c c a c c	a g g t g g c c g c	c c c c g t c g g g	2040
g t a t g t t c c g	g a c a g t g g g a	c a g c t c t a c a	a g g a g t c c c t	g a g c c g c c t c	a t g g c c a c a c	2100
t c a g c a a c a c	c a a c c c c a g t	t t t g t c c g g t	g c a t t g t c c c	c a a c c a c g a g	a a g a g g g c c g	2160
g g a a g c t g g a	g c c a c g g c t g	g t g c t g g a c c	a g c t t c g c t g	c a a c g g g g t c	c t g g a g g g c a	2220
t c c g c a t c t g	t c g c c a g g g c	t t c c c c a a c c	g c a t c c t c t t	c c a g g a g t t c	c g g c a g c g a t	2280
a c g a g a t c c t	g a c a c c c a a t	g c c a t c c c c a	a g g g c t t c a t	g g a t g g g a a g	c a g g c c t g t g	2340
a a a a g a t g a t	c c a g g c g c t g	g a a c t g g a c c	c c a a c c t c t a	c c g c g t g g g a	c a g a g c a a g a	2400
t c t t c t t c c g	g g c t g g g g t c	c t g g c c c a g c	t g g a a g a g g a	g c g a g a c c t g	a a g g t c a c c g	2460
a c a t c a t c g t	c t c c t t c c a g	g c a g c t g c c c	g g g g a t a c c t	g g c t c g c a g g	g c c t t c c a g a	2520
a g c g c c a g c a	g c a g c a g a g c	g c c c t g a g g g	t g a t g c a g c g	g a a c t g c g c g	g c c t a c c t c a	2580
a g c t g a g a c a	c t g g c a g t g g	t g g c g g c t g t	t t a c c a a g g t	g a a g c c a c t g	c t g c a g g t g a	2640
c g c g g c a g g a	t g a g g t g c t g	c a g g c a c g g g	c c c a g g a g c t	g c a g a a a g t g	c a g g a g c t a c	2700
a g c a g c a g a g	c g c c c g c g a a	g t t g g g g a g c	t c c a g g g c c g	a g t g g c a c a g	c t g g a a g a g g	2760
a g c g c g c c c g	c c t g g c a g a g	c a a t t g c g a g	c a g a g g c a g a	a c t g t g t g c a	g a g g c c g a g g	2820
a g a c g c g g g g	g a g g c t g g c a	g c c c g c a a g c	a g g a g c t g g a	g c t g g t g g t g	t c a g a g c t g g	2880
a g g c t c g c g t	g g g c g a g g a g	g a g g a g t g c a	g c c g t c a a a t	g c a a a c c g a g	a a g a a g a g g c	2940
t a c a g c a g c a	c a t a c a g g a g	c t a g a g g c c c	a c c t t g a g g c	t g a g g a g g g t	g c g c g g c a g a	3000
a g c t g c a g c t	g g a g a a g g t g	a c g a c a g a g g	c a a a a a t g a a	g a a a t t t g a a	g a g g a c c t g c	3060
t g c t c c t g g a	a g a c c a g a a t	t c c a a g c t g a	g c a a g a g c g g	a a g c t g c t g g	a a g a t c g t c t	3120
g g c c g a g t t c	t c a t c c c a g g	c a g c t g a g g a	g g a g g a g a a g	g t c a a g a g c c	t c a a t a a g c t	3180
a c g g c t c a a a	t a t g a g g c c a	c a a t c g c a g a	c a t g g a g g g a	c c g c c t a c g g	a a g g a g g a g a	3240
a g g g t c g c c a	g g a g c t g g a g	a a g c t g a a g c	g g a g g c t g g a	t g g g g a g a g c	t c a g a g c t g c	3300
a g g a g c a g a t	g g t g g a g c a g	c a a c a g c g g g	c a g a g g a g c t	g c g g g c c c a g	c t g g g c c g g a	3360
a g g a g g a g g a	g c t g c a g g c t	g c c c t g g c c a	g g g c a g a a g a	c g a g g g t g g g	g c c c g g g c c c	3420
a g c t g c t g a a	a t c c c t g c g g	g a g g c t c a a g	c a g c c c t g g c	c g a g g c c c a g	g a g g a c c t g g	3480
a g t c t g a g c g	t g t g g c c a g g	a c c a a g g c g g	a g a a g c a g c g	c c g g g a c c t g	g g c g a g g a g c	3540
t g g a g g c g c t	g c g g g g c g a g	c t g g a g g a c a	c g c t g g a c t c	c a c c a a c g c a	c a g c a g g a g c	3600

N3027PCT\_sequ. l i s t . . t x t

t ccggt ccaa gaggaacag gaggt gacgg agct gaagaa gact ct ggag gaggagact c	3660
gcat ccacga ggccggcagt g caggagct ga ggcagcgcca cggccaggcc ct gggggagc	3720
t ggccggagca gct ggagcag gcccgagggg gcaaaggt gc at gggagaag acccggt gg	3780
ccct ggaggc cgaggt gt cc gagct gcggg cagaact gag cagcct gcag act gcacgt c	3840
aggagggt ga gcagcggagg cgccgcct gg agt t acagct gcaggaggt g cagggccggg	3900
ct ggt gat gg ggagaggga cgagcggagg ct gct gagaa gct gcagcga gccagggt g	3960
aact ggagaa t gt gt ct ggg gcgct gaacg aggct gact c caaaacct c cgt ct t agca	4020
aggagct gag cagcacagaa gccagct gc acgat gcca ggagct gct g caggaggaga	4080
ccagggcgaa at t gccct t g ggg t cccggg t gcgagccat ggaggct gag gcagccgggc	4140
t gcgt gagca gct ggaggag gaggcagct g ccagggaacg ggccggccgt gaact gcaga	4200
ct gccaggc ccagct t t cc gact ggcggc ggcgccagga ggaggaggca ggggact gg	4260
aggcagggga ggaggcacgg cgccgggcag cccgggaggc cgaggccct g acccagcgcc	4320
t ggcagaaaa gacagagacc gt ggat cggc t ggagcgggg ccgccgccgg ct gcagcagg	4380
agct ggacga cgccacct g gacct ggagc agcagcggca gct t gt gagc accct ggaga	4440
agaagcagcg caagt t t gac cagct t ct gg cagaggagaa ggcagct gt a ct t cgggcag	4500
t ggaggaacg t gagcgggccc gaggcagagg gccgggagcg t gaggct cgg gccct gt cac	4560
t gacacgggc act ggaggag gagcaggagg cacgt gagga gct ggagcgg cagaaccggg	4620
ccct gcgggc t gagct ggag gact gct ga gcagcaagga t gacgt cggc aagagcgt gc	4680
at gagct gga acgagcct gc cgggt agcag aacaggcagc caat gat ct g cgagcacagg	4740
t gacagaact ggaggat gag ct gacagcgg ccgaggat gc caagct gcgt ct ggaggt ga	4800
ct gt gcaggc t ct caagact cagcat gagc gt gacct gca gggccgt gat gaggct ggt g	4860
aagagaggcg gaggcagct g gccaagcagc t gagagat gc agaggt ggag cgggat gagg	4920
agcgaagca gcgcact ct g gccgt ggct g cccgaagaa gct ggaggga gagct ggagg	4980
agct gaaggc t cagat ggcc t ct gccggcc agggcaagga ggaggcggg g aagcagct t c	5040
gcaagat gca ggccagat g aaggagct at ggcgggaggt ggaggagaca cgcacct ccc	5100
gggaggagat ct t ct cccag aat cgggaaa gt gaaaagcg cct caagggc ct ggaggct g	5160
aggt gct gcg gct gcaggag gaact ggccg cct cggaccg t gct cggcgg caggcccagc	5220
aggaccggga t gagat ggca gat gagggt gg ccaat ggt aa cct t agcaag gcagccat t c	5280
t ggaggagaa gcgt cagct g gaggggcgcc t ggggcagt t ggaggaagag ct ggaggagg	5340
agcagagcaa ct cagagct g ct caat gacc gct accgcaa gct gct cct g caggt agagt	5400
cact gaccac agagct gt ca gct gagcgca gt t t ct cagc caaggcagag agcgggcggc	5460
agcagct gga acggcagat c caggagct ac ggggacgcct ggggaggag gat gct gggg	5520
cccgt gcccg ccacaagat g accat t gct g ccct t gact c t aagt t ggcc caggct gagg	5580
agcagct aga gcaagagacc agagagcgca t cct ct ct gg aaagct ggt g cgcagagct g	5640
agaagcggct t aaagaggt g gt gct ccagg t ggaggagga gcggagggt g gct gaccagc	5700

N3027PCT\_sequ.list.txt

```

t ccgggacca gct ggagaag ggaaccttc gagt caagca gct gaagcgg cagct ggagg 5760
agggcgagga ggaggcatcc cgggctcagg ctggccgccg gaggctgcag cgt gagctgg 5820
aagatgtcac agagt cggcc gagtccatga accgtgaagt gaccacactg aggaaccggc 5880
ttcgacgcgg cccctcacc ttaccacccc gcacggcgcg ccaggctcttc cgact agagg 5940
agggcgtggc atccgacgag gaggcagagg aagcacagcc tgggtctggg ccatccccgg 6000
agcctgaggg gtccccacca gcccaccccc agtgacccta ccctgtcccc agatgcacta 6060
acagatgggg ccagaccccc ttcttccctg gacccacagg gccctgtcc caggaacccc 6120
gccctctgac ttcttggcct ttggaaatgg tgcagcactc tggcatttat cacccccacc 6180
tgggtcccct gcaacctccc atcaaaggat gaccctaaa cacagaggag cggggcagggc 6240
agggaggcaa ggactggagc taccttgctt gttgggggac tgggtacagt tggcaagctg 6300
tgtttccatc agctccctgt cctcctttct tccctcgtta ttgatctata gacattagga 6360
agggagtgag acggctcctc caccatcctc agccagtga acccatccc tctgcttctc 6420
tctctctctc tctctctccc tccctctcct tccctacct ctaccatct ttcttggcct 6480
ctctgagggg ctctctgtgc atctttttag gaatctcgct ctcaactctct acgtagccac 6540
tctccttccc ccatttctgc gtccaccct gaactcctga gcgacagaag cccagggcct 6600
ccaccagcct tgaaccttg caaaggggca ggacaagggg acccctctca ctctgctgc 6660
tgcccatgct ctgccctccc ttctggttgc tctgaggggt cggagcttcc ctctgggact 6720
aaaggagtgt cctttacct cccagcctcc aggctctggc agaaataaac tccaaccga 6780
ctggac 6786

```

<210> 12  
 <211> 1995  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1995)  
 <223> myosin heavy chain (MYH14)

<400> 12

Met Ala Ala Val Thr Met Ser Val Pro Gly Arg Lys Ala Pro Pro Arg  
1 5 10 15

Pro Gly Pro Val Pro Glu Ala Ala Gln Pro Phe Leu Phe Thr Pro Arg  
20 25 30

Gly Pro Ser Ala Gly Gly Gly Pro Gly Ser Gly Thr Ser Pro Gln Val  
35 40 45

Glu Trp Thr Ala Arg Arg Leu Val Trp Val Pro Ser Glu Leu His Gly  
50 55 60

N3027PCT\_sequ.list.txt

Phe 65 Glu Ala Ala Ala Leu 70 Arg Asp Glu Gly Glu Glu Glu Ala Glu Val 80  
 Glu Leu Ala Glu Ser 85 Gly Arg Arg Leu Arg 90 Leu Pro Arg Asp Gln Ile 95  
 Gln Arg Met Asn 100 Pro Pro Lys Phe Ser 105 Lys Ala Glu Asp Met 110 Ala Glu  
 Leu Thr Cys 115 Leu Asn Glu Ala Ser 120 Val Leu His Asn Leu 125 Arg Glu Arg  
 Tyr Tyr 130 Ser Gly Leu Ile Tyr 135 Thr Tyr Ser Gly Leu 140 Phe Cys Val Val  
 Ile 145 Asn Pro Tyr Lys Gln 150 Leu Pro Ile Tyr Thr 155 Glu Ala Ile Val Glu 160  
 Met Tyr Arg Gly Lys 165 Lys Arg His Glu Val 170 Pro Pro His Val Tyr 175 Ala  
 Val Thr Glu Gly 180 Ala Tyr Arg Ser Met 185 Leu Gln Asp Arg Glu 190 Asp Gln  
 Ser Ile Leu 195 Cys Thr Gly Glu Ser 200 Gly Ala Gly Lys Thr 205 Glu Asn Thr  
 Lys Lys 210 Val Ile Gln Tyr Leu 215 Ala His Val Ala Ser 220 Ser Pro Lys Gly  
 Arg 225 Lys Glu Pro Gly Val 230 Pro Gly Glu Leu Glu 235 Arg Gln Leu Leu Gln 240  
 Ala Asn Pro Ile Leu 245 Glu Ala Phe Gly Asn 250 Ala Lys Thr Val Lys 255 Asn  
 Asp Asn Ser Ser 260 Arg Phe Gly Lys Phe 265 Ile Arg Ile Asn Phe 270 Asp Val  
 Ala Gly Tyr 275 Ile Val Gly Ala Asn 280 Ile Glu Thr Tyr Leu 285 Leu Glu Lys  
 Ser Arg 290 Ala Ile Arg Gln Ala 295 Lys Asp Glu Cys Ser 300 Phe His Ile Phe  
 Tyr 305 Gln Leu Leu Gly Gly 310 Ala Gly Glu Gln Leu 315 Lys Ala Asp Leu Leu 320  
 Leu Glu Pro Cys Ser 325 His Tyr Arg Phe Leu 330 Thr Asn Gly Pro Ser 335 Ser  
 Ser Pro Gly Gln Glu Arg Glu Leu Phe Gln Glu Thr Leu Glu Ser Leu

340

345

350

Arg Val Leu Gly Phe Ser His Gu Gu Ile Ile Ser Met Leu Arg Met  
 355 360 365  
 Val Ser Ala Val Leu Gln Phe Gly Asn Ile Ala Leu Lys Arg Gu Arg  
 370 375 380  
 Asn Thr Asp Gln Ala Thr Met Pro Asp Asn Thr Ala Ala Gln Lys Leu  
 385 390 395 400  
 Cys Arg Leu Leu Gly Leu Gly Val Thr Asp Phe Ser Arg Ala Leu Leu  
 405 410 415  
 Thr Pro Arg Ile Lys Val Gly Arg Asp Tyr Val Gln Lys Ala Gln Thr  
 420 425 430  
 Lys Gu Gln Ala Asp Phe Ala Leu Gu Ala Leu Ala Lys Ala Thr Tyr  
 435 440 445  
 Gu Arg Leu Phe Arg Trp Leu Val Leu Arg Leu Asn Arg Ala Leu Asp  
 450 455 460  
 Arg Ser Pro Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala  
 465 470 475 480  
 Gly Phe Gu Ile Phe Gln Leu Asn Ser Phe Gu Gln Leu Cys Ile Asn  
 485 490 495  
 Tyr Thr Asn Gu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Val  
 500 505 510  
 Leu Gu Gln Gu Gu Tyr Gln Arg Gu Gly Ile Pro Trp Thr Phe Leu  
 515 520 525  
 Asp Phe Gly Leu Asp Leu Gln Pro Cys Ile Asp Leu Ile Gu Arg Pro  
 530 535 540  
 Ala Asn Pro Pro Gly Leu Leu Ala Leu Leu Asp Gu Gu Cys Trp Phe  
 545 550 555 560  
 Pro Lys Ala Thr Asp Lys Ser Phe Val Gu Lys Val Ala Gln Gu Gln  
 565 570 575  
 Gly Gly His Pro Lys Phe Gln Arg Pro Arg His Leu Arg Asp Gln Ala  
 580 585 590  
 Asp Phe Ser Val Leu His Tyr Ala Gly Lys Val Asp Tyr Lys Ala Asn  
 595 600 605  
 Gu Trp Leu Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Ala Ala  
 610 615 620

N3027PCT\_sequ.list.txt

Leu 625 Leu His Gln Ser Thr 630 Asp Arg Leu Thr Ala 635 Glu Ile Trp Lys Asp 640  
 Val Glu Gly Ile Val 645 Gly Leu Glu Gln Val 650 Ser Ser Leu Gly Asp 655 Gly  
 Pro Pro Gly Gly 660 Arg Pro Arg Arg Gly 665 Met Phe Arg Thr Val 670 Gly Gln  
 Leu Tyr Lys 675 Glu Ser Leu Ser Arg 680 Leu Met Ala Thr Leu 685 Ser Asn Thr  
 Asn 690 Pro Ser Phe Val Arg Cys 695 Ile Val Pro Asn His 700 Glu Lys Arg Ala  
 Gly 705 Lys Leu Glu Pro Arg 710 Leu Val Leu Asp Gln 715 Leu Arg Cys Asn Gly 720  
 Val Leu Glu Gly Ile 725 Arg Ile Cys Arg Gln 730 Gly Phe Pro Asn Arg 735 Ile  
 Leu Phe Gln Glu 740 Phe Arg Gln Arg Tyr 745 Glu Ile Leu Thr Pro 750 Asn Ala  
 Ile Pro Lys 755 Gly Phe Met Asp Gly 760 Lys Gln Ala Cys Glu 765 Lys Met Ile  
 Gln Ala 770 Leu Glu Leu Asp Pro 775 Asn Leu Tyr Arg Val 780 Gly Gln Ser Lys  
 Ile 785 Phe Phe Arg Ala Gly 790 Val Leu Ala Gln Leu 795 Glu Glu Glu Arg Asp 800  
 Leu Lys Val Thr 805 Asp Ile Ile Val Ser Phe 810 Gln Ala Ala Ala Arg 815 Gly  
 Tyr Leu Ala 820 Arg Arg Ala Phe Gln Lys 825 Arg Gln Gln Gln Gln 830 Ser Ala  
 Leu Arg Val 835 Met Gln Arg Asn Cys 840 Ala Ala Tyr Leu Lys 845 Leu Arg His  
 Trp Gln 850 Trp Trp Arg Leu Phe 855 Thr Lys Val Lys Pro 860 Leu Leu Gln Val  
 Thr 865 Arg Gln Asp Glu Val 870 Leu Gln Ala Arg Ala 875 Gln Glu Leu Gln Lys 880  
 Val Gln Glu Leu 885 Gln Gln Gln Ser Ala Arg 890 Glu Val Gly Glu Leu 895 Gln

## N3027PCT\_sequ.list.txt

Gly	Arg	Val	Ala	Gln	Leu	Glu	Glu	Arg	Ala	Arg	Leu	Ala	Glu	Gln	
			900					905					910		
Leu	Arg	Ala	Glu	Ala	Glu	Leu	Cys	Ala	Glu	Ala	Glu	Glu	Thr	Arg	Gly
		915					920					925			
Arg	Leu	Ala	Ala	Arg	Lys	Gln	Glu	Leu	Glu	Leu	Val	Val	Ser	Glu	Leu
	930					935					940				
Glu	Ala	Arg	Val	Gly	Glu	Glu	Glu	Glu	Cys	Ser	Arg	Gln	Met	Gln	Thr
945					950					955					960
Glu	Lys	Lys	Arg	Leu	Gln	Gln	His	Ile	Gln	Glu	Leu	Glu	Ala	His	Leu
				965					970					975	
Glu	Ala	Glu	Glu	Gly	Ala	Arg	Gln	Lys	Leu	Gln	Leu	Glu	Lys	Val	Thr
			980					985					990		
Thr	Glu	Ala	Lys	Met	Lys	Lys	Phe	Glu	Glu	Asp	Leu	Leu	Leu	Leu	Glu
		995					1000					1005			
Asp	Gln	Asn	Ser	Lys	Leu	Ser	Lys	Ser	Gly	Ser	Cys	Trp	Lys	Ile	
	1010					1015					1020				
Val	Trp	Pro	Ser	Ser	His	Pro	Arg	Gln	Leu	Arg	Arg	Arg	Arg	Arg	
	1025					1030					1035				
Ser	Arg	Ala	Ser	Ile	Ser	Tyr	Gly	Ser	Asn	Met	Arg	Pro	Gln	Ser	
	1040					1045					1050				
Gln	Thr	Trp	Arg	Asp	Arg	Leu	Arg	Lys	Glu	Glu	Lys	Gly	Arg	Gln	
	1055					1060					1065				
Glu	Leu	Glu	Lys	Leu	Lys	Arg	Arg	Leu	Asp	Gly	Glu	Ser	Ser	Glu	
	1070					1075					1080				
Leu	Gln	Glu	Gln	Met	Val	Glu	Gln	Gln	Gln	Arg	Ala	Glu	Glu	Leu	
	1085					1090					1095				
Arg	Ala	Gln	Leu	Gly	Arg	Lys	Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	
	1100					1105					1110				
Ala	Arg	Ala	Glu	Asp	Glu	Gly	Gly	Ala	Arg	Ala	Gln	Leu	Leu	Lys	
	1115					1120					1125				
Ser	Leu	Arg	Glu	Ala	Gln	Ala	Ala	Leu	Ala	Glu	Ala	Gln	Glu	Asp	
	1130					1135					1140				
Leu	Glu	Ser	Glu	Arg	Val	Ala	Arg	Thr	Lys	Ala	Glu	Lys	Gln	Arg	
	1145					1150					1155				

Arg Asp 1160 Leu Gly Gu Gu Leu 1165 Gu Ala Leu Arg Gly 1170 Gu Leu Gu  
 Asp Thr 1175 Leu Asp Ser Thr Asn 1180 Ala Gn Gn Gu Leu 1185 Arg Ser Lys  
 Arg Gu 1190 Gn Gu Val Thr Gu 1195 Leu Lys Lys Thr Leu 1200 Gu Gu Gu  
 Thr Arg 1205 Ile His Gu Ala Ala 1210 Val Gn Gu Leu Arg 1215 Gn Arg His  
 Gly Gn 1220 Ala Leu Gly Gu Leu 1225 Ala Gu Gn Leu Gu 1230 Gn Ala Arg  
 Arg Gly 1235 Lys Gly Ala Trp Gu 1240 Lys Thr Arg Leu Ala 1245 Leu Gu Ala  
 Gu Val 1250 Ser Gu Leu Arg Ala 1255 Gu Leu Ser Ser Leu 1260 Gn Thr Ala  
 Arg Gn 1265 Gu Gly Gu Gn Arg 1270 Arg Arg Arg Leu Gu 1275 Leu Gn Leu  
 Gn Gu 1280 Val Gn Gly Arg Ala 1285 Gly Asp Gly Gu Arg 1290 Ala Arg Ala  
 Gu Ala 1295 Ala Gu Lys Leu Gn 1300 Arg Ala Gn Ala Gu 1305 Leu Gu Asn  
 Val Ser 1310 Gly Ala Leu Asn Gu 1315 Ala Gu Ser Lys Thr 1320 Ile Arg Leu  
 Ser Lys 1325 Gu Leu Ser Ser Thr 1330 Gu Ala Gn Leu His 1335 Asp Ala Gn  
 Gu Leu 1340 Leu Gn Gu Gu Thr 1345 Arg Ala Lys Leu Ala 1350 Leu Gly Ser  
 Arg Val 1355 Arg Ala Met Gu Ala 1360 Gu Ala Ala Gly Leu 1365 Arg Gu Gn  
 Leu Gu 1370 Gu Gu Ala Ala Ala 1375 Arg Gu Arg Ala Gly 1380 Arg Gu Leu  
 Gn Thr 1385 Ala Gn Ala Gn Leu 1390 Ser Gu Trp Arg Arg 1395 Arg Gn Gu  
 Gu Gu 1400 Ala Gly Ala Leu Gu 1405 Ala Gly Gu Gu Ala 1410 Arg Arg Arg  
 Ala Ala Arg Gu Ala Gu Ala Leu Thr Gn Arg Leu Ala Gu Lys

1415						1420										1425
Thr	G u	Thr	Val	Asp	Arg	Leu	G u	Arg	G y	Arg	Arg	Arg	Leu	G n		
1430						1435					1440					
G n	G u	Leu	Asp	Asp	Al a	Thr	Met	Asp	Leu	G u	G n	G n	Arg	G n		
1445						1450					1455					
Leu	Val	Ser	Thr	Leu	G u	Lys	Lys	G n	Arg	Lys	Phe	Asp	G n	Leu		
1460						1465					1470					
Leu	Al a	G u	G u	Lys	Al a	Al a	Val	Leu	Arg	Al a	Val	G u	G u	Arg		
1475						1480					1485					
G u	Arg	Al a	G u	Al a	G u	G y	Arg	G u	Arg	G u	Al a	Arg	Al a	Leu		
1490						1495					1500					
Ser	Leu	Thr	Arg	Al a	Leu	G u	G u	G u	G n	G u	Al a	Arg	G u	G u		
1505						1510					1515					
Leu	G u	Arg	G n	Asn	Arg	Al a	Leu	Arg	Al a	G u	Leu	G u	Al a	Leu		
1520						1525					1530					
Leu	Ser	Ser	Lys	Asp	Asp	Val	G y	Lys	Ser	Val	Hi s	G u	Leu	G u		
1535						1540					1545					
Arg	Al a	Cys	Arg	Val	Al a	G u	G n	Al a	Al a	Asn	Asp	Leu	Arg	Al a		
1550						1555					1560					
G n	Val	Thr	G u	Leu	G u	Asp	G u	Leu	Thr	Al a	Al a	G u	Asp	Al a		
1565						1570					1575					
Lys	Leu	Arg	Leu	G u	Val	Thr	Val	G n	Al a	Leu	Lys	Thr	G n	Hi s		
1580						1585					1590					
G u	Arg	Asp	Leu	G n	G y	Arg	Asp	G u	Al a	G y	G u	G u	Arg	Arg		
1595						1600					1605					
Arg	G n	Leu	Al a	Lys	G n	Leu	Arg	Asp	Al a	G u	Val	G u	Arg	Asp		
1610						1615					1620					
G u	G u	Arg	Lys	G n	Arg	Thr	Leu	Al a	Val	Al a	Al a	Arg	Lys	Lys		
1625						1630					1635					
Leu	G u	G y	G u	Leu	G u	G u	Leu	Lys	Al a	G n	Met	Al a	Ser	Al a		
1640						1645					1650					
G y	G n	G y	Lys	G u	G u	Al a	Val	Lys	G n	Leu	Arg	Lys	Met	G n		
1655						1660					1665					
Al a	G n	Met	Lys	G u	Leu	Trp	Arg	G u	Val	G u	G u	Thr	Arg	Thr		
1670						1675					1680					

N3027PCT\_sequ.list.txt

Ser	Arg	Glu	Glu	Ile	Phe	Ser	Gln	Asn	Arg	Glu	Ser	Glu	Lys	Arg
	1685					1690					1695			
Leu	Lys	Gly	Leu	Glu	Ala	Glu	Val	Leu	Arg	Leu	Gln	Glu	Glu	Leu
	1700					1705					1710			
Ala	Ala	Ser	Asp	Arg	Ala	Arg	Arg	Gln	Ala	Gln	Gln	Asp	Arg	Asp
	1715					1720					1725			
Glu	Met	Ala	Asp	Glu	Val	Ala	Asn	Gly	Asn	Leu	Ser	Lys	Ala	Ala
	1730					1735					1740			
Ile	Leu	Glu	Glu	Lys	Arg	Gln	Leu	Glu	Gly	Arg	Leu	Gly	Gln	Leu
	1745					1750					1755			
Glu	Glu	Glu	Leu	Glu	Glu	Glu	Gln	Ser	Asn	Ser	Glu	Leu	Leu	Asn
	1760					1765					1770			
Asp	Arg	Tyr	Arg	Lys	Leu	Leu	Leu	Gln	Val	Glu	Ser	Leu	Thr	Thr
	1775					1780					1785			
Glu	Leu	Ser	Ala	Glu	Arg	Ser	Phe	Ser	Ala	Lys	Ala	Glu	Ser	Gly
	1790					1795					1800			
Arg	Gln	Gln	Leu	Glu	Arg	Gln	Ile	Gln	Glu	Leu	Arg	Gly	Arg	Leu
	1805					1810					1815			
Gly	Glu	Glu	Asp	Ala	Gly	Ala	Arg	Ala	Arg	His	Lys	Met	Thr	Ile
	1820					1825					1830			
Ala	Ala	Leu	Glu	Ser	Lys	Leu	Ala	Gln	Ala	Glu	Glu	Gln	Leu	Glu
	1835					1840					1845			
Gln	Glu	Thr	Arg	Glu	Arg	Ile	Leu	Ser	Gly	Lys	Leu	Val	Arg	Arg
	1850					1855					1860			
Ala	Glu	Lys	Arg	Leu	Lys	Glu	Val	Val	Leu	Gln	Val	Glu	Glu	Glu
	1865					1870					1875			
Arg	Arg	Val	Ala	Asp	Gln	Leu	Arg	Asp	Gln	Leu	Glu	Lys	Gly	Asn
	1880					1885					1890			
Leu	Arg	Val	Lys	Gln	Leu	Lys	Arg	Gln	Leu	Glu	Glu	Ala	Glu	Glu
	1895					1900					1905			
Glu	Ala	Ser	Arg	Ala	Gln	Ala	Gly	Arg	Arg	Arg	Leu	Gln	Arg	Glu
	1910					1915					1920			
Leu	Glu	Asp	Val	Thr	Glu	Ser	Ala	Glu	Ser	Met	Asn	Arg	Glu	Val
	1925					1930					1935			

N3027PCT\_sequ.list.txt

Thr Thr Leu Arg Asn Arg Leu Arg Arg Gly Pro Leu Thr Phe Thr  
1940 1945 1950

Thr Arg Thr Val Arg Gln Val Phe Arg Leu Glu Glu Gly Val Ala  
1955 1960 1965

Ser Asp Glu Glu Ala Glu Glu Ala Gln Pro Gly Ser Gly Pro Ser  
1970 1975 1980

Pro Glu Pro Glu Gly Ser Pro Pro Ala His Pro Gln  
1985 1990 1995

<210> 13  
<211> 3624  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(3624)  
<223> myosin I A (MYO1A)

<400> 13  
cagggagcct gggctggaag aggcagcaaa agggaaaatc agaagagtgg acaactggcaa 60  
gaggagggca gcctttttcc cagcttcctt gcaccatgga cagctcccat taagccacct 120  
ctccatcctg gggccaggac tcttatgcc catctcctgtc aaattgagat ttcattccacc 180  
attctccaag gacagtgaag ttatacccta gtctcagtggt tgggatcagt ggcccctctg 240  
gacatgcctc tcctggaagg ttctgtgggg gtggaggatc ttgtcctcct ggaacccttg 300  
gtggaggagt cactgctcaa gaatcttcag ctctcgctatg aaaacaagga gat ttat acc 360  
taccttggga atgtggtgat ctcagtgaat ccctatcaac agcttcccat ctatgggcca 420  
gagttcat tg ccaaatatca agactat act ttctatgagc tgaagcccca tatctacgca 480  
ttggcaaatg tggcgtacca gt cactgagg gacagggacc gagaccagt g tatcctcatc 540  
acaggcgaga gtggatcagg gaagactgag gccagcaagc tggatgatgtc ttatgtggct 600  
gccgtctgtg ggaaaggaga gcaggtgaac tctgtgaagg agcagctgct acagtctaac 660  
ccagtgtgg aggccttttg caatgccaag accattcgca acaacaattc ctcccgattt 720  
ggaaaataca tggatattga atttgacttc aagggatccc ccctcggtgg tgtcatcaca 780  
aactatctgc ttgagaaatc ccgattagt g aagcagctca aaggagaaag gaacttccac 840  
atcttctatc agctgctggc tggagcagat gaacagctgc tgaaggccct gaagcttgag 900  
cgggatacaa ctggctatgc ctatctgaat catgaagtat ccagagtgga tggcatggac 960  
gacgcctcca gcttcagggc tgtacagagt gcaatggcag tgattgggtt ctcgaggag 1020  
gagattcgac aagtgtaga ggtgacatcc atgggtgctaa agctggggaa cgtgttgggtg 1080  
gctgatgagt tccaggccag tgggatacca gcaagtggca tccgtgatgg gagaggtgtt 1140  
cgggagattg gggagatggt gggcttgaat tcagaagaag tagagagagc ttgtgtgctcg 1200

N3027PCT\_sequ. list .txt

aggaccat gg	aaacagccaa	ggaaaaggt g	gt cact gcac	t gaat gt t at	gcaggct cag	1260
t at gct cggg	acgccct ggc	t aagaacat c	t acagccgcc	t ct t t gact g	gat agt gaat	1320
cgaat caat g	agagcat caa	ggg gggcat c	ggggaaaaga	agaaggt aat	gggagt cct t	1380
gat at ct acg	gt t t t gagat	at t agaggat	aat agct t t g	agcaat t t gt	gat caact ac	1440
t gcaat gaga	agct gcagca	ggg gt t cat a	gagat gaccc	t gaaagaaga	gcaagaggaa	1500
t at aagagag	aaggcat acc	gt ggacaaag	gt ggact act	t t gat aat gg	cat cat t t gt	1560
aagct cat t g	agcat aat ca	gcgaggt at c	ct ggccat gt	t ggat gagga	gt gcct gcgg	1620
cct ggggt gg	t cagt gact c	cact t t cct a	gcaaagct ga	accagct ct t	ct ccaagcat	1680
ggccact acg	agagcaaagt	caccagaat	gcccagcgt c	agt at gacca	caccat gggc	1740
ct cagct gct	t ccgcat ct g	ccact at gcg	ggcaaggt ga	cat acaacgt	gaccagct t t	1800
at t gacaaga	at aat gacct	act ct t ccga	gacct gt t gc	aggccat gt g	gaaggccag	1860
cacccccct cc	t t cgggt cct t	gt t t cct gag	ggcaat cct a	agcaggcat c	t ct caaacgc	1920
cccccgact g	ct ggggcca	gt t caagagt	t ct gt ggcca	t cct cat gaa	gaat ct gt at	1980
t ccaagagcc	ccaact acat	caggt gcat a	aagcccaat g	agcat cagca	gcgaggt cag	2040
t t ct ct t cag	acct ggt ggc	aaccaggct	cgggt acct gg	gact gct gga	gaacgt acgg	2100
gt gcgacggg	caggct at gc	ccaccgccag	ggg t at gggc	cct t cct gga	aaggt accga	2160
t t gct gagcc	ggagcacct g	gcct cact gg	aat gggggag	accgggaagg	t gt t gagaag	2220
gt cct ggggg	agct gagcat	gt cct cgggg	gagct ggcct	t t ggcaagac	aaagat ct t c	2280
at t agaagcc	ccaagact ct	t t t ct acct c	gaagaacaga	ggcgct gag	act ccagcag	2340
ct ggccacac	t cat acagaa	gat t t accga	ggct ggcgt	gccgcacca	ct accaact g	2400
at gcgaaaga	gt cagat cct	cat ct cct ct	t ggt t t cggg	gaaacat gca	aaagaaat gc	2460
t at gggaaga	t aaaggcat c	cgt gt t at t g	at ccaggct t	t t gt gagagg	gt ggaaggcc	2520
cgaagaat t	at cgcaaata	t t t ccgggt ca	gaggct gccc	t cacct t ggc	agat t t cat c	2580
t acaagagca	t ggt acagaa	at t cct act g	gggct gaaga	acaat t t gcc	at ccacaaac	2640
gt ct t agaca	agacat ggcc	agccgcccc	t acaagt gcc	t cagcacagc	aaat caggag	2700
ct gcagcagc	t ct t ct acca	gt ggaagt gc	aagaggt t cc	gggat cagct	gt cccgaag	2760
caggt agaga	t cct gaggga	aaagct ct gt	gccagt gaac	t gt t caaggg	caagaaggct	2820
t cat at cccc	agagt gt ccc	cat t ccat t c	t gt ggt gact	acat t gggct	gcaagggaac	2880
cccaagct gc	agaagct gaa	aggcggggag	gaggggcct g	t t ct gat ggc	agaggccgt g	2940
aagaaggt ca	at cgt ggcaa	t ggcaagact	t ct t ct cgga	t t ct cct cct	gaccaagggc	3000
cat gt gat t c	t cacagacac	caagaagt cc	caggccaaaa	t t gt cat t gg	gct agacaat	3060
gt ggct gggg	t gt cagt cac	cagcct caag	gat gggct ct	t t agct t gca	t ct gagt gag	3120
at gt cat cgg	t gggct ccaa	gggggact t c	ct gct ggt ca	gcgagcat gt	gat t gaact g	3180
ct gacaaaaa	t gt accgggc	t gt gct ggat	gccacgcaga	ggcagct t ac	agt caccgt g	3240
act gagaagt	t ct cagt gag	gt t caaggag	aacagt gt gg	ct gt caaggt	cgt ccagggc	3300

N3027PCT\_sequ.list.txt

```
cctgcagggtg gtgacaacag caagctacgc taaaaaaaaa aggggagtcattgcttggag 3360
gtgactgtgc agtgaggagg gggcaccatg cagagatggc agttgcttcc tctgaacca 3420
gcactaatcc ccctctgccc tctgtgtgg gaggatctct aaccctctg atcgtggcgc 3480
atggcttggg gattaaacta cccttgaaga ggacccttgt cccaaaccct tcttgttctc 3540
tctccaaaa gtacttctt ccaaccgcga gcctctctgc aactaat aa aacatgtggc 3600
ttggaaaggt tcaaaaaaaaa aaaa 3624
```

```
<210> 14
<211> 1043
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> MSC_FEATURE
<222> (1)..(1043)
<223> myosin I A (MYO1A)
```

```
<400> 14
```

```
Met Pro Leu Leu Glu Gly Ser Val Gly Val Glu Asp Leu Val Leu Leu
1 5 10 15
```

```
Glu Pro Leu Val Glu Glu Ser Leu Leu Lys Asn Leu Gln Leu Arg Tyr
20 25 30
```

```
Glu Asn Lys Glu Ile Tyr Thr Tyr Ile Gly Asn Val Val Ile Ser Val
35 40 45
```

```
Asn Pro Tyr Gln Gln Leu Pro Ile Tyr Gly Pro Glu Phe Ile Ala Lys
50 55 60
```

```
Tyr Gln Asp Tyr Thr Phe Tyr Glu Leu Lys Pro His Ile Tyr Ala Leu
65 70 75 80
```

```
Ala Asn Val Ala Tyr Gln Ser Leu Arg Asp Arg Asp Arg Asp Gln Cys
85 90 95
```

```
Ile Leu Ile Thr Gly Glu Ser Gly Ser Gly Lys Thr Glu Ala Ser Lys
100 105 110
```

```
Leu Val Met Ser Tyr Val Ala Ala Val Cys Gly Lys Gly Glu Gln Val
115 120 125
```

```
Asn Ser Val Lys Glu Gln Leu Leu Gln Ser Asn Pro Val Leu Glu Ala
130 135 140
```

```
Phe Gly Asn Ala Lys Thr Ile Arg Asn Asn Asn Ser Ser Arg Phe Gly
145 150 155 160
```

```
Lys Tyr Met Asp Ile Glu Phe Asp Phe Lys Gly Ser Pro Leu Gly Gly
165 170 175
```

N3027PCT\_sequ.list.txt

Val Ile Thr Asn Tyr Leu Leu Glu Lys Ser Arg Leu Val Lys Glu Leu  
180 185 190

Lys Gly Glu Arg Asn Phe His Ile Phe Tyr Glu Leu Leu Ala Gly Ala  
195 200 205

Asp Glu Glu Leu Leu Lys Ala Leu Lys Leu Glu Arg Asp Thr Thr Gly  
210 215 220

Tyr Ala Tyr Leu Asn His Glu Val Ser Arg Val Asp Gly Met Asp Asp  
225 230 235 240

Ala Ser Ser Phe Arg Ala Val Glu Ser Ala Met Ala Val Ile Gly Phe  
245 250 255

Ser Glu Glu Glu Ile Arg Glu Val Leu Glu Val Thr Ser Met Val Leu  
260 265 270

Lys Leu Gly Asn Val Leu Val Ala Asp Glu Phe Glu Ala Ser Gly Ile  
275 280 285

Pro Ala Ser Gly Ile Arg Asp Gly Arg Gly Val Arg Glu Ile Gly Glu  
290 295 300

Met Val Gly Leu Asn Ser Glu Glu Val Glu Arg Ala Leu Cys Ser Arg  
305 310 315 320

Thr Met Glu Thr Ala Lys Glu Lys Val Val Thr Ala Leu Asn Val Met  
325 330 335

Glu Ala Glu Tyr Ala Arg Asp Ala Leu Ala Lys Asn Ile Tyr Ser Arg  
340 345 350

Leu Phe Asp Trp Ile Val Asn Arg Ile Asn Glu Ser Ile Lys Val Gly  
355 360 365

Ile Gly Glu Lys Lys Lys Val Met Gly Val Leu Asp Ile Tyr Gly Phe  
370 375 380

Glu Ile Leu Glu Asp Asn Ser Phe Glu Glu Phe Val Ile Asn Tyr Cys  
385 390 395 400

Asn Glu Lys Leu Glu Glu Val Phe Ile Glu Met Thr Leu Lys Glu Glu  
405 410 415

Glu Glu Glu Tyr Lys Arg Glu Gly Ile Pro Trp Thr Lys Val Asp Tyr  
420 425 430

Phe Asp Asn Gly Ile Ile Cys Lys Leu Ile Glu His Asn Glu Arg Gly  
435 440 445

N3027PCT\_sequ.list.txt

Ile Leu Ala Met Leu Asp Glu Glu Cys Leu Arg Pro Gly Val Val Ser  
 450 455 460  
 Asp Ser Thr Phe Leu Ala Lys Leu Asn Gln Leu Phe Ser Lys His Gly  
 465 470 475 480  
 His Tyr Glu Ser Lys Val Thr Gln Asn Ala Gln Arg Gln Tyr Asp His  
 485 490 495  
 Thr Met Gly Leu Ser Cys Phe Arg Ile Cys His Tyr Ala Gly Lys Val  
 500 505 510  
 Thr Tyr Asn Val Thr Ser Phe Ile Asp Lys Asn Asn Asp Leu Leu Phe  
 515 520 525  
 Arg Asp Leu Leu Gln Ala Met Trp Lys Ala Gln His Pro Leu Leu Arg  
 530 535 540  
 Ser Leu Phe Pro Glu Gly Asn Pro Lys Gln Ala Ser Leu Lys Arg Pro  
 545 550 555 560  
 Pro Thr Ala Gly Ala Gln Phe Lys Ser Ser Val Ala Ile Leu Met Lys  
 565 570 575  
 Asn Leu Tyr Ser Lys Ser Pro Asn Tyr Ile Arg Cys Ile Lys Pro Asn  
 580 585 590  
 Glu His Gln Gln Arg Gly Gln Phe Ser Ser Asp Leu Val Ala Thr Gln  
 595 600 605  
 Ala Arg Tyr Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly  
 610 615 620  
 Tyr Ala His Arg Gln Gly Tyr Gly Pro Phe Leu Glu Arg Tyr Arg Leu  
 625 630 635 640  
 Leu Ser Arg Ser Thr Trp Pro His Trp Asn Gly Gly Asp Arg Glu Gly  
 645 650 655  
 Val Glu Lys Val Leu Gly Glu Leu Ser Met Ser Ser Gly Glu Leu Ala  
 660 665 670  
 Phe Gly Lys Thr Lys Ile Phe Ile Arg Ser Pro Lys Thr Leu Phe Tyr  
 675 680 685  
 Leu Glu Glu Gln Arg Arg Leu Arg Leu Gln Gln Leu Ala Thr Leu Ile  
 690 695 700  
 Gln Lys Ile Tyr Arg Gly Trp Arg Cys Arg Thr His Tyr Gln Leu Met  
 705 710 715 720

N3027PCT\_sequ.list.txt

Arg Lys Ser Gln Ile Leu Ile Ser Ser Trp Phe Arg Gly Asn Met Gln  
725 730 735

Lys Lys Cys Tyr Gly Lys Ile Lys Ala Ser Val Leu Leu Ile Gln Ala  
740 745 750

Phe Val Arg Gly Trp Lys Ala Arg Lys Asn Tyr Arg Lys Tyr Phe Arg  
755 760 765

Ser Glu Ala Ala Leu Thr Leu Ala Asp Phe Ile Tyr Lys Ser Met Val  
770 775 780

Gln Lys Phe Leu Leu Gly Leu Lys Asn Asn Leu Pro Ser Thr Asn Val  
785 790 795 800

Leu Asp Lys Thr Trp Pro Ala Ala Pro Tyr Lys Cys Leu Ser Thr Ala  
805 810 815

Asn Gln Glu Leu Gln Gln Leu Phe Tyr Gln Trp Lys Cys Lys Arg Phe  
820 825 830

Arg Asp Gln Leu Ser Pro Lys Gln Val Glu Ile Leu Arg Glu Lys Leu  
835 840 845

Cys Ala Ser Glu Leu Phe Lys Gly Lys Lys Ala Ser Tyr Pro Gln Ser  
850 855 860

Val Pro Ile Pro Phe Cys Gly Asp Tyr Ile Gly Leu Gln Gly Asn Pro  
865 870 875 880

Lys Leu Gln Lys Leu Lys Gly Gly Glu Glu Gly Pro Val Leu Met Ala  
885 890 895

Glu Ala Val Lys Lys Val Asn Arg Gly Asn Gly Lys Thr Ser Ser Arg  
900 905 910

Ile Leu Leu Leu Thr Lys Gly His Val Ile Leu Thr Asp Thr Lys Lys  
915 920 925

Ser Gln Ala Lys Ile Val Ile Gly Leu Asp Asn Val Ala Gly Val Ser  
930 935 940

Val Thr Ser Leu Lys Asp Gly Leu Phe Ser Leu His Leu Ser Glu Met  
945 950 955 960

Ser Ser Val Gly Ser Lys Gly Asp Phe Leu Leu Val Ser Glu His Val  
965 970 975

Ile Glu Leu Leu Thr Lys Met Tyr Arg Ala Val Leu Asp Ala Thr Gln  
980 985 990

Arg Gln Leu Thr Val Thr Val Thr Glu Lys Phe Ser Val Arg Phe Lys

G u Asn Ser Val Al a Val Lys Val Val G n G y Pro Al a G y G y  
 1010 1015 1020

Asp Asn Ser Lys Leu Arg Tyr Lys Lys Lys G y Ser Hi s Oys Leu  
 1025 1030 1035

G u Val Thr Val G n  
 1040

<210> 15  
 <211> 4825  
 <212> DNA  
 <213> Homo sapi ens

<220>  
 <221> mi sc\_f eat ure  
 <222> ( 1) . . ( 4825)  
 <223> myosi n I B ( MYO1B)

<400> 15  
 gagcact ccg cagct gggg g cgcacgggag cct caaccgc ggcgcgt gga ggcagt acca 60  
 gagcgcgcgg cgcgcagt cg gccggcagcc gcgggacagc ct t ggcagaa cagccgcggc 120  
 gggagccccg cagccccggg ct gggccccg gt cccggagc gccaccggag agcgaggacg 180  
 acgt ggaggc ggagt ggcgc cggcgagggt agcgccaggc gagct ggaga ccat ggccaa 240  
 aat ggagggt g aaaacct cac t t ct ggacaa t at gat t gga gt t ggggat a t ggt t ct t t t 300  
 agaacct ct c aat gaggaga cct t cat caa caacct caag aagcgct t t g accacagt ga 360  
 aat at acaca t acat t ggaa gt gt ggt t at at ct gt t aac ccat accggt ct t t acccat 420  
 t t at t cacca gagaaagt gg aagaat acag gaacagaaat t t t t at gaac t gagccct ca 480  
 cat ct t t gcc ct t t cggat g aagcat acag at ccct acga gat caagat a aggaccaat g 540  
 t at t ct cat t act ggggaaa gt ggagcagg aaaaacagag gccagt aagc t t gt cat gt c 600  
 ct at gt ggca gct gt t t gt g gaaaaggagc agaagt t aat caagt t aaag aacagct t t t 660  
 acagt ccaac ccggt cct gg aagct t t t gg aaat gccaaa act gt aagga at gacaact c 720  
 ct ct agat t t ggcaaat at a t ggat at t ga at t t gact t t aaaggcgat c cact aggagg 780  
 agt aat aagt aact at ct t t t agagaaat c t cgggt t gt t aaacagccaa gaggt gaaag 840  
 aaact t ccat gt gt t ct at c agct gct ct c t ggt gcct ct gaagagct cc t caat aaact 900  
 t aagct t gag agggat t t ca gcaggat at aa ct acct gagt ct ggat t cgg ccaaagt gaa 960  
 t ggagt ggat gat gcagcaa at t t t agaac cgt gcggaat gccat gcaga t t gt gggct t 1020  
 t at ggat cat gaagct gagt ct gt ct t ggc ggt ggt ggca gcagt gt t ga aact ggggaa 1080  
 cat t gagt t c aagcccgaat ct cgagt gaa t ggt ct agat gaaagcaaaa t caaagat aa 1140  
 aaat gagt t a aaagaaat t t gt gaat t gac cggcat t gat caat cagt t c t agaacgagc 1200  
 at t cagt t t c cgaacagt t g aggccaaaca ggagaaagt t t caact acac t gaat gt ggc 1260

N3027PCT\_sequ. list.txt

t caggct t at t at gcccg t g at gct ct ggc t aaaaacct c t acagcaggt t g t t t t cat g	1320
gt t ggt aaat cgaat caat g aaagcat t aa ggcacaaaca aaagt gagaa agaaggt cat	1380
gggt gt t ct g gacat t t at g gct t t gagat t t t cgaggac aacagct t t g agcagt t cat	1440
t at t aat t at t gt aacgaaa agct gcaaca aat ct t cat t gaact t act c t t aaagaaga	1500
gcaggaggag t at at acggg aggat at aga at ggact cac at t gact act t caat aat gc	1560
t at cat t t gt gacct aat ag aaaat aacac aaat ggaat c ct ggccat gc t ggat gaaga	1620
gt gcct caga cct ggcacag t cact gat ga gacct t ct t a gaaaagct ga accaagt at g	1680
t gccaccac cagcat t t t g agagcaggat gagcaagt gc t ct cgg t t cc t caat gacac	1740
gt ct ct gcct cacagct gct t caggat cca gcat t at gct ggaaaggt gc t gt accaggt	1800
ggaaggat t c gt t gacaaaa acaat gacct t ct ct at cga gacct gt ccc aagccat gt g	1860
gaaggccagc cat gccct ca t caagt ct t t gt t ccccgaa gggaaat cccg ccaagat caa	1920
cct gaaaagg cct cct acag caggct caca gt t caaggca t ccgt ggcca ct ct gat gaa	1980
aaacct acag accaagaacc caaact at at t aggt gt at c aaaccgaat g at aaaaaagc	2040
agcacacat c t t caacgagg ct ct agt gt g t cat cagat c aggt acct gg ggct t t t gga	2100
gaacgt ccga gt gcggaggg caggct acgc ct t caggcag gcct at gaac ct t gcct aga	2160
aagat acaaa at gct t t gt a aacaaacat g gcct cat t gg aaaggaccag ccaggt ct gg	2220
t gt ggaggt c ct at t t aat g aat t agaaat t cccgt ggaa gaat act cct t t ggt agat c	2280
aaagat at t c at ccgaaacc caagaacat t at t caaat t a gaagacct ga ggaagcaacg	2340
cct ggaggac t t ggccact c t cat t cagaa gat at at cgg ggggt ggaaat gccgcacaca	2400
ct t cct gct a at gaaaaaaaa gccaaat t gt gat t gccgcc t ggt acagga gat at gcgca	2460
acaaaagagg t accagcaga caaagagt t c cgcct t agt a at t cagt ct t at at ccgggg	2520
t t ggaaggct cgaaaaat t c t gcgggaact gaagcat caa aagcgct gt a aggaagcagt	2580
cacgaccat t gct gcat at t ggcat gggac ccaggt acgt agagaat aca ggaaat t ct t	2640
cagagccaat gct ggaaaga aaat ct at ga gt t t acgct t cagagaat t g t gcaaaaat a	2700
ct t ct t ggaa at gaaaaat a agat gcct t c ct t at ct cca at agacaaga at t ggccct c	2760
aagacct t ac t t at t ct t gg at t ct act ca caaggagct a aaaaggat t t t cact t gt g	2820
gaggt gt aaa aaat acaggg accaat t cac agaccagcag aaact t at t t at gaagagaa	2880
act agaagcc agt gaact ct t caaagacaa gaaggct t t a t acccat ct a gt gt t gggca	2940
accat t ccaa ggggct t acc t ggaaat caa caagaacccc aagt at aaga aact caaaga	3000
t gccat t gaa gaaaagat ca t cat t gct ga agt cgt gaac aaaat t aacc gt gct aat gg	3060
gaagagt aca t ct cggat t t t cct ct t aac aaacaat aat ct cct t ct t g ct gacaaaaa	3120
gt ct ggacaa at caagt cag aggt t ccat t ggt ggat gt g accaaggt at caat gagct c	3180
acaaaat gat ggct t ct t cg ccgt ccacct caaagagggc t cagaagcag ct agt aaagg	3240
agact t t ct c t t cagcagt g at cacct gat t gaaat ggcc accaagct ct at cgcacaac	3300
t ct cagccaa accaaacaga agct caat at t gagat t t cc gat gagt t cc t ggt acagt t	3360

N3027PCT\_sequ.list.txt

cagacaggac aaagt atgtg tgaagtttat tcagggaac cagaaaaatg ggagtgtccc 3420  
aacatgtaaa cgaaaaaaca accgtctcct tgaagttgct gtcccttaac tggcgccctcc 3480  
tctctacttt catggacttg ttcctttgta atagtgaat ttggttttgt tttatttggg 3540  
gttcatitga tgtttgggaa tcaccaaagg cttttagagt tctttggcaa aataaaaat a 3600  
tttgactaat caatttttat tatgggaata gttttaacct ttcaaataca tgttctgtcc 3660  
tggagcagga ttgtagaaac taacagtgtc tattttcatg tctgatgtgt tcttccttta 3720  
gtcatcatgt taggtctgtg taccctaaat cagcatatta ctcataaatc attaattaat 3780  
ataagcatag gaaatggctc taaaagat ac tgcattcatt catcagatatt ttattccatg 3840  
cctactctat gctaggcact gtgctagatg gtatgaaaac ttattaggaa cctttttgtt 3900  
tttgagacca ttgcatctg gctggtttgt gctggtttaa cgacatctaa gaaggtttag 3960  
aaatggtagag accaaaacaa taactgttaa tgaaggacag cattattagg aaccctgtag 4020  
tatgatattt aacaatatag gcttcaagaa gggctggtcc taagaggggg cagaaatgaa 4080  
tgaccagggtt aaatccctct acatgtggtt tctgtttgaa aaaaagaaaa ctgacatttg 4140  
aacaggactt ttaattttgt taaaactctg gtaattactt gtacagt ag aaaatagaag 4200  
tcatcttat tttagaaaaa gtgacagaag cagtcagta agattat atg tttctgtttc 4260  
tggtaaat ac catatatgat cctcgaaatg ataatatctc cagaatatg tttcaccca 4320  
aatttgagta gatatttt aa acacctaca aagt aaagggt ctaaaagcca ttcagatagc 4380  
agtaaaacat tctgtatgat gtgcaataaa acatccaaga tcttttttga aagttttatt 4440  
tataatat ac atttttgtat gagaaagggtg attggtagag ggtgcctatt ttagtcatgg 4500  
atcaaaattt gtgt aacttg cagggtttc tttctttttc ttcaaattta caagggttca 4560  
ttttggaaac tacatttt aa actttggaat caaattgttt ctattttggg aggat aatgt 4620  
atatacattg gtattatgtt aaataataaa attgttctaa tttggtgcca tttcctgaat 4680  
cacaactgta tttttgtatc tcaagctatt ttcatatgtt atgtgtcaat gtatcatctc 4740  
tcagaaagggt tttacaatcc aaacattata tgttctctgt gtaactgaat ttcacttatc 4800  
ttttataaac cagaaacatt aattg 4825

<210> 16  
<211> 1078  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1078)  
<223> myosin IB (MYO1B)

<400> 16

Met Ala Lys Met Glu Val Lys Thr Ser Leu Leu Asp Asn Met Ile Gly  
1 5 10 15

N3027PCT\_sequ.list.txt

Val Gly Asp Met Val Leu Leu Glu Pro Leu Asn Glu Glu Thr Phe Ile  
20 25 30

Asn Asn Leu Lys Lys Arg Phe Asp His Ser Glu Ile Tyr Thr Tyr Ile  
35 40 45

Gly Ser Val Val Ile Ser Val Asn Pro Tyr Arg Ser Leu Pro Ile Tyr  
50 55 60

Ser Pro Glu Lys Val Glu Glu Tyr Arg Asn Arg Asn Phe Tyr Glu Leu  
65 70 75 80

Ser Pro His Ile Phe Ala Leu Ser Asp Glu Ala Tyr Arg Ser Leu Arg  
85 90 95

Asp Gln Asp Lys Asp Gln Cys Ile Leu Ile Thr Gly Glu Ser Gly Ala  
100 105 110

Gly Lys Thr Glu Ala Ser Lys Leu Val Met Ser Tyr Val Ala Ala Val  
115 120 125

Cys Gly Lys Gly Ala Glu Val Asn Gln Val Lys Glu Gln Leu Leu Gln  
130 135 140

Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn  
145 150 155 160

Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Ile Glu Phe Asp Phe  
165 170 175

Lys Gly Asp Pro Leu Gly Gly Val Ile Ser Asn Tyr Leu Leu Glu Lys  
180 185 190

Ser Arg Val Val Lys Gln Pro Arg Gly Glu Arg Asn Phe His Val Phe  
195 200 205

Tyr Gln Leu Leu Ser Gly Ala Ser Glu Glu Leu Leu Asn Lys Leu Lys  
210 215 220

Leu Glu Arg Asp Phe Ser Arg Tyr Asn Tyr Leu Ser Leu Asp Ser Ala  
225 230 235 240

Lys Val Asn Gly Val Asp Asp Ala Ala Asn Phe Arg Thr Val Arg Asn  
245 250 255

Ala Met Gln Ile Val Gly Phe Met Asp His Glu Ala Glu Ser Val Leu  
260 265 270

Ala Val Val Ala Ala Val Leu Lys Leu Gly Asn Ile Glu Phe Lys Pro  
275 280 285

Glu Ser Arg Val Asn Gly Leu Asp Glu Ser Lys Ile Lys Asp Lys Asn

290

295

300

G u Leu Lys G u I l e C y s G u Leu Thr G y I l e A s p G n Ser Val Leu  
305 310 315 320

G u Arg A l a P h e S e r P h e Arg Thr Val G u A l a L y s G n G u L y s Val  
325 330 335

Ser Thr Thr L e u A s n Val A l a G n A l a T y r T y r A l a Arg A s p A l a Leu  
340 345 350

A l a L y s A s n L e u T y r S e r Arg L e u P h e S e r T r p L e u Val A s n Arg I l e  
355 360 365

A s n G u S e r I l e L y s A l a G n Thr L y s Val Arg L y s L y s Val M e t G y  
370 375 380

Val Leu A s p I l e T y r G y P h e G u I l e P h e G u A s p A s n Ser P h e G u  
385 390 395 400

G n P h e I l e I l e A s n T y r C y s A s n G u L y s L e u G n G n I l e P h e I l e  
405 410 415

G u Leu Thr L e u L y s G u G u G n G u G u T y r I l e Arg G u A s p I l e  
420 425 430

G u T r p Thr H i s I l e A s p T y r P h e A s n A s n A l a I l e I l e C y s A s p Leu  
435 440 445

I l e G u A s n A s n Thr A s n G y I l e L e u A l a M e t L e u A s p G u G u C y s  
450 455 460

L e u Arg P r o G y Thr Val Thr A s p G u Thr P h e L e u G u L y s L e u A s n  
465 470 475 480

G n Val C y s A l a Thr H i s G n H i s P h e G u Ser Arg M e t Ser L y s C y s  
485 490 495

Ser Arg P h e L e u A s n A s p Thr Ser L e u P r o H i s Ser C y s P h e Arg I l e  
500 505 510

G n H i s T y r A l a G y L y s Val L e u T y r G n Val G u G y P h e Val A s p  
515 520 525

L y s A s n A s n A s p L e u L e u T y r Arg A s p L e u Ser G n A l a M e t T r p L y s  
530 535 540

A l a Ser H i s A l a L e u I l e L y s Ser L e u P h e P r o G u G y A s n P r o A l a  
545 550 555 560

L y s I l e A s n L e u L y s Arg P r o P r o Thr A l a G y Ser G n P h e L y s A l a  
565 570 575

N3027PCT\_sequ.list.txt

Ser Val Ala Thr 580 Leu Met Lys Asn Leu 585 Gln Thr Lys Asn Pro 590 Asn Tyr

Ile Arg Cys 595 Ile Lys Pro Asn Asp 600 Lys Lys Ala Ala His 605 Ile Phe Asn

Glu Ala 610 Leu Val Cys His Gln 615 Ile Arg Tyr Leu Gly 620 Leu Leu Glu Asn

Val 625 Arg Val Arg Arg Ala 630 Gly Tyr Ala Phe Arg 635 Gln Ala Tyr Glu Pro 640

Cys Leu Glu Arg Tyr 645 Lys Met Leu Cys Lys 650 Gln Thr Trp Pro His 655 Trp

Lys Gly Pro Ala 660 Arg Ser Gly Val Glu 665 Val Leu Phe Asn Glu 670 Leu Glu

Ile Pro Val 675 Glu Glu Tyr Ser Phe 680 Gly Arg Ser Lys Ile Phe 685 Ile Arg

Asn Pro 690 Arg Thr Leu Phe Lys 695 Leu Glu Asp Leu Arg 700 Lys Gln Arg Leu

Glu 705 Asp Leu Ala Thr Leu 710 Ile Gln Lys Ile Tyr 715 Arg Gly Trp Lys Cys 720

Arg Thr His Phe Leu 725 Leu Met Lys Lys Ser 730 Gln Ile Val Ile Ala 735 Ala

Trp Tyr Arg Arg 740 Tyr Ala Gln Gln Lys 745 Arg Tyr Gln Gln Thr 750 Lys Ser

Ser Ala Leu 755 Val Ile Gln Ser Tyr 760 Ile Arg Gly Trp Lys 765 Ala Arg Lys

Ile Leu 770 Arg Glu Leu Lys His 775 Gln Lys Arg Cys Lys 780 Glu Ala Val Thr

Thr Ile Ala Ala Tyr Trp 790 His Gly Thr Gln Val 795 Arg Arg Glu Tyr Arg 800

Lys Phe Phe Arg Ala 805 Asn Ala Gly Lys Lys 810 Ile Tyr Glu Phe Thr 815 Leu

Gln Arg Ile Val 820 Gln Lys Tyr Phe Leu 825 Glu Met Lys Asn Lys 830 Met Pro

Ser Leu Ser 835 Pro Ile Asp Lys Asn 840 Trp Pro Ser Arg Pro 845 Tyr Leu Phe

N3027PCT\_sequ.list.txt

Leu Asp Ser Thr His Lys Glu Leu Lys Arg Ile Phe His Leu Trp Arg  
 850 855 860  
 Cys Lys Lys Tyr Arg Asp Gln Phe Thr Asp Gln Gln Lys Leu Ile Tyr  
 865 870 875 880  
 Glu Glu Lys Leu Glu Ala Ser Glu Leu Phe Lys Asp Lys Lys Ala Leu  
 885 890 895  
 Tyr Pro Ser Ser Val Gly Gln Pro Phe Gln Gly Ala Tyr Leu Glu Ile  
 900 905 910  
 Asn Lys Asn Pro Lys Tyr Lys Lys Leu Lys Asp Ala Ile Glu Glu Lys  
 915 920 925  
 Ile Ile Ile Ala Glu Val Val Asn Lys Ile Asn Arg Ala Asn Gly Lys  
 930 935 940  
 Ser Thr Ser Arg Ile Phe Leu Leu Thr Asn Asn Asn Leu Leu Leu Ala  
 945 950 955 960  
 Asp Gln Lys Ser Gly Gln Ile Lys Ser Glu Val Pro Leu Val Asp Val  
 965 970 975  
 Thr Lys Val Ser Met Ser Ser Gln Asn Asp Gly Phe Phe Ala Val His  
 980 985 990  
 Leu Lys Glu Gly Ser Glu Ala Ala Ser Lys Gly Asp Phe Leu Phe Ser  
 995 1000 1005  
 Ser Asp His Leu Ile Glu Met Ala Thr Lys Leu Tyr Arg Thr Thr  
 1010 1015 1020  
 Leu Ser Gln Thr Lys Gln Lys Leu Asn Ile Glu Ile Ser Asp Glu  
 1025 1030 1035  
 Phe Leu Val Gln Phe Arg Gln Asp Lys Val Cys Val Lys Phe Ile  
 1040 1045 1050  
 Gln Gly Asn Gln Lys Asn Gly Ser Val Pro Thr Cys Lys Arg Lys  
 1055 1060 1065  
 Asn Asn Arg Leu Leu Glu Val Ala Val Pro  
 1070 1075  
 <210> 17  
 <211> 4973  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature

N3027PCT\_sequ. list . . txt

<222> (1) . . (4973)

<223> myosin IC (MYO1C)

<400> 17

```

gggccaagag gcctcccagt cagacctgga cggctccagc cgtgtcctga ggagctggac      60
cagccacatc ccctggggct gcagttgaag cagaaccaag tggccatccc ggcgttagac      120
cgtaggttcc tggctccgga gtggtcggag cccgccagt gggcaggcagc tcttgctcac      180
aggccgcggt gcccaggccg ctggctctcc gcagggcgga atggcgctgc aagtggagct      240
ggtaccacc ggggagatca tccgcgtggt tcatccccac aggcctgca agcttgcct      300
gggcagt gac ggggttcggg tgaccatgga gagtgcgctc accgccctg accgggtggg      360
ggtgcaggat ttctgtgctgc ttggagaactt caccagcgag gccgccttca tcgagaacct      420
gcggcggcga tttcgggaga atctcatcta cacctacatt ggccccgtcc tggctctgt      480
caatccctac cgggacctgc agatctacag ccggcagcat atggagcgtt accgtggcgt      540
cagcttctat gaagtcccc ctcacctgtt tggcgtggcg gacactgtgt accgagcact      600
gcgcacggag cgtcgggacc aggtgtgat gatctctggg gagagcgggg caggcaagac      660
cgaggccacc aagaggctgc tgcagttcta tgcagagacc tggccagccc ccgagcgcgg      720
aggtgccgtg cgggaccggc tgcctacagag caaccgggtg ctggaggcct ttggaaatgc      780
caagaccctc cggaacgat a actccagcag gttcggaag tcatggatg tgcagtttga      840
cttcaagggg gccccgtgg gtggccacat cctcagttac ctctggaaa agtcacgagt      900
ggtgcaccag aatcatgggg agcggaaactt ccacatcttc taccagctgc tggagggggg      960
cgaggaggag actcttcgca ggctgggctt ggaacggaac cccagagct acctgtacct      1020
ggtgaagggc cagtgtgcca aagtctcctc catcaacgac aagagt gact ggaaggtcgt      1080
caggaaggct ctgacagtca ttgat ttcac cgaggatgaa gtggaggacc tgcctgagcat      1140
cgtggccagc gtccttcat t tgggcaacat ccactttgct gccaacgagg agagcaatgc      1200
ccaggtcacc accgagaacc agctcaagt a tctgaccagg ctctcagcg tggagggtc      1260
gacgctgcga gaagccctga cacacaggaa gatcatcgcc aagggggagg agctcctgag      1320
cccgtgaac ctggagcagg ccgcgtacgc acgagacgcc ctcgccaagg ctgtgtacag      1380
ccgcactttt acctggctcg t cgggaagat caacaggctcg ctggcctcca aggacgtgga      1440
gagccccagc tggcggagca ccacggttct cgggctcctg gatatttat g gctttgaagt      1500
gtttcagcat aacagctttg agcagttctg catcaattac tgcaacgaga agctgcagca      1560
gctcttcatc gagctcacgc tcaagtcgga gcaggaggag tacgaggcag agggcatcgc      1620
gtgggagccc gtccagtatt tcaacaacaa aatcatctgt gatctggtgg aggagaagt t      1680
taagggcatc atctcgattt tggatgagga gtgtctgcgc cccggggagg ccacagacct      1740
gaccttctg gagaagctgg aggatactgt caagcaccat ccacacttcc tgacgcacaa      1800
gctggctgac cagcggacca ggaaatctct gggccgaggg gaattccgcc t tctgacta      1860
tgccgggggag gtgacctaca gcgtgaccgg gtttctggac aaaaacaatg accttctctt      1920
ccggaacctt aaggagacca tgtgtagctc aaagaatccc attatgagcc agtgctttga      1980

```

N3027PCT\_sequ. list . . txt

ccggagcgag	ct cagt gaca	agaagcggcc	agagacggt c	gccacccagt	t caagat gag	2040
cct cct gcag	ct ggt ggaga	t cct gcagt c	t aaggagccc	gcct acgt cc	gct gcat caa	2100
acccaat gat	gccaaacagc	ccggccgct t	t gacgaggt g	ct gat ccgcc	accaggt gaa	2160
gt acct gggg	ct gt t ggaaa	acct gcgcgt	gcgcagagcc	ggct t t gcct	at cgccgcaa	2220
at acgaagct	t t cct gcaaa	ggt acaagt c	act gt gccca	gagacgt ggc	ccacgt gggc	2280
aggacggccg	caggat gggg	t ggct gt gct	ggt ccgacac	ct gggct aca	agccagaaga	2340
gt acaagat g	ggcaggacca	agat ct t cat	ccgct t cccc	aagaccct gt	t t gccacaga	2400
ggat gccct g	gaggt ccggc	ggcagagcct	ggccacaaag	at ccaagct g	cct ggagggg	2460
ct t t cact gg	cggcagaaat	t cct ccgggt	gaagagat ca	gccat ct gca	t ccagt cgt g	2520
gt ggcgt gga	acact gggcc	ggaggaaggc	agccaagagg	aagt gggcgg	cacagaccat	2580
ccggcggct c	at ccgaggct	t cgt cct gcg	ccacgcccc	cgct gccccg	agaacgcct t	2640
ct t cct ggac	cat gt gcgca	cct ct t t t t	gct aaacct g	aggcggcagc	t gccccagaa	2700
t gt cct ggac	acct cgt ggc	ccacgcccc	acct gccct g	cgt gaggcct	cagagct t ct	2760
gcgggagt t g	t gcat aaaga	acat ggt gt g	gaaat act gc	cggagt at ca	gccct gagt g	2820
gaagcagcag	ct gcagcaga	aggccgt ggc	t agt gagat c	t t caagggca	agaaggat aa	2880
t t accct cag	agt gt accca	ggct ct t cat	cagcact cgg	ct t ggt acag	at gagat cag	2940
cccccgagt g	ct gcaggcct	t gggct ct ga	gccccat t cag	t at gcggt gc	ct gt t gt gaa	3000
at acgaccgc	aagggt aca	agcct cgct c	ccggcagct g	ct gct cacgc	ccaacgccgt	3060
cgt cat cgt g	gaggacgcc	aagt caagca	gaggat t gat	t acgccaacc	t gaccggaat	3120
ct ct gt cagc	agcct gagcg	acagt ct t t t	t gt gct t cat	gt acagcgt g	cggacaat aa	3180
gcaaaaggga	gat gt ggt gc	t gcagagt ga	ccacgt gat t	gagacgct ga	ccaagacagc	3240
cct cagt gcc	aaccgcgt ga	acagcat caa	cat caaccag	ggcagcat ca	cgt t t gcagg	3300
gggccccggc	aggat ggca	ccat t gact t	cacacccggc	t cggagct gc	t cat caccaa	3360
ggccaagaac	gggcacct gg	ct gt ggt cgc	cccacggct g	aat t ct cgg	gat aaaggcg	3420
cccact ggac	cct cccaacg	cccaat gct t	t gct t t t ct c	ct cct cccct	t cccagt t ac	3480
caaagact cg	aact t ccaga	cagggacca	gggacacccc	gaagcccacc	t gcaat ct cc	3540
cacct cct gc	ccat ccct ct	ct t gaggag	cagcaggggc	caggagct ac	cccaggagt g	3600
ggccaggccg	ggccacagca	at aggaaagc	caggggccaga	gcgagccat g	ccagccct ac	3660
t gccgat gcc	aaat at t t ga	gagaaggga	ct t t t gct ga	gggt t t t ct ct	gaggt t t t t t	3720
t gat gct t t a	t aggaact a	t t t t t aaaa	aaagccat t t	cccacccaag	gacacagt gg	3780
at gt gt t t t c	cct gact cca	gcagggcaag	gaat gt agcc	gagaggt t gt	gt gggct ggg	3840
ct ct ggt gcc	ct ct t ccct g	gccaggacac	ct ct cct cct	gat t ccct t g	gcacct t gt c	3900
t t t ct gt ct g	t t t acct gt c	t cct gcct g	cccat ct gca	t ct t t t gcag	cccact ct ga	3960
ct t ccat ct g	ggggct gaga	ccaccct t gc	ct gccccct t	ct t t ct gcct	t aagaat gt c	4020

N3027PCT\_sequ.list.txt

```

cttttaggct gggcatggtg gctcacgcct gtaacccag cactttggga ggcggagacg 4080
ggcagat aac ctgaggtcag gat ttcgaga ccaacctgac ctacatggag aaactccgcc 4140
tctagt aaaa atacaaaatt agccgggcat ggtggtgcac gcctctaatc ccagctactc 4200
gggaggctga ggcaggagaa t cacttgaac ccgggaagt g gaggttgcag t gagccaaga 4260
gtacaccact gcactccagc ctgggcaaca gagcgagact ccgtctt aaa aaaaaaaaaa 4320
aagaacgccc ttttactgtc ctcatcatcc cagtttgagg cagtgtgga gtggggaagg 4380
ccgtcttaga ccatagaggt t ggaagacgc tgagagatca tccagcccag ccccttgatg 4440
ttacagagca gaagacagat gcccaaacag gagaaggcac ttgccacgg tcatacggca 4500
ggttgccaca aaaccaagat ggcagccctt cctcagcgtg cctcactgcc actcccagag 4560
ccaggagacc ccataaaacc cacatcatgt cttaagagta tatctggctc cttgaccagc 4620
aatcgccct gggagccacc aggtgggaaa agcgccctctg ccagagtcga ggccttggga 4680
tgacagacag cttgcccgca cactcgggcc ccactcaagg atgtagggcc ttttctggcc 4740
cctgaccct cctggcatg ggagcgtggg gacggggctg gccttgggag gagcggcagg 4800
ggcatcacct ccttctgctg cttctccctg ctctaccct caagggcctg ggggctgcc 4860
agctgcctct atgcccttct gggggctctca gccactgct gacacttctg caatccagag 4920
aaacactaaa taaagcaata cgtgtttgcc aaaaaaaaaa aaaaaaaaaa aaa 4973

```

<210> 18  
 <211> 1063  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1063)  
 <223> myosin IC (MYO1C)

<400> 18

Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val  
1 5 10 15

Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val  
20 25 30

Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val  
35 40 45

Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile  
50 55 60

Glu Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile  
65 70 75 80

Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr  
85 90 95

N3027PCT\_sequ.list.txt

Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val  
100 105 110

Pro Pro His Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg  
115 120 125

Thr Glu Arg Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala  
130 135 140

Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr  
145 150 155 160

Cys Pro Ala Pro Glu Arg Gly Gly Ala Val Arg Asp Arg Leu Leu Gln  
165 170 175

Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn  
180 185 190

Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Val Gln Phe Asp Phe  
195 200 205

Lys Gly Ala Pro Val Gly Gly His Ile Leu Ser Tyr Leu Leu Glu Lys  
210 215 220

Ser Arg Val Val His Gln Asn His Gly Glu Arg Asn Phe His Ile Phe  
225 230 235 240

Tyr Gln Leu Leu Glu Gly Gly Glu Glu Glu Thr Leu Arg Arg Leu Gly  
245 250 255

Leu Glu Arg Asn Pro Gln Ser Tyr Leu Tyr Leu Val Lys Gly Gln Cys  
260 265 270

Ala Lys Val Ser Ser Ile Asn Asp Lys Ser Asp Trp Lys Val Val Arg  
275 280 285

Lys Ala Leu Thr Val Ile Asp Phe Thr Glu Asp Glu Val Glu Asp Leu  
290 295 300

Leu Ser Ile Val Ala Ser Val Leu His Leu Gly Asn Ile His Phe Ala  
305 310 315 320

Ala Asn Glu Glu Ser Asn Ala Gln Val Thr Thr Glu Asn Gln Leu Lys  
325 330 335

Tyr Leu Thr Arg Leu Leu Ser Val Glu Gly Ser Thr Leu Arg Glu Ala  
340 345 350

Leu Thr His Arg Lys Ile Ile Ala Lys Gly Glu Glu Leu Leu Ser Pro  
355 360 365

N3027PCT\_sequ.list.txt

Leu Asn Leu Glu Gln Ala Ala Tyr Ala Arg Asp Ala Leu Ala Lys Ala  
370 375 380

Val Tyr Ser Arg Thr Phe Thr Trp Leu Val Gly Lys Ile Asn Arg Ser  
385 390 395 400

Leu Ala Ser Lys Asp Val Glu Ser Pro Ser Trp Arg Ser Thr Thr Val  
405 410 415

Leu Gly Leu Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln His Asn Ser  
420 425 430

Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu  
435 440 445

Phe Ile Glu Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Glu Ala Glu  
450 455 460

Gly Ile Ala Trp Glu Pro Val Gln Tyr Phe Asn Asn Lys Ile Ile Cys  
465 470 475 480

Asp Leu Val Glu Glu Lys Phe Lys Gly Ile Ile Ser Ile Leu Asp Glu  
485 490 495

Glu Cys Leu Arg Pro Gly Glu Ala Thr Asp Leu Thr Phe Leu Glu Lys  
500 505 510

Leu Glu Asp Thr Val Lys His His Pro His Phe Leu Thr His Lys Leu  
515 520 525

Ala Asp Gln Arg Thr Arg Lys Ser Leu Gly Arg Gly Glu Phe Arg Leu  
530 535 540

Leu His Tyr Ala Gly Glu Val Thr Tyr Ser Val Thr Gly Phe Leu Asp  
545 550 555 560

Lys Asn Asn Asp Leu Leu Phe Arg Asn Leu Lys Glu Thr Met Cys Ser  
565 570 575

Ser Lys Asn Pro Ile Met Ser Gln Cys Phe Asp Arg Ser Glu Leu Ser  
580 585 590

Asp Lys Lys Arg Pro Glu Thr Val Ala Thr Gln Phe Lys Met Ser Leu  
595 600 605

Leu Gln Leu Val Glu Ile Leu Gln Ser Lys Glu Pro Ala Tyr Val Arg  
610 615 620

Cys Ile Lys Pro Asn Asp Ala Lys Gln Pro Gly Arg Phe Asp Glu Val  
625 630 635 640

Leu Ile Arg His Gln Val Lys Tyr Leu Gly Leu Leu Glu Asn Leu Arg  
Page 73

645

650

655

Val Arg Arg Ala Gly Phe Ala Tyr Arg Arg Lys Tyr Glu Ala Phe Leu  
660 665 670

Gln Arg Tyr Lys Ser Leu Cys Pro Glu Thr Trp Pro Thr Trp Ala Gly  
675 680 685

Arg Pro Gln Asp Gly Val Ala Val Leu Val Arg His Leu Gly Tyr Lys  
690 695 700

Pro Glu Glu Tyr Lys Met Gly Arg Thr Lys Ile Phe Ile Arg Phe Pro  
705 710 715 720

Lys Thr Leu Phe Ala Thr Glu Asp Ala Leu Glu Val Arg Arg Gln Ser  
725 730 735

Leu Ala Thr Lys Ile Gln Ala Ala Trp Arg Gly Phe His Trp Arg Gln  
740 745 750

Lys Phe Leu Arg Val Lys Arg Ser Ala Ile Cys Ile Gln Ser Trp Trp  
755 760 765

Arg Gly Thr Leu Gly Arg Arg Lys Ala Ala Lys Arg Lys Trp Ala Ala  
770 775 780

Gln Thr Ile Arg Arg Leu Ile Arg Gly Phe Val Leu Arg His Ala Pro  
785 790 795 800

Arg Cys Pro Glu Asn Ala Phe Phe Leu Asp His Val Arg Thr Ser Phe  
805 810 815

Leu Leu Asn Leu Arg Arg Gln Leu Pro Gln Asn Val Leu Asp Thr Ser  
820 825 830

Trp Pro Thr Pro Pro Pro Ala Leu Arg Glu Ala Ser Glu Leu Leu Arg  
835 840 845

Glu Leu Cys Ile Lys Asn Met Val Trp Lys Tyr Cys Arg Ser Ile Ser  
850 855 860

Pro Glu Trp Lys Gln Gln Leu Gln Gln Lys Ala Val Ala Ser Glu Ile  
865 870 875 880

Phe Lys Gly Lys Lys Asp Asn Tyr Pro Gln Ser Val Pro Arg Leu Phe  
885 890 895

Ile Ser Thr Arg Leu Gly Thr Asp Glu Ile Ser Pro Arg Val Leu Gln  
900 905 910

Ala Leu Gly Ser Glu Pro Ile Gln Tyr Ala Val Pro Val Val Lys Tyr  
915 920 925

N3027PCT\_sequ.list.txt

Asp Arg Lys Gly Tyr Lys Pro Arg Ser Arg Gln Leu Leu Leu Thr Pro  
930 935 940

Asn Ala Val Val Ile Val Glu Asp Ala Lys Val Lys Gln Arg Ile Asp  
945 950 955 960

Tyr Ala Asn Leu Thr Gly Ile Ser Val Ser Ser Leu Ser Asp Ser Leu  
965 970 975

Phe Val Leu His Val Gln Arg Ala Asp Asn Lys Gln Lys Gly Asp Val  
980 985 990

Val Leu Gln Ser Asp His Val Ile Glu Thr Leu Thr Lys Thr Ala Leu  
995 1000 1005

Ser Ala Asn Arg Val Asn Ser Ile Asn Ile Asn Gln Gly Ser Ile  
1010 1015 1020

Thr Phe Ala Gly Gly Pro Gly Arg Asp Gly Thr Ile Asp Phe Thr  
1025 1030 1035

Pro Gly Ser Glu Leu Leu Ile Thr Lys Ala Lys Asn Gly His Leu  
1040 1045 1050

Ala Val Val Ala Pro Arg Leu Asn Ser Arg  
1055 1060

<210> 19  
<211> 5182  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(5182)  
<223> myosin ID (MYO1D)

<400> 19  
cgcgctggcg ccatggcgga gcaggagagc ctggaattcg gcaaggcaga cttcgtgctg 60  
atggacaccg tctccatgcc cgagttcatg gccaacctca ggctcagatt tgaaaaaggg 120  
cgcatctata cgttcat tgg agaagtcgtc gt t t c t g t g a accct t a c a a g t t g t t g a a c 180  
atctatggaa gagacacaat tgagcagtat aaaggccgtg agctgtatga gagaccgcct 240  
cacctttttg ctattgcgga tgctgcttac aaggctatga agaggcgatc aaaagacact 300  
tgtattgtga tatcagggga aagtggagct ggtaaaacgg aagccagt aa gtacattatg 360  
cagtatattg cggccatcac caacccagc cagagagcag aggttgaaag agtgaagaat 420  
atgttgctta agtccaactg tgttttggaa gcttttggaa atgccaaaac caaccgtaat 480  
gacaactcaa gcaggtttgg aaaatacatg gatatacaact ttgacttcaa gggtgaccct 540  
attgggtgggc atatacaataa ctacttacta gaaaagtc c gagtgattgt gcaacagcca 600

N3027PCT\_sequ.list.txt

ggagaaagaa gctttcat tctctatcag ctactccaag gaggttcaga acaaatgct a	660
cgctctctac atctccagaa atccctttca tctctacaact atattcatgt gggagct caa	720
ttaaagtctt ctatcaatga t gctgccgaa ttcagagttg t t gct gat gc cat gaaagt c	780
attggcttca aacctgagga gatccaaaca gtgtataga ttttggctgc t attctgcac	840
ttgggaaatt taaaattt gt agtagatggg gacacgcctc t t att gagaa tggcaaagt a	900
gtatctatca tagcagaatt gctctctact aagacagat a tgggt gagaa agcccttctt	960
taccggactg tggccacagg ccgtgacatc attgacaagc agcacacaga acaagaggcc	1020
agctacggca gagacgcctt tggcaaggca atatagagc gccttttttg ttggatcgtt	1080
actcgcatca atgatattat tggaggtcaag aactatgaca ccacaatcca tgggaaaaac	1140
actgttattg gtgtcttggg tatctatggc tttgaaatct tgcacaacaa cagttttgaa	1200
caattctgta tcaattactg caatgagaaa ctgcagcagc tatttattca gctggttctg	1260
aagcaagaac aagaggaata ccagcgggaa gggatccct ggaaacat at t gact act t c	1320
aacaatcaga tcat t g t ga cctcgtggag caacagcaca aagggtat cat t gcaat cct t	1380
gatgatgctt gcatgaatgt cggcaaagt c accgat gaaa t g t t c t t ga agcact t aac	1440
agt aaat t gg gcaaacacgc ccat t t t cc agccgaaagc tctgtgcctc agacaaaatt	1500
ctggagtttg atcgagattt t cgaattcga cattatgcag gcgatgtagt ctattctgtc	1560
attggtttta ttgacaaaaa taaagat act t t att t caag atttcaagcg cctt atgtat	1620
aacagttcaa atcctgtgct caagaat at g tggcctgaag gcaaact gag cattacagag	1680
gtgaccaagc gacctctgac t gctgctacc t t g t t t aaga attctatgat t gctctagt a	1740
gacaaccttg catcaaagga accatattac gt t cgt t gca tcaaacccaa t gacaagaaa	1800
tctccacaga tatttgatga tgaacgctgc cggcaccaag tagaatatct tggactactg	1860
gaaaatgtga gagtgcgtcg ggcaggattt gccttccgcc agacat acga gaagt t t c t t	1920
cacaggtat a agatgatctc tgaattcacc tggcccaacc atgaccttcc ttcagacaaa	1980
gaggctgtca agaaactaat tgaacgggtgt ggttttcagg atgatgtagc t t at gggaag	2040
acaaaaattt tcat t cgaac accccgaaca t t g t t t acct t ggaagaact ccgtgccag	2100
atgctcat aa ggattgtcct ct t t c t acaa aaggtgtggc ggggcaccct ggcccgcag	2160
cggtacaaaa gaaccaaggc agctctgaca ataatcaggt actaccggcg ctacaaagt g	2220
aagt cgt aca tccacgaggt ggccagacgc t t ccatggcg tcaagaccat gcgagact ac	2280
gggaagcacg tgaagtggcc aagccctcct aaagt t c t t c gccgt t t t ga ggaggccct g	2340
cagacgattt tcaatagatg gagagcatcc cagctcatca agagcat t cc ggcctcagac	2400
ctgccccagg t cagggcaaa ggt t gcagcc gtggaaatgt tgaagggtca aagggtgac	2460
ctcgggctcc agagggcctg ggagggaac t at c t t g c t t caaagccaga t acacctcag	2520
acctcaggca cttttgtccc t g t t g c t aat gaattgaaac ggaaggacaa atacatgaat	2580
gtcctctttt cctgtcacgt ccgt aaggt a aatcgattt a gt aaggt gga agacagagca	2640

N3027PCT\_sequ. list .txt

at t t t t gt ca ct gaccgt ca cct gt at aaa at ggat ccca ct aaacagt a caaggt gat g	2700
aagact at cc ct ct at acaa t t t gact ggt ct gagt gt ct ccaat ggaaa ggaccaact t	2760
gt agt gt t cc at acgaaaga caacaaagac ct cat t gt ct gcct ct t cag caaacagcca	2820
acccat gaga gt cgaat t gg agaact t gt t ggagt gct gg t gaat cat t t caagagt gag	2880
aagcgccacc t t caagt gaa cgt caccaac ccagt acagt gcagcct gca cgggaagaag	2940
t gcaccgt ct ccgt ggagac gcggt caac cagccccagc ccgact t cac caagaat cgc	3000
t cgggct t ca t cct cagcgt gcccgggaac t gacgccccg cggaggcct g gcccggagcc	3060
cggccacact ccgagt cct g ggt cccagt c cagct gct gc ct cccaaccc at gcccgct a	3120
gaaacct gct gcgagggccc ct cccagagg agccccgccc ct gt aagat t t cct t cct gg	3180
t t t t ct gcct t t ggt at cat ct t cct ct gt cct t act gt c cacggt ccct gt t caat aag	3240
ccaaagaccc t ggt gccccg cccagacccc t gggct gacg t ccagaccaa t ct cacccca	3300
gaggcaact g gat ggt gcct t t agt t ggt g cggat gcccc gt ggccaggt caagt cagag	3360
cacct ggaca ggt gt cct cc ct gct gct ga ccct gcagag ggaaggggt g gggat gcagg	3420
accccgct ct gcgggagccc cat agccacc t ct ct t gccc aaggt gagcc agccct gggg	3480
accagct ca gggaggct ct gct cagagt t cggcggaccc accccaaccc aact cccagc	3540
cgccagccaa agccact ggg t gagcagagt caccacaggg gccagcccct cagccaggag	3600
ccagt ggag gagcggaaca gcccat ccag cagagt gagt ccat cct t cc caggt t ct cc	3660
cct gggagac t ccc t t t gcc accaaggccc ccaccagggc ct ct gaccac cgct ct ggag	3720
aggacagt gt ggc at gct cc aaggat cat c t t act t aact cgcagcct gt ggct gt ggt c	3780
ct ct t at aga t act t t cacc gt t t gcaggg t t gct aat ca gat acct gct gt caccacac	3840
t t ggg t cagg aacct aat g agaacgggga gct gccaggg t gagggcagc cct caggg t c	3900
ggccgct t t c cct ct ggacc acct cccgct gcgt t t cct a ct cagagaaa cagcaagggc	3960
gggg t caaga cacgggat ga cgggaagcag gaagcggggc agcagcacag cgt ggggt cc	4020
t ggcact gca ggccaggcca ggat gccac cccgccct ct acacggcccc t t ggggcct g	4080
cgcccg t gaa act ggt gcc a gggagcact g ccagct t gcc agt t t ct gcc cagcaaaagc	4140
acgt at gct t caggggcct t ct gagaccac ct t cccact gagccccagc t gct gagaag	4200
gcct t gaggg aagt agaggc t gggagcaaa t gccccat gc ggt gagagga t gaggggagc	4260
ct acgcct ca ggcat gt ggt gagaggat ga gggggaggga gccacgcct caggt ggagt	4320
gggcagaggt gcaagagagg gat gt act ga agct t ct t cc cgt cct gcc a cagacact t c	4380
t cct gcct t c ccacct gac ccggcagaac ccaccaagt g cct gt gt gca gcct cct gt g	4440
cct caccag ggcct gaccc cagagt ggt c ccaacaaccc ggt ct cat gc ccact cccca	4500
t cct gct t c ccaaaaat t g cact gt gt gc agt t t gcaac aaagaat ccc gct ggcat cc	4560
t gt cct t ggg aacct t t ct cat t ct ccaa gcct ggt cag ct gcct gcac aggcagaggt	4620
gccct cagcc caggt t agca acact cat ag t t t t gccaat t accagt aga cact agt gga	4680
accat ct aac t ggaact t cc t ct ct cct t c cact t at t t c ct caaact t g t t gct t t aca	4740

N3027PCT\_sequ.list.txt

ct agacacat gcaaatgtat gttttaaaca caccaaaaca gatcatgcca aatgagttgc 4800  
ctgtcaaagg ctggaggggca ggaggagggc ctgggtttgg gttctttcct cccagccttt 4860  
ggatggtgcc ttggggccct tagccccagc gccagggcct cccagctgag gccacaggac 4920  
aagcactttt ttatgatgta ctaaaagcca cagtatgtgg caactgcaaa aggatcagga 4980  
atttagggtat tgatctcggc cacgtgtccc gggcgctgag gggaaaggaa gcgggcatga 5040  
ttgtagacaa tgaggggggtt ctcttgatgt aatgaaatgc aattttatgg ttggtgcaa 5100  
aaactcctat ttccagtaaa attaacttta ttctaaagc atattttgat ttgccatcaa 5160  
gagcaataaa gcattaaatc tt 5182

<210> 20  
<211> 1006  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1006)  
<223> myosin ID (MYO1D)

<400> 20

Met Ala Glu Gln Glu Ser Leu Glu Phe Gly Lys Ala Asp Phe Val Leu  
1 5 10 15

Met Asp Thr Val Ser Met Pro Glu Phe Met Ala Asn Leu Arg Leu Arg  
20 25 30

Phe Glu Lys Gly Arg Ile Tyr Thr Phe Ile Gly Glu Val Val Val Ser  
35 40 45

Val Asn Pro Tyr Lys Leu Leu Asn Ile Tyr Gly Arg Asp Thr Ile Glu  
50 55 60

Gln Tyr Lys Gly Arg Glu Leu Tyr Glu Arg Pro Pro His Leu Phe Ala  
65 70 75 80

Ile Ala Asp Ala Ala Tyr Lys Ala Met Lys Arg Arg Ser Lys Asp Thr  
85 90 95

Cys Ile Val Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Ser  
100 105 110

Lys Tyr Ile Met Gln Tyr Ile Ala Ala Ile Thr Asn Pro Ser Gln Arg  
115 120 125

Ala Glu Val Glu Arg Val Lys Asn Met Leu Leu Lys Ser Asn Cys Val  
130 135 140

Leu Glu Ala Phe Gly Asn Ala Lys Thr Asn Arg Asn Asp Asn Ser Ser  
145 150 155 160

N3027PCT\_sequ.list.txt

Arg Phe Gly Lys Tyr<sub>165</sub> Met Asp Ile Asn Phe<sub>170</sub> Asp Phe Lys Gly Asp<sub>175</sub> Pro  
Ile Gly Gly His<sub>180</sub> Ile Asn Asn Tyr<sub>185</sub> Leu Leu Glu Lys Ser Arg<sub>190</sub> Val Ile  
Val Gln Gln<sub>195</sub> Pro Gly Glu Arg Ser<sub>200</sub> Phe His Ser Phe Tyr<sub>205</sub> Gln Leu Leu  
Gln Gly<sub>210</sub> Gly Ser Glu Gln Met<sub>215</sub> Leu Arg Ser Leu His<sub>220</sub> Leu Gln Lys Ser  
Leu Ser Ser Tyr Asn Tyr<sub>230</sub> Ile His Val Gly Ala<sub>235</sub> Gln Leu Lys Ser Ser<sub>240</sub>  
Ile Asn Asp Ala Ala<sub>245</sub> Glu Phe Arg Val Val<sub>250</sub> Ala Asp Ala Met<sub>255</sub> Lys Val  
Ile Gly Phe Lys<sub>260</sub> Pro Glu Glu Ile Gln Thr Val Tyr Lys Ile<sub>270</sub> Leu Ala  
Ala Ile Leu<sub>275</sub> His Leu Gly Asn Leu<sub>280</sub> Lys Phe Val Val Asp<sub>285</sub> Gly Asp Thr  
Pro Leu<sub>290</sub> Ile Glu Asn Gly Lys<sub>295</sub> Val Val Ser Ile Ile<sub>300</sub> Ala Glu Leu Leu  
Ser Thr Lys Thr Asp Met<sub>310</sub> Val Glu Lys Ala Leu<sub>315</sub> Leu Tyr Arg Thr Val<sub>320</sub>  
Ala Thr Gly Arg Asp<sub>325</sub> Ile Ile Asp Lys Gln His Thr Glu Gln Glu Ala<sub>335</sub>  
Ser Tyr Gly Arg<sub>340</sub> Asp Ala Phe Ala Lys<sub>345</sub> Ala Ile Tyr Glu Arg<sub>350</sub> Leu Phe  
Cys Trp Ile<sub>355</sub> Val Thr Arg Ile Asn<sub>360</sub> Asp Ile Ile Glu Val<sub>365</sub> Lys Asn Tyr  
Asp Thr Thr Ile His Gly Lys<sub>375</sub> Asn Thr Val Ile Gly<sub>380</sub> Val Leu Asp Ile  
Tyr Gly Phe Glu Ile Phe<sub>390</sub> Asp Asn Asn Ser Phe<sub>395</sub> Glu Gln Phe Cys Ile<sub>400</sub>  
Asn Tyr Cys Asn Glu<sub>405</sub> Lys Leu Gln Gln Leu Phe Ile Gln Leu Val<sub>415</sub> Leu  
Lys Gln Glu Gln<sub>420</sub> Glu Glu Tyr Gln Arg<sub>425</sub> Glu Gly Ile Pro Trp<sub>430</sub> Lys His

N3027PCT\_sequ.list.txt

I l e A s p T y r P h e A s n A s n G n I l e I l e V a l A s p L e u V a l G l u G n G n  
435 440 445

H i s L y s G l y I l e I l e A l a I l e L e u A s p A s p A l a C y s M e t A s n V a l G l y  
450 455 460

L y s V a l T h r A s p G l u M e t P h e L e u G l u A l a L e u A s n S e r L y s L e u G l y  
465 470 475 480

L y s H i s A l a H i s P h e S e r S e r A r g L y s L e u C y s A l a S e r A s p L y s I l e  
485 490 495

L e u G l u P h e A s p A r g A s p P h e A r g I l e A r g H i s T y r A l a G l y A s p V a l  
500 505 510

V a l T y r S e r V a l I l e G l y P h e I l e A s p L y s A s n L y s A s p T h r L e u P h e  
515 520 525

G n A s p P h e L y s A r g L e u M e t T y r A s n S e r S e r A s n P r o V a l L e u L y s  
530 535 540

A s n M e t T r p P r o G l u G l y L y s L e u S e r I l e T h r G l u V a l T h r L y s A r g  
545 550 555 560

P r o L e u T h r A l a A l a T h r L e u P h e L y s A s n S e r M e t I l e A l a L e u V a l  
565 570 575

A s p A s n L e u A l a S e r L y s G l u P r o T y r T y r V a l A r g C y s I l e L y s P r o  
580 585 590

A s n A s p L y s L y s S e r P r o G n I l e P h e A s p A s p G l u A r g C y s A r g H i s  
595 600 605

G n V a l G l u T y r L e u G l y L e u L e u G l u A s n V a l A r g V a l A r g A r g A l a  
610 615 620

G l y P h e A l a P h e A r g G n T h r T y r G l u L y s P h e L e u H i s A r g T y r L y s  
625 630 635 640

M e t I l e S e r G l u P h e T h r T r p P r o A s n H i s A s p L e u P r o S e r A s p L y s  
645 650 655

G l u A l a V a l L y s L y s L e u I l e G l u A r g C y s G l y P h e G n A s p A s p V a l  
660 665 670

A l a T y r G l y L y s T h r L y s I l e P h e I l e A r g T h r P r o A r g T h r L e u P h e  
675 680 685

T h r L e u G l u G l u L e u A r g A l a G n M e t L e u I l e A r g I l e V a l L e u P h e  
690 695 700

Leu 705 G n Lys Val Trp Arg 710 G y Thr Leu Ala Arg 715 Met Arg Tyr Lys Arg 720

Thr Lys Ala Ala Leu 725 Thr Ile Ile Arg Tyr 730 Tyr Arg Arg Tyr Lys 735 Val

Lys Ser Tyr Ile 740 His Glu Val Ala Arg 745 Arg Phe His Gly Val 750 Lys Thr

Met Arg Asp 755 Tyr Gly Lys His Val 760 Lys Trp Pro Ser Pro 765 Lys Val

Leu Arg 770 Arg Phe Glu Glu Ala 775 Leu G n Thr Ile Phe 780 Asn Arg Trp Arg

Ala 785 Ser G n Leu Ile Lys 790 Ser Ile Pro Ala Ser 795 Asp Leu Pro G n Val 800

Arg Ala Lys Val Ala 805 Ala Val Glu Met Leu 810 Lys Gly G n Arg Ala 815 Asp

Leu Gly Leu G n 820 Arg Ala Trp Glu Gly 825 Asn Tyr Leu Ala Ser 830 Lys Pro

Asp Thr Pro 835 G n Thr Ser Gly Thr 840 Phe Val Pro Val Ala 845 Asn Glu Leu

Lys Arg 850 Lys Asp Lys Tyr Met 855 Asn Val Leu Phe Ser 860 Cys His Val Arg

Lys Val Asn Arg Phe Ser 870 Lys Val Glu Asp Arg 875 Ala Ile Phe Val Thr 880

Asp Arg His Leu Tyr 885 Lys Met Asp Pro Thr 890 Lys G n Tyr Lys Val 895 Met

Lys Thr Ile Pro 900 Leu Tyr Asn Leu Thr 905 Gly Leu Ser Val Ser 910 Asn Gly

Lys Asp G n 915 Leu Val Val Phe His 920 Thr Lys Asp Asn Lys 925 Asp Leu Ile

Val Cys 930 Leu Phe Ser Lys G n 935 Pro Thr His Glu Ser 940 Arg Ile Gly Glu

Leu 945 Val Gly Val Leu Val 950 Asn His Phe Lys Ser 955 Glu Lys Arg His Leu 960

G n Val Asn Val Thr 965 Asn Pro Val G n Cys 970 Ser Leu His Gly Lys 975 Lys

Cys Thr Val Ser Val Glu Thr Arg Leu Asn G n Pro G n Pro Asp Phe

Thr Lys Asn Arg Ser Gly Phe Ile Leu Ser Val Pro Gly Asn  
 995 1000 1005

<210> 21  
 <211> 4729  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mi sc\_f eature  
 <222> (1)..(4729)  
 <223> myosi n I E (MYOIE)

<400> 21  
 cgagactcag ccagaggagt acggatt aag tggccgaaga aagaggagt g aggcagggga 60  
 gcgaggcgga cgct ccgagc gcat cggact cacct gggcc ggcggcgagc ggcgagt acg 120  
 agt ggact ct t gccct ccgc agcat gcgcc ccgcct gct a agt cgccgcc gt ct cgccct 180  
 cacct agcac cgccaat ccc gcct ggat gg agt cccct ct ggggt t cccat t ggct cct gt 240  
 gagt gct t gg gt gt cgggag cct gt t t t t g gcgaggggaa ccaact t t t g aagt t cgccc 300  
 agaagact gc gt t ccagccc cagt t ccccg gcagcgggac ccggcgaaga cgcgaccgcg 360  
 gcgcgagt ca ccat gggaag caaagggt gt c t accagt acc act ggcaaag ccacaat gt c 420  
 aagcacagt g gt gt ggacga cat ggt gct a ct gt ccaaga t cacagagaa ct ccat cgt g 480  
 gagaat ct ga agaagagat a cat ggat gac t acat t t t t a cat at at agg at ct gt at t a 540  
 at ct cagt ca accct t t caa gcagat gcca t at t t t gggg aaaaggaaat t gaaat gt ac 600  
 caaggagcgg cacagt at ga aaaccaccca cat at ct at g ccct t gcaga t aat at gt ac 660  
 agaaacat ga t cat t gacag agagaaccag t gcgt cat t a t cagt ggt ga aagt ggt gct 720  
 ggaaaaacag t ggct gccaa at at at cat g agct acat ct ccagagt gt c t ggaggaggg 780  
 accaaagt cc agcacgt gaa ggacat t at c ct gcagt cca acccgct gct ggaggcct t c 840  
 gggaacgcca agaccgt ccg gaacaacaac t ccagccgat t t ggaaaat a ct t t gaaat c 900  
 cagt t cagt c cagggt gggga accagat ggt ggaaagat ct ccaact t cct t ct ggaaaaa 960  
 t ct aggggt gg t gat gaggaa cccaggagag cggagt t t t c acat at t t t a ccagct cat c 1020  
 gagggcgct ct gcagagca gaaacacagc ct t ggcat ca ccagcat gga ct at t at t ac 1080  
 t acct gagcc t ct cgggct c at acaagggt t gat gacat t g acgacaggcg ggagt t t cag 1140  
 gaaact ct gc acgcat gaa t gt gat t ggg at ct t t gcag aagagcaaac gct ggt gt t g 1200  
 cagat agt gg cgggt at t ct ccacct ggga aacat cagct t caaagaagt t ggcaact ac 1260  
 gcggct gt gg agagt gaaga gt t t t t agct t t t cct gcat at ct gct agg gat aaaccag 1320  
 gaccggt t ga aagaaaagct aacaagccgg cagat ggat a gcaagt gggg aggcaaat cc 1380  
 gaat ccat cc acgt gaccct caacgt agag caggcct gt t acaccggga t gcgct cgcc 1440  
 aaggccct gc acgcccgggt ct t t gat t t c t t ggt agat t ccat caat aa agccat ggag 1500

N3027PCT\_sequ. list .txt

aaagaccat g	aagaat acaa	cat tggcgt c	ct agacat ct	at ggct t t ga	aat at t ccag	1560
aaaaat ggct	t t gaacagt t	t t gt at caat	t t t gt t aat g	aaaaact gca	gcagat t t t t	1620
at t gaact ga	cat t aaaggc	agaacaggaa	gaat at gt t c	aagaggggaat	aagat ggaca	1680
cccat t gagt	act t t aat aa	t aaaat cgt a	t gt gacct ca	t agagaacaa	agt gaaccct	1740
cct ggcat ca	t gagcat cct	ggat gacgt g	t gcgccacga	t gcat gcggt	gggt gagggg	1800
gcagat caga	cgct gct cca	gaaact t cag	at gcagat t g	ggagt cat ga	gcact t caac	1860
agt t ggaacc	aaggct t cat	cat t cat cat	t at gct ggga	aggt at cct a	t gacat ggat	1920
ggct t t t gt g	aaaggaaccg	ggat gt gct t	t t t at ggat c	t cat cgagct	t at gcagagc	1980
agcgagct gc	ct t t cat aaa	gt ct t t at t t	ccggaaaat c	t gcaggct ga	caagaaaggg	2040
cgcccaact a	ct gccggaag	caaaat aaag	aaacaagcca	at gacct t gt	gagcaccct g	2100
at gaaat gt a	cgccccact a	cat t cgct gc	at caagccaa	acgaaaccaa	gaagcccaga	2160
gact gggagg	aaagcagggg	aaagcat caa	gt cgaat at t	t ggggt ct gaa	agagaacat t	2220
cgagt gagaa	gagct ggct a	t gcct at cgg	cgcat ct t cc	aaaaat t cct	acagaggt at	2280
gccat t ct ga	ccaaagccac	ct ggcct t ct	t ggcagggag	aggagaagca	aggcgt cct g	2340
cacct gct gc	agt cgggt caa	cat ggacagc	gaccagt t cc	agct ggggag	gagt aaagt g	2400
t t cat caaag	cccccgagt c	t ct at t t ct t	t t agaagaga	t gagagagag	aaagt at gat	2460
gggt at gct c	gagt gat aca	gaaat cat gg	aggaaat t cg	t ggcccggaa	gaaat acgt t	2520
caaat gagag	aagaagcct c	agacct ct t a	t t gaacaaga	aggagagaag	gagaaacagt	2580
at t aacagga	act t t at agg	ggat t at at t	gggat ggaag	agcaccacaga	act ccagcag	2640
t t cgt gggca	agagggagaa	gat t gat t t c	gcagacacag	t caccaagt a	t gacaggagg	2700
t t caagggg	t aaagcgaga	cct gct cct t	accccaaagt	gct t gt act t	aat cggacga	2760
gaaaaagt ca	aacagggccc	agacaagggc	ct ggt gaaag	aagt cct gaa	gcggaaaat c	2820
gagat agaac	ggat ct t gt c	t gt gt ccct c	agt act at gc	aggat gacat	t t t t at t ct c	2880
cat gagcaag	agt at gacag	t t t gct t gaa	t ct gt ct t ca	aaact gaat t	cct aagcct c	2940
t t agcaaagc	gt t acgagga	gaagaccag	aagcaact ac	ct ct gaaat t	cagcaat acg	3000
ct t gaact ga	agt t gaaaaa	ggaaaact gg	ggccct gga	gt gcaggggg	ct cccggcaa	3060
gt gcagt t cc	accaagggg	t t ggggacct g	gct gt cct ca	agcccagt aa	caaagt gct g	3120
caggt cagca	t cggacct gg	act gcccaag	aact cccgt c	ct accagaag	gaacact acc	3180
caaaat acag	gt t at t ccag	t gggact caa	aat gccaaact	acccagt gag	agct gccct	3240
cct cccccag	gat accat ca	gaacggagt c	at cagaaacc	agt at gt gcc	at at ccccat	3300
gct cct ggaa	gccagaggt c	caat cagaaa	agcct gt aca	cct ccat ggc	ccgcccggcc	3360
t t gcct cggc	agcagt ct ac	cagt t cagac	cgagt gt cac	agacgccaga	gagcct ggat	3420
t t cct caagg	t cccggacca	gggagct gca	gggggt cagga	gacaaacaac	cagt cggcct	3480
ccccagcag	ggggcagacc	caagccccag	cccaagccca	agcct caggt	gccacagt gc	3540
aaggct t t gt	at gcct at ga	cgct caggac	acagacgaac	t cagct t t aa	t gccaat gac	3600

N3027PCT\_sequ.list.txt

```

attattgata ttatcaaaga agatccttct ggctggtgga cgggtcgact acgaggcaag 3660
cagggcctgt tccccaaaca ctatgtgacc aagatctgag gtgcccgtaga ctctgacaca 3720
tggggcagag gagctccagg cacagaccag gggaggggat atttaggggc tccccttaca 3780
atccacaatg agcaattgct tctccaaggc ctggagctat tctggtacct tccccatgga 3840
ggacactgaa aaggctgggt tggggacagg gagtatcact ccatagtga tctaaaagg 3900
tagcctcttc ataggaaccc aggaggacaa aaccacatg cattaatatt tatttattgt 3960
atttaaacct ggtgagagga caagtgaggt ctgctcagac cttgtaggct tctatcaaaa 4020
cagcacctgt cttgctcacc aggcctagag aatggctga ggtggccgct gacaagtgcc 4080
tttagttgaa gagcacattt ctttcatctc tcttgtccat acctgataga cacattcctc 4140
tctgccacct tcttccaggg aggacccgcc ctctgcagac tgggcttagc gtgagcaggc 4200
acttcccatg tacgtgccaa gggtaagctg gcctgctgag cccagggcgga cagaggggca 4260
ctggtttaca ctttgccggg accatcaggg ccgccaagca ggtcaggggc tgggggctgg 4320
gggctgggct gctggctttg ctttctctgg gtcttcaatt agaatgtggc tggcccatat 4380
tggtttgtgt ttaaagtctg tacttactac aagaaggatc ttttttcaag ctgtacattt 4440
ataaaaacag atcatatact gtatatataa aaatcttgag atggtagaaa catgtatgaa 4500
tgtactaagt agtatccac tgtactcatt cataaagt aggtttcttac aaaactcaca 4560
ccaggtaactt aaagatgtgc tctgcttttt tccaactacg gagtgtcact gctttctagg 4620
tcagtccctg cagactcttc tcaactcttt ccctatagga aacttactcc gcgtcctgcc 4680
cccacctctt aaataaataa aggaatcggc gaacaaaaaa aaaaaaaaaa 4729

```

<210> 22  
 <211> 1108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1108)  
 <223> myosin IE (MYO1E)

<400> 22

```

Met Gly Ser Lys Gly Val Tyr Gln Tyr His Trp Gln Ser His Asn Val
1          5          10
Lys His Ser Gly Val Asp Asp Met Val Leu Leu Ser Lys Ile Thr Glu
20         25         30
Asn Ser Ile Val Glu Asn Leu Lys Lys Arg Tyr Met Asp Asp Tyr Ile
35         40         45
Phe Thr Tyr Ile Gly Ser Val Leu Ile Ser Val Asn Pro Phe Lys Gln
50         55         60

```

N3027PCT\_sequ.list.txt

Met Pro Tyr Phe Gly Gu Lys Gu Ile Gu Met Tyr Gln Gly Ala Ala  
65 70 75 80

Gln Tyr Gu Asn Pro Pro His Ile Tyr Ala Leu Ala Asp Asn Met Tyr  
85 90 95

Arg Asn Met Ile Ile Asp Arg Gu Asn Gln Cys Val Ile Ile Ser Gly  
100 105 110

Gu Ser Gly Ala Gly Lys Thr Val Ala Ala Lys Tyr Ile Met Ser Tyr  
115 120 125

Ile Ser Arg Val Ser Gly Gly Gly Thr Lys Val Gln His Val Lys Asp  
130 135 140

Ile Ile Leu Gln Ser Asn Pro Leu Leu Gu Ala Phe Gly Asn Ala Lys  
145 150 155 160

Thr Val Arg Asn Asn Asn Ser Ser Arg Phe Gly Lys Tyr Phe Gu Ile  
165 170 175

Gln Phe Ser Pro Gly Gly Gu Pro Asp Gly Gly Lys Ile Ser Asn Phe  
180 185 190

Leu Leu Gu Lys Ser Arg Val Val Met Arg Asn Pro Gly Gu Arg Ser  
195 200 205

Phe His Ile Phe Tyr Gln Leu Ile Gu Gly Ala Ser Ala Gu Gln Lys  
210 215 220

His Ser Leu Gly Ile Thr Ser Met Asp Tyr Tyr Tyr Tyr Leu Ser Leu  
225 230 235 240

Ser Gly Ser Tyr Lys Val Asp Asp Ile Asp Asp Arg Arg Gu Phe Gln  
245 250 255

Gu Thr Leu His Ala Met Asn Val Ile Gly Ile Phe Ala Gu Gu Gln  
260 265 270

Thr Leu Val Leu Gln Ile Val Ala Gly Ile Leu His Leu Gly Asn Ile  
275 280 285

Ser Phe Lys Gu Val Gly Asn Tyr Ala Ala Val Gu Ser Gu Gu Phe  
290 295 300

Leu Ala Phe Pro Ala Tyr Leu Leu Gly Ile Asn Gln Asp Arg Leu Lys  
305 310 315 320

Gu Lys Leu Thr Ser Arg Gln Met Asp Ser Lys Trp Gly Gly Lys Ser  
325 330 335

Gu Ser Ile His Val Thr Leu Asn Val Gu Gln Ala Cys Tyr Thr Arg

340

345

350

Asp Ala Leu Ala Lys Ala Leu His Ala Arg Val Phe Asp Phe Leu Val  
 355 360 365  
 Asp Ser Ile Asn Lys Ala Met Glu Lys Asp His Glu Glu Tyr Asn Ile  
 370 375 380  
 Gly Val Leu Asp Ile Tyr Gly Phe Glu Ile Phe Glu Lys Asn Gly Phe  
 385 390 395 400  
 Glu Glu Phe Cys Ile Asn Phe Val Asn Glu Lys Leu Glu Glu Ile Phe  
 405 410 415  
 Ile Glu Leu Thr Leu Lys Ala Glu Glu Glu Tyr Val Glu Glu Gly  
 420 425 430  
 Ile Arg Trp Thr Pro Ile Glu Tyr Phe Asn Asn Lys Ile Val Cys Asp  
 435 440 445  
 Leu Ile Glu Asn Lys Val Asn Pro Pro Gly Ile Met Ser Ile Leu Asp  
 450 455 460  
 Asp Val Cys Ala Thr Met His Ala Val Gly Glu Gly Ala Asp Glu Thr  
 465 470 475 480  
 Leu Leu Glu Lys Leu Glu Met Glu Ile Gly Ser His Glu His Phe Asn  
 485 490 495  
 Ser Trp Asn Glu Gly Phe Ile Ile His His Tyr Ala Gly Lys Val Ser  
 500 505 510  
 Tyr Asp Met Asp Gly Phe Cys Glu Arg Asn Arg Asp Val Leu Phe Met  
 515 520 525  
 Asp Leu Ile Glu Leu Met Glu Ser Ser Glu Leu Pro Phe Ile Lys Ser  
 530 535 540  
 Leu Phe Pro Glu Asn Leu Glu Ala Asp Lys Lys Gly Arg Pro Thr Thr  
 545 550 555 560  
 Ala Gly Ser Lys Ile Lys Lys Glu Ala Asn Asp Leu Val Ser Thr Leu  
 565 570 575  
 Met Lys Cys Thr Pro His Tyr Ile Arg Cys Ile Lys Pro Asn Glu Thr  
 580 585 590  
 Lys Lys Pro Arg Asp Trp Glu Glu Ser Arg Val Lys His Glu Val Glu  
 595 600 605  
 Tyr Leu Gly Leu Lys Glu Asn Ile Arg Val Arg Arg Ala Gly Tyr Ala  
 610 615 620

N3027PCT\_sequ.list.txt

Tyr Arg Arg Ile Phe Gln Lys Phe Leu Gln Arg Tyr Ala Ile Leu Thr  
 625 630 635 640  
 Lys Ala Thr Trp Pro Ser Trp Gln Gly Glu Glu Lys Gln Gly Val Leu  
 645 650 655  
 His Leu Leu Gln Ser Val Asn Met Asp Ser Asp Gln Phe Gln Leu Gly  
 660 665 670  
 Arg Ser Lys Val Phe Ile Lys Ala Pro Glu Ser Leu Phe Leu Leu Glu  
 675 680 685  
 Glu Met Arg Glu Arg Lys Tyr Asp Gly Tyr Ala Arg Val Ile Gln Lys  
 690 695 700  
 Ser Trp Arg Lys Phe Val Ala Arg Lys Lys Tyr Val Gln Met Arg Glu  
 705 710 715 720  
 Glu Ala Ser Asp Leu Leu Leu Asn Lys Lys Glu Arg Arg Arg Asn Ser  
 725 730 735  
 Ile Asn Arg Asn Phe Ile Gly Asp Tyr Ile Gly Met Glu Glu His Pro  
 740 745 750  
 Glu Leu Gln Gln Phe Val Gly Lys Arg Glu Lys Ile Asp Phe Ala Asp  
 755 760 765  
 Thr Val Thr Lys Tyr Asp Arg Arg Phe Lys Gly Val Lys Arg Asp Leu  
 770 775 780  
 Leu Leu Thr Pro Lys Cys Leu Tyr Leu Ile Gly Arg Glu Lys Val Lys  
 785 790 795 800  
 Gln Gly Pro Asp Lys Gly Leu Val Lys Glu Val Leu Lys Arg Lys Ile  
 805 810 815  
 Glu Ile Glu Arg Ile Leu Ser Val Ser Leu Ser Thr Met Gln Asp Asp  
 820 825 830  
 Ile Phe Ile Leu His Glu Gln Glu Tyr Asp Ser Leu Leu Glu Ser Val  
 835 840 845  
 Phe Lys Thr Glu Phe Leu Ser Leu Leu Ala Lys Arg Tyr Glu Glu Lys  
 850 855 860  
 Thr Gln Lys Gln Leu Pro Leu Lys Phe Ser Asn Thr Leu Glu Leu Lys  
 865 870 875 880  
 Leu Lys Lys Glu Asn Trp Gly Pro Trp Ser Ala Gly Gly Ser Arg Gln  
 885 890 895

N3027PCT\_sequ.list.txt

Val Gln Phe His Gln Gly Phe Gly Asp Leu Ala Val Leu Lys Pro Ser  
900 905 910

Asn Lys Val Leu Gln Val Ser Ile Gly Pro Gly Leu Pro Lys Asn Ser  
915 920 925

Arg Pro Thr Arg Arg Asn Thr Thr Gln Asn Thr Gly Tyr Ser Ser Gly  
930 935 940

Thr Gln Asn Ala Asn Tyr Pro Val Arg Ala Ala Pro Pro Pro Pro Gly  
945 950 955 960

Tyr His Gln Asn Gly Val Ile Arg Asn Gln Tyr Val Pro Tyr Pro His  
965 970 975

Ala Pro Gly Ser Gln Arg Ser Asn Gln Lys Ser Leu Tyr Thr Ser Met  
980 985 990

Ala Arg Pro Pro Leu Pro Arg Gln Gln Ser Thr Ser Ser Asp Arg Val  
995 1000 1005

Ser Gln Thr Pro Glu Ser Leu Asp Phe Leu Lys Val Pro Asp Gln  
1010 1015 1020

Gly Ala Ala Gly Val Arg Arg Gln Thr Thr Ser Arg Pro Pro Pro  
1025 1030 1035

Ala Gly Gly Arg Pro Lys Pro Gln Pro Lys Pro Lys Pro Gln Val  
1040 1045 1050

Pro Gln Cys Lys Ala Leu Tyr Ala Tyr Asp Ala Gln Asp Thr Asp  
1055 1060 1065

Glu Leu Ser Phe Asn Ala Asn Asp Ile Ile Asp Ile Ile Lys Glu  
1070 1075 1080

Asp Pro Ser Gly Trp Trp Thr Gly Arg Leu Arg Gly Lys Gln Gly  
1085 1090 1095

Leu Phe Pro Asn Asn Tyr Val Thr Lys Ile  
1100 1105

<210> 23  
<211> 3860  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(3860)  
<223> myosin IF (MYO1F)

<400> 23

N3027PCT\_sequ. list .txt

gt gaacgggc	agaagcaggg	ccat gcccaa	gccaccccca	agat cccct	gaacct gcac	60
ct ccat cacg	acccat t cag	gagcct ccag	gagcccagac	accagccccc	caccat gggc	120
agcaaggagc	gct t ccact g	gcagagccac	aacgt gaagc	agagcggcgt	ggat gacat g	180
gt gct t ct t c	cccagat cac	cgaagacgcc	at t gccgcca	acct ccggaa	gcgct t cat g	240
gacgact aca	t ct t cacct a	cat cggct ct	gt gct cat ct	ct gt aaaccc	ct t caagcag	300
at gccct act	t caccgaccg	t gagat cgac	ct ct at cagg	gcgcggccca	gt at gagaat	360
ccccgcaca	t ct acgccct	cacggacaac	at gt accgga	acat gct t at	cgact gt gag	420
aaccagt gt g	t cat cat t ag	t ggagagagt	ggagct ggga	agacagt ggc	agccaaat at	480
at cat gggct	acat ct ccaa	gggt gt ct ggc	ggaggcgaga	aggt ccagca	cgt caaagat	540
at cat cct gc	agt ccaaccc	gct gct cgag	gcct t cgga	acgccaagac	t gt gcgcaac	600
aacaat t cca	gccgct t t gg	caagt act t t	gagat ccagt	t cagccgagg	t ggggagcca	660
gat gggggca	agat ct ccaa	ct t ct t gct g	gagaagt ccc	gcgt ggt cat	gcaaaat gaa	720
aat gagagga	act t ccacat	ct act accag	ct gct ggaag	gggcct ccca	ggagcaaagg	780
cagaacct gg	gcct cat gac	accggact ac	t at t act acc	t caaccaat c	ggacacct ac	840
caggt ggacg	gcacggacga	cagaagcgac	t t t ggt gaga	ct ct gagt gc	t at gcaggt t	900
at t gggat cc	cgcccagcat	ccagcagct g	gt cct gcagc	t cgt ggcggg	gat ct t gcac	960
ct ggggaaca	t cagt t t ct g	t gaagacggg	aat t acgccc	gagt ggagag	t gt ggacct c	1020
ct ggcct t t c	ccgcct acct	gct gggcat t	gacagcgggc	gact gcagga	gaagct gacc	1080
agccgcaaga	t ggacagccg	ct ggggcggg	cgcagcgagt	ccat caat gt	gacct caac	1140
gt ggagcagg	cagcct acac	ccgt gat gcc	ct ggccaagg	ggct ct at gc	ccgcct ct t c	1200
gact t cct cg	t ggaggccat	caaccgt gct	at gcagaaac	cccaggaaga	gt acagcat c	1260
gggt gt gct gg	acat t t acgg	ct t cgagat c	t t ccagaaaa	at ggct t cga	gcagt t t t gc	1320
at caact t cg	t caat gagaa	gct gcagcaa	at ct t t at cg	aact t accct	gaaggccgag	1380
caggaggagt	at gt gcagga	aggcat ccgc	t ggact ccaa	t ccagt act t	caacaacaag	1440
gt cgt ct gt g	acct cat cga	aaacaagct g	agccccccag	gcat cat gag	cgt ct t ggac	1500
gacgt gt gcg	ccacat gca	cgccacgggc	gggggagcag	accagacact	gct gcagaag	1560
ct gcaggcgg	ct gt ggggac	ccacgagcat	t t caacagct	ggagcgccgg	ct t cgt cat c	1620
caccact acg	ct ggcaaggt	ct cct acgac	gt cagcggct	t ct gcgagag	gaaccgagac	1680
gt t ct ct t ct	ccgacct cat	agagct gat g	cagaccagt g	agcaggcct t	cct ccggat g	1740
ct ct t ccccg	agaagct gga	t ggagacaag	aaggggcgcc	ccagcaccgc	cggct ccaag	1800
at caagaaac	aagccaacga	cct ggt ggcc	acact gat ga	gggt gcacacc	ccact acat c	1860
cgct gcat ca	aaccaacga	gaccaagagg	ccccgagact	gggaggagaa	cagagt caag	1920
caccaggt gg	aat acct ggg	cct gaaggag	aacat caggg	t gcgcagagc	cggct t cgcc	1980
t accgccgcc	agt t cgccaa	at t cct gcag	aggt at gcca	t t ct gacccc	cgagacgt gg	2040
ccgcgggt ggc	gt ggggacga	acgccagggc	gt ccagcacc	t gct t cgggc	gggt caacat g	2100

N3027PCT\_sequ. list . . txt

gagcccgacc agt accagat ggggagcacc aaggt ctttg t caagaaccc agagt cgct t	2160
tt cct cct gg aggaggt gcg agagcgaaag tt cgat ggct tt gccgaac cat ccagaag	2220
gcct ggcggc gccacgt ggc t gt ccggaag t acgaggaga t gcgggagga agct t ccaac	2280
at cct gct ga acaagaagga gcggaggcgc aacagcat ca at cggaact t cgt cggggac	2340
t acct ggggc t ggaggagcg gcccagct g cgt cagt t cc t gggcaagag ggagcgggt g	2400
gact t cgccg att cggt cac caagt acgac cgccgct t ca agcccat caa gcgggact t g	2460
at cct gacgc ccaagt gt gt gt at gt gat t gggcgagaga aagt gaagaa gggacct gag	2520
aagggccagg t gt gt gaagt ct t gaagaag aaagt ggaca t ccaggct ct gcggggagt c	2580
t ccct cagca cgcgacagga cgact t ct t c at cct ccaag aggat gccgc cgacagct t c	2640
ct ggagagcg t ct t caagac cgagt t t gt c agcct t ct gt gcaagcgct t cgaggaggcg	2700
acgcggaggc ccct gcccct cacct t cagc gacacact ac agt t t cgggt gaagaaggag	2760
ggct ggggcg gt ggcggcac ccgcagcgt c acct t ct ccc gcggct t cgg cgact t ggca	2820
gt gct caagg t t ggcgggt cg gaccct cacg gt cagcgt gg gcgat gggct gcccaagagc	2880
t ccaagcct a cgcggaagg aat ggccaag ggaaaacct c ggaggt cgt c ccaagcccct	2940
acccgggcgg ccct gcgcc cccagaggc at ggat cgca at ggggt gcc ccct ct gcc	3000
agagggggcc ccct gcccct ggagat cat g t ct ggagggg gcacccacag gcct ccccg	3060
ggccct ccgt ccacat ccct gggagccagc agacgacccc gggcacgt cc gccct cagag	3120
cacaacacag aat t cct caa cgt gcct gac cagggcat gg ccggcat gca gaggaagcgc	3180
agcgt ggggc aacggccagt gcct ggt gt g ggccgaccca agccccagcc t cggacacat	3240
ggc cccaggt gccgggccct at accagt ac gt gggccaag at gt ggacga gct gagct t c	3300
aacgt gaacg aggt cat t ga gat cct cat g gaagat ccct cgggct ggt g gaagggccgg	3360
ct t cacggcc aggaggccct t t t cccagga aact acgt gg agaagat ct g agct gggccc	3420
t gggat act g cct t ct ct t t cggccgcct a t ct gcct gcc ggcct ggt gg ggagccaggc	3480
cct gccaat g agagcct cgt t t acct gggc t gcaat agcc t aaaagt cca gt cct t t ggc	3540
ct ccagt cct gcccaggccc t gggc cacca ggt cact gct gcagcccccg ccct gggcc	3600
ct ggt ct t cc t ccaacat ca cacct gct gc ccat t ct cca t t t ct gt gt g t gt caaagg	3660
gact aacagc agaat ct acc t cccaact gc cat gt gat t a agaaat gggc ct t gact cct	3720
gt gct gt t gg caaagt gcc ggcacagt t g gggagggggg ggt cct t aac aagcgt gact	3780
tt gct cat t c t gt cat cact aaggcaat aa acct t t gcc ggt gaaaaaa aaaaaaaaaa	3840
aaaaaaaaaa aaaaaaaaaa	3860

<210> 24  
 <211> 1098  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; M SC FEATURE

&lt;222&gt; (1)..(1098)

&lt;223&gt; myosin IF (MYO1F)

&lt;400&gt; 24

Met Gly Ser Lys Glu Arg Phe His Trp Gln Ser His Asn Val Lys Gln  
1 5 10 15Ser Gly Val Asp Asp Met Val Leu Leu Pro Gln Ile Thr Glu Asp Ala  
20 25 30Ile Ala Ala Asn Leu Arg Lys Arg Phe Met Asp Asp Tyr Ile Phe Thr  
35 40 45Tyr Ile Gly Ser Val Leu Ile Ser Val Asn Pro Phe Lys Gln Met Pro  
50 55 60Tyr Phe Thr Asp Arg Glu Ile Asp Leu Tyr Gln Gly Ala Ala Gln Tyr  
65 70 75 80Glu Asn Pro Pro His Ile Tyr Ala Leu Thr Asp Asn Met Tyr Arg Asn  
85 90 95Met Leu Ile Asp Cys Glu Asn Gln Cys Val Ile Ile Ser Gly Glu Ser  
100 105 110Gly Ala Gly Lys Thr Val Ala Ala Lys Tyr Ile Met Gly Tyr Ile Ser  
115 120 125Lys Val Ser Gly Gly Gly Glu Lys Val Gln His Val Lys Asp Ile Ile  
130 135 140Leu Gln Ser Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val  
145 150 155 160Arg Asn Asn Asn Ser Ser Arg Phe Gly Lys Tyr Phe Glu Ile Gln Phe  
165 170 175Ser Arg Gly Gly Glu Pro Asp Gly Gly Lys Ile Ser Asn Phe Leu Leu  
180 185 190Glu Lys Ser Arg Val Val Met Gln Asn Glu Asn Glu Arg Asn Phe His  
195 200 205Ile Tyr Tyr Gln Leu Leu Glu Gly Ala Ser Gln Glu Gln Arg Gln Asn  
210 215 220Leu Gly Leu Met Thr Pro Asp Tyr Tyr Tyr Tyr Leu Asn Gln Ser Asp  
225 230 235 240Thr Tyr Gln Val Asp Gly Thr Asp Asp Arg Ser Asp Phe Gly Glu Thr  
245 250 255

N3027PCT\_sequ.list.txt

Leu Ser Ala Met 260 Gln Val Ile Gly 265 Ile Pro Pro Ser Ile Gln Gln Leu 270  
 Val Leu Gln 275 Leu Val Ala Gly 280 Ile Leu His Leu Gly Asn 285 Ile Ser Phe  
 Cys Gu 290 Asp Gly Asn Tyr Ala 295 Arg Val Gu Ser Val 300 Asp Leu Leu Ala  
 Phe 305 Pro Ala Tyr Leu Leu 310 Gly Ile Asp Ser Gly 315 Arg Leu Gln Gu Lys 320  
 Leu Thr Ser Arg 325 Lys Met Asp Ser Arg Trp 330 Gly Gly Arg Ser Gu 335 Ser  
 Ile Asn Val Thr 340 Leu Asn Val Gu Gln 345 Ala Ala Tyr Thr Arg 350 Asp Ala  
 Leu Ala Lys 355 Gly Leu Tyr Ala Arg 360 Leu Phe Asp Phe Leu 365 Val Gu Ala  
 Ile Asn Arg Ala Met Gln Lys 375 Pro Gln Gu Gu Tyr 380 Ser Ile Gly Val  
 Leu 385 Asp Ile Tyr Gly Phe 390 Gu Ile Phe Gln Lys 395 Asn Gly Phe Gu Gln 400  
 Phe Cys Ile Asn Phe 405 Val Asn Gu Lys Leu 410 Gln Gln Ile Phe Ile Gu 415  
 Leu Thr Leu Lys 420 Ala Gu Gln Gu Gu Tyr Val Gln Gu Gly 430 Ile Arg  
 Trp Thr Pro 435 Ile Gln Tyr Phe Asn 440 Asn Lys Val Val Cys 445 Asp Leu Ile  
 Gu Asn 450 Lys Leu Ser Pro Pro 455 Gly Ile Met Ser Val 460 Leu Asp Asp Val  
 Cys 465 Ala Thr Met His Ala 470 Thr Gly Gly Gly Ala 475 Asp Gln Thr Leu Leu 480  
 Gln Lys Leu Gln Ala 485 Ala Val Gly Thr His 490 Gu His Phe Asn Ser Trp 495  
 Ser Ala Gly Phe 500 Val Ile His His Tyr 505 Ala Gly Lys Val Ser 510 Tyr Asp  
 Val Ser Gly 515 Phe Cys Gu Arg Asn 520 Arg Asp Val Leu Phe 525 Ser Asp Leu

Ile Glu Leu Met Gln Thr Ser Glu Gln Ala Phe Leu Arg Met Leu Phe  
 530 535 540

Pro Glu Lys Leu Asp Gly Asp Lys Lys Gly Arg Pro Ser Thr Ala Gly  
 545 550 555 560

Ser Lys Ile Lys Lys Gln Ala Asn Asp Leu Val Ala Thr Leu Met Arg  
 565 570 575

Cys Thr Pro His Tyr Ile Arg Cys Ile Lys Pro Asn Glu Thr Lys Arg  
 580 585 590

Pro Arg Asp Trp Glu Glu Asn Arg Val Lys His Gln Val Glu Tyr Leu  
 595 600 605

Gly Leu Lys Glu Asn Ile Arg Val Arg Arg Ala Gly Phe Ala Tyr Arg  
 610 615 620

Arg Gln Phe Ala Lys Phe Leu Gln Arg Tyr Ala Ile Leu Thr Pro Glu  
 625 630 635 640

Thr Trp Pro Arg Trp Arg Gly Asp Glu Arg Gln Gly Val Gln His Leu  
 645 650 655

Leu Arg Ala Val Asn Met Glu Pro Asp Gln Tyr Gln Met Gly Ser Thr  
 660 665 670

Lys Val Phe Val Lys Asn Pro Glu Ser Leu Phe Leu Leu Glu Glu Val  
 675 680 685

Arg Glu Arg Lys Phe Asp Gly Phe Ala Arg Thr Ile Gln Lys Ala Trp  
 690 695 700

Arg Arg His Val Ala Val Arg Lys Tyr Glu Glu Met Arg Glu Glu Ala  
 705 710 715 720

Ser Asn Ile Leu Leu Asn Lys Lys Glu Arg Arg Arg Asn Ser Ile Asn  
 725 730 735

Arg Asn Phe Val Gly Asp Tyr Leu Gly Leu Glu Glu Arg Pro Glu Leu  
 740 745 750

Arg Gln Phe Leu Gly Lys Arg Glu Arg Val Asp Phe Ala Asp Ser Val  
 755 760 765

Thr Lys Tyr Asp Arg Arg Phe Lys Pro Ile Lys Arg Asp Leu Ile Leu  
 770 775 780

Thr Pro Lys Cys Val Tyr Val Ile Gly Arg Glu Lys Val Lys Lys Gly  
 785 790 795 800

Pro Glu Lys Gly Gln Val Cys Glu Val Leu Lys Lys Lys Val Asp Ile

805

810

815

Gln Ala Leu Arg Gly Val Ser Leu Ser Thr Arg Gln Asp Asp Phe Phe  
 820 825 830  
 Ile Leu Gln Glu Asp Ala Ala Asp Ser Phe Leu Glu Ser Val Phe Lys  
 835 840 845  
 Thr Glu Phe Val Ser Leu Leu Cys Lys Arg Phe Glu Glu Ala Thr Arg  
 850 855 860  
 Arg Pro Leu Pro Leu Thr Phe Ser Asp Thr Leu Gln Phe Arg Val Lys  
 865 870 875 880  
 Lys Glu Gly Trp Gly Gly Gly Gly Thr Arg Ser Val Thr Phe Ser Arg  
 885 890 895  
 Gly Phe Gly Asp Leu Ala Val Leu Lys Val Gly Gly Arg Thr Leu Thr  
 900 905 910  
 Val Ser Val Gly Asp Gly Leu Pro Lys Ser Ser Lys Pro Thr Arg Lys  
 915 920 925  
 Gly Met Ala Lys Gly Lys Pro Arg Arg Ser Ser Gln Ala Pro Thr Arg  
 930 935 940  
 Ala Ala Pro Ala Pro Pro Arg Gly Met Asp Arg Asn Gly Val Pro Pro  
 945 950 955 960  
 Ser Ala Arg Gly Gly Pro Leu Pro Leu Glu Ile Met Ser Gly Gly Gly  
 965 970 975  
 Thr His Arg Pro Pro Arg Gly Pro Pro Ser Thr Ser Leu Gly Ala Ser  
 980 985 990  
 Arg Arg Pro Arg Ala Arg Pro Pro Ser Glu His Asn Thr Glu Phe Leu  
 995 1000 1005  
 Asn Val Pro Asp Gln Gly Met Ala Gly Met Gln Arg Lys Arg Ser  
 1010 1015 1020  
 Val Gly Gln Arg Pro Val Pro Gly Val Gly Arg Pro Lys Pro Gln  
 1025 1030 1035  
 Pro Arg Thr His Gly Pro Arg Cys Arg Ala Leu Tyr Gln Tyr Val  
 1040 1045 1050  
 Gly Gln Asp Val Asp Glu Leu Ser Phe Asn Val Asn Glu Val Ile  
 1055 1060 1065  
 Glu Ile Leu Met Glu Asp Pro Ser Gly Trp Trp Lys Gly Arg Leu  
 1070 1075 1080

N3027PCT\_sequ.list.txt

His Gly Gln Glu Gly Leu Phe Pro Gly Asn Tyr Val Glu Lys Ile  
1085 1090 1095

<210> 25  
<211> 3259  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_f eat ur e  
<222> (1)..(3259)  
<223> myosi n I G (MYO1G)

```

<400> 25
ggggcagggc gggggcggt g gggcct cccc tagcct tccc tccccct ct c ct t cact gt c 60
ct t ccagcag gcacaggaag gt gaggcaag gt gt t t ccag ccggcaggat ggaggacgag 120
gaaggccct g agt at ggcaa acct gact t t gt gct t t t gg accaagt gac cat ggaggac 180
t t cat gagga acct gcagct caggt t cgag aagggccgca t ct acacct a cat cggt gag 240
gt gct ggt gt ccgt gaaccc ct accaggag ct gccct gt at gggcct ga ggccat cgcc 300
aggt accagg gccgt gagct ct at gagcgg ccaccccat c t ct at gct gt ggccaacgcc 360
gcct acaagg caat gaagca ccggt ccagg gacacct gca t cgt cat ct c aggggagagt 420
ggggcagggg agacagaagc cagt aagcac at cat gcagt acat cgct gc t gt caccaat 480
ccaagccaga gggct gaggt ggagaggg t aaggacgt gc t gct caagt c cacct gt gt g 540
ct ggaggcct t t ggcaat gc ccgcaccaac cgcaat caca act ccagccg ct t t ggcaag 600
t acat ggaca t caact t t ga ct t caagggg gacccgat cg gaggacacat ccacagct ac 660
ct act ggaga agt ct cgggt cct caagcag cacgt ggggt g aaagaaact t ccacgcct t c 720
t accaat t gc t gagaggcag t gaggacaag cagct gcat g aact gcact t ggagagaaac 780
cct gct gt at acaat t t cac acaccaggga gcaggact ca acat gact gt gcacagt gcc 840
t t ggacagt g at gagcagag ccaccaggca gt gaccgagg ccat gaggggt cat cggct t c 900
agt cct gaag aggt ggagt c t gt gcat cgc at cct ggct g ccat at t gca cct gggaaac 960
at cgagt t t g t ggagacgga ggaggggt ggg ct gcagaagg agggcct ggc agt ggccgag 1020
gaggcact gg t ggacat gt ggct gagct g acggccacac cccgggacct cgt gct ccgc 1080
t ccct gct gg ct cgcacagt t gcct cggga ggcagggaac t cat agagaa gggccacact 1140
gcagct gagg ccagct at gc ccgggat gcc t gt gccaagg cagt gt acca gcggct gt t t 1200
gagt ggggt gg t gaacaggat caacagt gt c at ggaacccc ggggcccggga t cct cggcgt 1260
gat ggcaagg acacagt cat t ggcgt gct g gacat ct at g gct t cgaggt gt t t cccgt c 1320
aacagt t t cg agcagt t ct g cat caact ac t gcaacgaga agct gcagca gct at t cat c 1380
cagct cat cc t gaagcagga acaggaagag t acgagcgcg agggcat cac ct ggcagagc 1440
gt t gagt at t t caacaacgc caccat t gt g gat ct ggt gg agcggcccca ccgt ggcat c 1500
ct ggccgt gc t ggacgaggc ct gcagct ct gct ggcacca t cact gaccg aat ct t cct g 1560

```

N3027PCT\_sequ. list . . txt

cagaccct gg	acacgcacca	ccgccat cac	ct aact aca	ccagccgcca	gct ct gcccc	1620
acagacaaga	ccat ggagt t	t ggccgagac	t t ccggat ca	agcact at gc	aggggacgt c	1680
acgt act ccg	t ggaaggct t	cat cgacaag	aacagagat t	t cct ct t cca	ggact t caag	1740
cggct gct gt	acaacagcac	ggacccact	ct acgggcca	t gt ggccgga	cgggcagcag	1800
gacat cacag	aggt gaccaa	gcgccccct g	acggct ggca	cact ct t caa	gaact ccat g	1860
gt ggccct gg	t ggagaacct	t gcct ccaag	gagccct t ct	acgt ccgct g	cat caagccc	1920
aat gaggaca	aggt agct gg	gaagct ggat	gagaaccact	gt cgccacca	ggc cgcat ac	1980
ct ggggct gc	t ggagaat gt	gagggt ccgc	agggct ggct	t cgct t cccg	ccagccct ac	2040
t ct cgat t cc	t gct caggt a	caagat gacc	t gt gaat aca	cat ggcccaa	ccacct gct g	2100
ggct ccgaca	aggcagccgt	gagcgt ct c	ct ggagcagc	acgggct gca	gggggacgt g	2160
gcct t t ggcc	acagcaagct	gt t cat ccgc	t caccgccga	cact ggt cac	act ggagcag	2220
agccgagccc	gcct cat ccc	cat cat t gt g	ct gct at t gc	agaaggcat g	gcggggcacc	2280
t t ggcgaggt	ggcgct gccg	gagggt gagg	gct at ct aca	ccat cat gcg	ct ggt t ccgg	2340
agacacaagg	t gcgggct ca	cct ggct gag	ct gcagcggc	gat t ccaggc	t gcaaggcag	2400
ccgccact ct	acgggcgt ga	cct t gt gt gg	ccgct gcccc	ct gct gt gct	gcagccct t c	2460
caggacacct	gccacgcact	ct t ct gcagg	t ggccgggccc	ggcagct ggt	gaagaacat c	2520
ccccct t cag	acat gcccc	gat caaggcc	aagggt ggccg	ccat gggggc	cct gcaaggg	2580
ct t cgt cagg	act ggggct g	ccgacggggc	t gggcccag	act acct gt c	ct ct gccact	2640
gacaat ccca	cagcat caag	cct gt t t gct	cagcgact aa	agacact t cg	ggacaaagat	2700
ggct t cgggg	ct gt gct ct t	t t caagccat	gt ccgcaagg	t gaaccgct t	ccacaagat c	2760
cggaaaccggg	ccct cct gct	cacagaccag	cacct ct aca	agct ggaccc	t gaccggcag	2820
t accgggt ga	t gcggggcgt	gcccc t gag	gcggt gacgg	ggct gagcgt	gaccagcgga	2880
ggagaccagc	t ggt ggt gct	gcacgcccgc	ggccaggacg	acct cgt ggt	gt gcct gcac	2940
cgct cccggc	cgccat t gga	caaccgcgt t	ggggagct gg	t gggcgt gct	ggccgcacac	3000
t gccaggggg	agggccgcac	cct ggaggt t	cgcgt ct ccg	act gcat ccc	act aagccat	3060
cgcggggt cc	ggcgct cat	ct ccgt ggag	cccaggccgg	agcagccaga	gcccgat t t c	3120
cgct gcgct c	gcggct cct t	caccct gct c	t ggcccagcc	gct gagcgcc	cgcacccgcc	3180
gcaccccgag	gccgccaat t	gt ccgccccg	ccagcgct gc	aaat aaacct	t ct gagt cag	3240
ccaaaaaaaa	aaaaaaaaa					3259

<210> 26  
 <211> 1018  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> M SC\_FEATURE  
 <222> (1) . . (1018)

&lt;223&gt; myosin I G (MYO1G)

&lt;400&gt; 26

Met Glu Asp Glu Glu Gly Pro Glu Tyr Gly Lys Pro Asp Phe Val Leu  
1 5 10 15

Leu Asp Gln Val Thr Met Glu Asp Phe Met Arg Asn Leu Gln Leu Arg  
20 25 30

Phe Glu Lys Gly Arg Ile Tyr Thr Tyr Ile Gly Glu Val Leu Val Ser  
35 40 45

Val Asn Pro Tyr Gln Glu Leu Pro Leu Tyr Gly Pro Glu Ala Ile Ala  
50 55 60

Arg Tyr Gln Gly Arg Glu Leu Tyr Glu Arg Pro Pro His Leu Tyr Ala  
65 70 75 80

Val Ala Asn Ala Ala Tyr Lys Ala Met Lys His Arg Ser Arg Asp Thr  
85 90 95

Cys Ile Val Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Ser  
100 105 110

Lys His Ile Met Gln Tyr Ile Ala Ala Val Thr Asn Pro Ser Gln Arg  
115 120 125

Ala Glu Val Glu Arg Val Lys Asp Val Leu Leu Lys Ser Thr Cys Val  
130 135 140

Leu Glu Ala Phe Gly Asn Ala Arg Thr Asn Arg Asn His Asn Ser Ser  
145 150 155 160

Arg Phe Gly Lys Tyr Met Asp Ile Asn Phe Asp Phe Lys Gly Asp Pro  
165 170 175

Ile Gly Gly His Ile His Ser Tyr Leu Leu Glu Lys Ser Arg Val Leu  
180 185 190

Lys Gln His Val Gly Glu Arg Asn Phe His Ala Phe Tyr Gln Leu Leu  
195 200 205

Arg Gly Ser Glu Asp Lys Gln Leu His Glu Leu His Leu Glu Arg Asn  
210 215 220

Pro Ala Val Tyr Asn Phe Thr His Gln Gly Ala Gly Leu Asn Met Thr  
225 230 235 240

Val His Ser Ala Leu Asp Ser Asp Glu Gln Ser His Gln Ala Val Thr  
245 250 255

Glu Ala Met Arg Val Ile Gly Phe Ser Pro Glu Glu Val Glu Ser Val  
Page 97

260

265

270

His	Arg	Ile	Leu	Ala	Ala	Ile	Leu	His	Leu	Gly	Asn	Ile	Glu	Phe	Val
		275					280					285			
Glu	Thr	Glu	Glu	Gly	Gly	Leu	Gln	Lys	Glu	Gly	Leu	Ala	Val	Ala	Glu
	290					295					300				
Glu	Ala	Leu	Val	Asp	His	Val	Ala	Glu	Leu	Thr	Ala	Thr	Pro	Arg	Asp
	305				310					315					320
Leu	Val	Leu	Arg	Ser	Leu	Leu	Ala	Arg	Thr	Val	Ala	Ser	Gly	Gly	Arg
				325					330					335	
Glu	Leu	Ile	Glu	Lys	Gly	His	Thr	Ala	Ala	Glu	Ala	Ser	Tyr	Ala	Arg
			340					345					350		
Asp	Ala	Cys	Ala	Lys	Ala	Val	Tyr	Gln	Arg	Leu	Phe	Glu	Trp	Val	Val
		355					360					365			
Asn	Arg	Ile	Asn	Ser	Val	Met	Glu	Pro	Arg	Gly	Arg	Asp	Pro	Arg	Arg
	370					375					380				
Asp	Gly	Lys	Asp	Thr	Val	Ile	Gly	Val	Leu	Asp	Ile	Tyr	Gly	Phe	Glu
					390					395					400
Val	Phe	Pro	Val	Asn	Ser	Phe	Glu	Gln	Phe	Cys	Ile	Asn	Tyr	Cys	Asn
				405					410					415	
Glu	Lys	Leu	Gln	Gln	Leu	Phe	Ile	Gln	Leu	Ile	Leu	Lys	Gln	Glu	Gln
			420					425					430		
Glu	Glu	Tyr	Glu	Arg	Glu	Gly	Ile	Thr	Trp	Gln	Ser	Val	Glu	Tyr	Phe
		435					440					445			
Asn	Asn	Ala	Thr	Ile	Val	Asp	Leu	Val	Glu	Arg	Pro	His	Arg	Gly	Ile
	450					455					460				
Leu	Ala	Val	Leu	Asp	Glu	Ala	Cys	Ser	Ser	Ala	Gly	Thr	Ile	Thr	Asp
	465				470					475					480
Arg	Ile	Phe	Leu	Gln	Thr	Leu	Asp	Thr	His	His	Arg	His	His	Leu	His
				485					490					495	
Tyr	Thr	Ser	Arg	Gln	Leu	Cys	Pro	Thr	Asp	Lys	Thr	Met	Glu	Phe	Gly
			500					505					510		
Arg	Asp	Phe	Arg	Ile	Lys	His	Tyr	Ala	Gly	Asp	Val	Thr	Tyr	Ser	Val
		515					520					525			
Glu	Gly	Phe	Ile	Asp	Lys	Asn	Arg	Asp	Phe	Leu	Phe	Gln	Asp	Phe	Lys
	530					535					540				

N3027PCT\_sequ.list.txt

Arg Leu Leu Tyr Asn Ser Thr Asp Pro Thr Leu Arg Ala Met Trp Pro  
 545 550 555 560  
 Asp Gly Gln Gln Asp Ile Thr Gu Val Thr Lys Arg Pro Leu Thr Ala  
 565 570 575  
 Gly Thr Leu Phe Lys Asn Ser Met Val Ala Leu Val Glu Asn Leu Ala  
 580 585 590  
 Ser Lys Glu Pro Phe Tyr Val Arg Cys Ile Lys Pro Asn Glu Asp Lys  
 595 600 605  
 Val Ala Gly Lys Leu Asp Glu Asn His Cys Arg His Gln Val Ala Tyr  
 610 615 620  
 Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly Phe Ala Ser  
 625 630 635 640  
 Arg Gln Pro Tyr Ser Arg Phe Leu Leu Arg Tyr Lys Met Thr Cys Glu  
 645 650 655  
 Tyr Thr Trp Pro Asn His Leu Leu Gly Ser Asp Lys Ala Ala Val Ser  
 660 665 670  
 Ala Leu Leu Glu Gln His Gly Leu Gln Gly Asp Val Ala Phe Gly His  
 675 680 685  
 Ser Lys Leu Phe Ile Arg Ser Pro Arg Thr Leu Val Thr Leu Glu Gln  
 690 695 700  
 Ser Arg Ala Arg Leu Ile Pro Ile Ile Val Leu Leu Leu Gln Lys Ala  
 705 710 715 720  
 Trp Arg Gly Thr Leu Ala Arg Trp Arg Cys Arg Arg Leu Arg Ala Ile  
 725 730 735  
 Tyr Thr Ile Met Arg Trp Phe Arg Arg His Lys Val Arg Ala His Leu  
 740 745 750  
 Ala Glu Leu Gln Arg Arg Phe Gln Ala Ala Arg Gln Pro Pro Leu Tyr  
 755 760 765  
 Gly Arg Asp Leu Val Trp Pro Leu Pro Pro Ala Val Leu Gln Pro Phe  
 770 775 780  
 Gln Asp Thr Cys His Ala Leu Phe Cys Arg Trp Arg Ala Arg Gln Leu  
 785 790 795 800  
 Val Lys Asn Ile Pro Pro Ser Asp Met Pro Gln Ile Lys Ala Lys Val  
 805 810 815

N3027PCT\_sequ.list.txt

Ala Ala Met Gly Ala Leu Gln Gly Leu Arg Gln Asp Trp Gly Cys Arg  
820 825 830

Arg Ala Trp Ala Arg Asp Tyr Leu Ser Ser Ala Thr Asp Asn Pro Thr  
835 840 845

Ala Ser Ser Leu Phe Ala Gln Arg Leu Lys Thr Leu Arg Asp Lys Asp  
850 855 860

Gly Phe Gly Ala Val Leu Phe Ser Ser His Val Arg Lys Val Asn Arg  
865 870 875 880

Phe His Lys Ile Arg Asn Arg Ala Leu Leu Leu Thr Asp Gln His Leu  
885 890 895

Tyr Lys Leu Asp Pro Asp Arg Gln Tyr Arg Val Met Arg Ala Val Pro  
900 905 910

Leu Glu Ala Val Thr Gly Leu Ser Val Thr Ser Gly Gly Asp Gln Leu  
915 920 925

Val Val Leu His Ala Arg Gly Gln Asp Asp Leu Val Val Cys Leu His  
930 935 940

Arg Ser Arg Pro Pro Leu Asp Asn Arg Val Gly Glu Leu Val Gly Val  
945 950 955 960

Leu Ala Ala His Cys Gln Gly Glu Gly Arg Thr Leu Glu Val Arg Val  
965 970 975

Ser Asp Cys Ile Pro Leu Ser His Arg Gly Val Arg Arg Leu Ile Ser  
980 985 990

Val Glu Pro Arg Pro Glu Gln Pro Glu Pro Asp Phe Arg Cys Ala Arg  
995 1000 1005

Gly Ser Phe Thr Leu Leu Trp Pro Ser Arg  
1010 1015

<210> 27  
<211> 3807  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(3807)  
<223> myosin IH (MYO1H)

<400> 27  
aaagaagacg tgaggaggaa acacatccgt ctgcacatgg aaggggacgct gactgcccgg 60  
gacaagggtcg ggggttcagga ttttgtgcta ttggacgcgt acaccagcga atctgccttt 120

N3027PCT\_sequ. list.txt

gt cgacaacc t ccgcaagcg t t t cagcgag aacct cat at acacat at at t ggcaccct c	180
ct t gt gt ct g t gaat ccat a ccaggagct c ggaat ct aca ct gt gagcca gat ggaact t	240
t at caagggg t caat t t ct t t gaact gcca ccacat gt ct acgct at agc cgacaacgct	300
t accgaat ga t gt gt gct ga act aaat aac cat t t cat cc t cat t t ct gg agagagt ggg	360
gcagggaaaa cagaggcct c caagaaaat t ct cgagt at t t t gcagt gac ct gcccaat g	420
accagt cac t acaaat agc ccgt gacaga ct gct gt t ct ccaaccagt gct ggaggct	480
t t t ggaaat g ccagaacgct ccggaat gac aact ccagca gat t t gggaa at acat ggat	540
at acaat t t g at t t t caggg cat t cccgt a ggt gggcat a t cat cagt t a ct t gat agag	600
aagt cccgag t t gt ct acca aaacgaaggc gagcggaat t t ccacat ct t ct accagct g	660
ct ggcaggt g gcgaagagga ggcct gt ct t acct gggac t cgagcgaga cccccagct g	720
t at aaat acc t ct cacaggg t cat t gt gcc aaagagt cat ccatt agt ga caagaat gac	780
t ggaaaact g t t t ccaacgc ct t t t ct gt c at t gat t t t a ct gaagct ga cct cgagaat	840
ct ct t t ggaa t t at t gccag t gt ct t acac ct ggggaaca t t ggt t t t ga agaagacgac	900
caaggct gt g ccact at ccc agacacccat gagat caagt ggat agccaa gct cct gggg	960
gt ccacccat cagt cct t ct ggaagct ct c acccacagaa aaat t gaagc caaaact gag	1020
gaggt gat ct gcccgt t gac act agaact c t ct gt ct acg ct agagat gc aat ggcaaag	1080
gct gt t t at g gacgaacgt t t act t ggct g gt caacaaaa t caat t cct c ct t agt t aac	1140
aaggt t ggt c aacgcat t t t ggat ccct t g ct ct t gct ca cgt ggaaaac t gt aat t gga	1200
t t act ggaca t ct at ggggt t t gaagt ct t t gacaagaat g gt t t t gaaca gt t ct gt at a	1260
aat t act gca at gagaaact ccagcaact g t t aat t gaga ggact ct aaa agcagaacag	1320
gcagaat at g aaat ggaagg cat agagt gg gagccaat t a aat at t t caa caacaagat c	1380
at ct gt gat t t ggt agaaga gagacat aaa ggaat cat at ct at t ct gga t gaagaat gc	1440
at t cggcct g gt cct gct ac agact t gagt t t cct ggaga aat t ggaaga gaaagt gggc	1500
aaacat gcac act t cgaaac ccgt aagct g gct ggt ccaa agggccgaaa gaggat t ggc	1560
t ggat ggagt t ccgact cct ccact at gca ggagaggt ca cat act gcac caagggat t c	1620
t t ggaaaaaa acaat gat ct t ct t t acaga cat ct gaaag aagt gct gt g caagt ccaag	1680
aacat t at cc t gagggaat g ct t cct gct g gccgagt t ag aaaaccggag gaggccccc	1740
acagt gggga ct cagt t t aa aaacagt ct g agcagcct t c t agaaaccct cat ct ct aag	1800
gagccct cct acat ccgt t g cat caagccc aacgacagga aagaaccag caaat t t gat	1860
gact t cct ca t aaggcat ca gat caaat ac ct ggggct ga t ggagcacct gcgggt gaga	1920
cgggct ggt t t t gcat accg aaggaaat ac gagcat t t ct t gcaaaggt a caagt cct t a	1980
t gccagaca cct ggccgca ct ggcacggg cct ccagcag agggcgt gga acggct gat c	2040
aagt acat cg gct acaaacc cgaggaat ac aagt t aggca aaaccaaaat at t cat t cgt	2100
t t ccccagaa ct ct gt t t gc t accgaagat gcct t t gaat t t agt aaaca t caact agt t	2160
gcaagaat cc aagccact t a caaacgct gc ct aggaagga gagaat acgt gaaaaaaga	2220

N3027PCT\_sequ. list . . txt

caagcagcca t caaact gga agcccact gg cgt ggggccc t ggct cggaa ggcaat ccaa 2280  
aggagaaagt gggccgt gcg gat t at caga aagt t cat t a aaggat t cat cagt cgcaac 2340  
aaacccct ct gt cct gacaa cgaggaat t t at cgt gt t t g t gcggaagaa t t acat ct t g 2400  
aat ct ccggt at cacct t cc aaagact gt c ct ggacaaga gct ggct gag gcct cct ggc 2460  
at ct t ggaaa at gcat caga t ct gct cagg aaaat gt gcg t gaggaacct ggt gcagaag 2520  
t act gccgcg ggat cacagc t gagcggaaa gcaat gat gc agcaaaaggt agt t acaagt 2580  
gaaat ct t ca ggggaaggaa agacggct ac acagaaagt t t aaat caacc ct t t gt caac 2640  
agt cggat ag at gaaggaga cat t aat ccg aaagt gct t c agct aat t ag ccat gagaaa 2700  
at ccagt at g gt gt cccggt cat t aaat at gacagaaaag gct t caaagc acggcagcgg 2760  
caact cat t c t t act cagaa agcagct t ac gt ggt ggaac t t gccaaaat caagcagaaa 2820  
at agagt act cagct ct caa aggt gt ct cc act agcaat c t gagt gat gg aat ct t agt c 2880  
at t cat gt t t caccagagga cagcaagcaa aagggggat g ccgt t t t gca gt gt ggacac 2940  
gt gt t t gaag cagt t act aa act cgt cat g ct ggt t aaga aggagaacat t gt caat gt t 3000  
gt t caaggaa gt t t acagt t t t t at t agt ccgggaaaag aaggcacaat agt t t t cgac 3060  
act ggact gg aagaacaagt ct at aaaaat aaaaat ggac aat t aacagt ggt gt cagt c 3120  
cggaggaagt cct gat agag gat gacgt ct gacct ct acc at cgccat t t t t gct ccaac 3180  
t gaggaaact acaggggaag t ggggat t gg at ccagt t ag ct acct ct t c aaggt accag 3240  
gcccgcagca ct aacagat c acat ct gcaa ccct gaacgt gcaggt t gga gaacgaat ga 3300  
at acaaat t t t at t gt aaaa t aaaaat gt a t at aaagcat at gagcacac aaat ggacaa 3360  
t aaat gccac agcgcaaaag cgt gt agcga gcct gccacg ct t gt gact g gggaggggct 3420  
ccgt at aat c t cacct t t gc aagcgt t t at t t act gat gt at gcggccac cact gt gacc 3480  
accat cact t accgat t cac caaaact t ag gt aat at ggt ct t at t t t t g at t t aat t aa 3540  
at at acgt gt agct cat gt a t t t cacagt t t aat at gaga agt gct t t gg t ct t t at t t a 3600  
gaaat t ggggt gat gt t t t t g t gccagcaa cat gct gt ag gaat t t aact ct t gt t t aca 3660  
t ccat t agcc t cat ggt t t t gct t caagt c t cagct t cca agaacct at c gat gact t ac 3720  
t gt gcat ggt ct gagact aa gt aaaggaaa t t t cct aaag ct gt gaaat t t gaat t t t gc 3780  
t t t aaat aaa t ggaact cac at gt gt c 3807

<210> 28  
<211> 1032  
<212> PRT  
<213> Homo sapi ens

<220>  
<221> M SC FEATURE  
<222> (1) . . (1032)  
<223> myosi n I H (MYO1H)

<400> 28

Met Glu Gly Ala Leu Thr Ala Arg Asp Lys Val Gly Val Gln Asp Phe  
 1 5 10 15  
 Val Leu Leu Asp Ala Tyr Thr Ser Glu Ser Ala Phe Val Asp Asn Leu  
 20 25 30  
 Arg Lys Arg Phe Ser Glu Asn Leu Ile Tyr Thr Tyr Ile Gly Thr Leu  
 35 40 45  
 Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Gly Ile Tyr Thr Val Ser  
 50 55 60  
 Gln Met Glu Leu Tyr Gln Gly Val Asn Phe Phe Glu Leu Pro Pro His  
 65 70 75 80  
 Val Tyr Ala Ile Ala Asp Asn Ala Tyr Arg Met Met Cys Ala Glu Leu  
 85 90 95  
 Asn Asn His Phe Ile Leu Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr  
 100 105 110  
 Glu Ala Ser Lys Lys Ile Leu Glu Tyr Phe Ala Val Thr Cys Pro Met  
 115 120 125  
 Thr Gln Ser Leu Gln Ile Ala Arg Asp Arg Leu Leu Phe Ser Asn Pro  
 130 135 140  
 Val Leu Glu Ala Phe Gly Asn Ala Arg Thr Leu Arg Asn Asp Asn Ser  
 145 150 155 160  
 Ser Arg Phe Gly Lys Tyr Met Asp Ile Gln Phe Asp Phe Gln Gly Ile  
 165 170 175  
 Pro Val Gly Gly His Ile Ile Ser Tyr Leu Ile Glu Lys Ser Arg Val  
 180 185 190  
 Val Tyr Gln Asn Glu Gly Glu Arg Asn Phe His Ile Phe Tyr Gln Leu  
 195 200 205  
 Leu Ala Gly Gly Glu Glu Glu Arg Leu Ser Tyr Leu Gly Leu Glu Arg  
 210 215 220  
 Asp Pro Gln Leu Tyr Lys Tyr Leu Ser Gln Gly His Cys Ala Lys Glu  
 225 230 235 240  
 Ser Ser Ile Ser Asp Lys Asn Asp Trp Lys Thr Val Ser Asn Ala Phe  
 245 250 255  
 Ser Val Ile Asp Phe Thr Glu Ala Asp Leu Glu Asn Leu Phe Gly Ile  
 260 265 270  
 Ile Ala Ser Val Leu His Leu Gly Asn Ile Gly Phe Glu Glu Asp Asp

275

G n G y Oys Ala Thr Ile Pro Asp Thr His G u Ile Lys Trp Ile Ala  
290 295 300

Lys Leu Leu G y Val His Pro Ser Val Leu Leu G u Ala Leu Thr His  
305 310 315 320

Arg Lys Ile G u Ala Lys Thr G u G u Val Ile Oys Pro Leu Thr Leu  
325 330 335

G u Leu Ser Val Tyr Ala Arg Asp Ala Met Ala Lys Ala Val Tyr G y  
340 345 350

Arg Thr Phe Thr Trp Leu Val Asn Lys Ile Asn Ser Ser Leu Val Asn  
355 360 365

Lys Val G y G n Arg Ile Leu Asp Pro Leu Leu Leu Leu Thr Trp Lys  
370 375 380

Thr Val Ile G y Leu Leu Asp Ile Tyr G y Phe G u Val Phe Asp Lys  
385 390 395 400

Asn G y Phe G u G n Phe Oys Ile Asn Tyr Oys Asn G u Lys Leu G n  
405 410 415

G n Leu Leu Ile G u Arg Thr Leu Lys Ala G u G n Ala G u Tyr G u  
420 425 430

Met G u G y Ile G u Trp G u Pro Ile Lys Tyr Phe Asn Asn Lys Ile  
435 440 445

Ile Oys Asp Leu Val G u G u Arg His Lys G y Ile Ile Ser Ile Leu  
450 455 460

Asp G u G u Oys Ile Arg Pro G y Pro Ala Thr Asp Leu Ser Phe Leu  
465 470 475 480

G u Lys Leu G u G u Lys Val G y Lys His Ala His Phe G u Thr Arg  
485 490 495

Lys Leu Ala G y Pro Lys G y Arg Lys Arg Ile G y Trp Met G u Phe  
500 505 510

Arg Leu Leu His Tyr Ala G y G u Val Thr Tyr Oys Thr Lys G y Phe  
515 520 525

Leu G u Lys Asn Asn Asp Leu Leu Tyr Arg His Leu Lys G u Val Leu  
530 535 540

Oys Lys Ser Lys Asn Ile Ile Leu Arg G u Oys Phe Leu Leu Ala G u  
545 550 555 560

N3027PCT\_sequ.list.txt

Leu Glu Asn Arg Arg 565 Arg Pro Pro Thr Val 570 Gly Thr Glu Phe Lys 575 Asn  
 Ser Leu Ser Ser 580 Leu Leu Glu Thr Leu 585 Ile Ser Lys Glu 590 Pro Ser Tyr  
 Ile Arg Cys 595 Ile Lys Pro Asn Asp 600 Arg Lys Glu Pro Ser 605 Lys Phe Asp  
 Asp Phe 610 Leu Ile Arg His Glu 615 Ile Lys Tyr Leu Gly 620 Leu Met Glu His  
 Leu 625 Arg Val Arg Arg Ala 630 Gly Phe Ala Tyr Arg 635 Arg Lys Tyr Glu His 640  
 Phe Leu Glu Arg Tyr 645 Lys Ser Leu Cys Pro 650 Asp Thr Trp Pro His 655 Trp  
 His Gly Pro 660 Pro Ala Glu Gly Val Glu 665 Arg Leu Ile Lys Tyr 670 Ile Gly  
 Tyr Lys Pro 675 Glu Glu Tyr Lys Leu 680 Gly Lys Thr Lys Ile 685 Phe Ile Arg  
 Phe Pro 690 Arg Thr Leu Phe Ala 695 Thr Glu Asp Ala Phe 700 Glu Phe Ser Lys  
 His 705 Glu Leu Val Ala Arg 710 Ile Glu Ala Thr Tyr 715 Lys Arg Cys Leu Gly 720  
 Arg Arg Glu Tyr Val 725 Lys Lys Arg Glu Ala 730 Ala Ile Lys Leu Glu Ala 735  
 His Trp Arg Gly 740 Ala Leu Ala Arg Lys 745 Ala Ile Glu Arg Arg 750 Lys Trp  
 Ala Val Arg 755 Ile Ile Arg Lys Phe 760 Ile Lys Gly Phe Ile 765 Ser Arg Asn  
 Lys Pro 770 Leu Cys Pro Asp Asn 775 Glu Glu Phe Ile Val 780 Phe Val Arg Lys  
 Asn 785 Tyr Ile Leu Asn Leu 790 Arg Tyr His Leu Pro 795 Lys Thr Val Leu Asp 800  
 Lys Ser Trp Leu Arg 805 Pro Pro Gly Ile Leu 810 Glu Asn Ala Ser Asp 815 Leu  
 Leu Arg Lys Met 820 Cys Val Arg Asn Leu 825 Val Glu Lys Tyr Cys 830 Arg Gly

N3027PCT\_sequ.list.txt

I l e Thr A l a G l u A r g L y s A l a M e t M e t G n G n L y s V a l V a l T h r S e r  
835 840 845

G l u I l e P h e A r g G y A r g L y s A s p G y T y r T h r G l u S e r L e u A s n G n  
850 855 860

P r o P h e V a l A s n S e r A r g I l e A s p G l u G y A s p I l e A s n P r o L y s V a l  
865 870 875 880

L e u G n L e u I l e S e r H i s G l u L y s I l e G n T y r G y V a l P r o V a l I l e  
885 890 895

L y s T y r A s p A r g L y s G y P h e L y s A l a A r g G n A r g G n L e u I l e L e u  
900 905 910

T h r G n L y s A l a A l a T y r V a l V a l G l u L e u A l a L y s I l e L y s G n L y s  
915 920 925

I l e G l u T y r S e r A l a L e u L y s G y V a l S e r T h r S e r A s n L e u S e r A s p  
930 935 940

G y I l e L e u V a l I l e H i s V a l S e r P r o G l u A s p S e r L y s G n L y s G y  
945 950 955 960

A s p A l a V a l L e u G n C y s G y H i s V a l P h e G l u A l a V a l T h r L y s L e u  
965 970 975

V a l M e t L e u V a l L y s L y s G l u A s n I l e V a l A s n V a l V a l G n G y S e r  
980 985 990

L e u G n P h e P h e I l e S e r P r o G y L y s G l u G y T h r I l e V a l P h e A s p  
995 1000 1005

T h r G y L e u G l u G l u G n V a l T y r L y s A s n L y s A s n G y G n L e u  
1010 1015 1020

T h r V a l V a l S e r V a l A r g A r g L y s S e r  
1025 1030

<210> 29  
<211> 5798  
<212> DNA  
<213> Homo sapiens

<220>  
<221> m i s c \_ f e a t u r e  
<222> (1)..(5798)  
<223> myosin IIIA (MYO3A)

<400> 29  
ggatggcgcg gatggcgcgg cctccacctg cgggcagtg agagagcggc gagaggaaga 60  
atattccccg cgagccggga taaggggcc cttcggctcg gttgaccag gt cagat cct 120

N3027PCT\_sequelist.txt

cccgccgacc	ttcgggccgc	cctctacagg	cgggccagtt	cttcccctgc	t cggct gccc	180
ctgcccgccc	ctcgagggag	cgcccgt agc	cagcgccccc	gt aaagaaat	aaggaggcgc	240
ccggcttccc	gcccaggccc	agggccccag	tgcagcctgg	acacagttat	caaagttttg	300
gcgtctgagc	attgttatgc	gttattttca	agctttgcta	acggttttta	aacctttgag	360
atgtttccat	t aattggaaa	aacaatcatc	tttgataact	ttcctgatcc	ttctgataca	420
tgggaaatca	ctgagacaat	tggcaaagga	acttatggga	aagtttttaa	agtattgaat	480
aagaaaaatg	gccaaaaagc	agcagtcaaa	attcttgatc	caattcacga	tattgacgaa	540
gagattgaag	cagaatat aa	catcttaaaa	gcactttctg	accaccctaa	tgt ggt caga	600
ttctatggga	t atacttt aa	gaaggat aaa	gt aaat ggag	acaagctgtg	gtt ggt tctt	660
gagctctgca	gtggaggatc	agt gact gac	ctt gt gaaag	gatttctgaa	gaggggt gaa	720
agaatgagt g	agcctctaat	tgcctatatt	ttacatgaag	cactaatggg	acttcaacat	780
ttgcat aaca	acaaaactat	ccacagagat	gtgaaaggca	ataacattct	attgaccacg	840
gaagggtggag	t gaaact agt	agattttggg	gtgtctgcac	agctcaccag	t acccggcac	900
cgtcggaaca	catccgtagg	aacaccgttt	tggatggctc	ctgaggtgat	t gcat gt gaa	960
cagcaattgg	at accactta	t gacgccaga	tgt gacactt	gggtccctggg	t at cacggcc	1020
attgagctgg	gtgatggaga	tcctccacta	gct gaccttc	atcccatgag	agcactcttc	1080
aaaat accaa	ggaatccacc	cccaaaacta	aggcagcctg	agctatggtc	agcagaattc	1140
aatgacttca	t aagcaagt g	cttgactaaa	gattatgaaa	agcgtccaac	agtgtcagaa	1200
cttttacagc	ataaattcat	t actcaaat	gagggc aaag	atgtgatgct	acaaaaacaa	1260
ctaacggaat	t cattggcat	ccatcaatgc	atgggaggca	cagaaaaggc	cagacgt gaa	1320
cgtattcaca	cgaagaaagg	gaacttcaac	cgacctctaa	t atccaatct	gaaggatgta	1380
gatgatttag	caaccctaga	aattttggat	gagaat acag	tctcagagca	acttgagaag	1440
tgttattcca	gagatcagat	ctacgtctat	gtgggagaca	t actcattgc	tcttaaccct	1500
tttcagagtc	tgggtcttta	ctccacaaag	cattccaaac	t at atattgg	atcaaagaga	1560
actgccagtc	ctcctcacat	ttttgcaatg	gctgacttag	gatataatc	t at gat aaca	1620
tataattcag	atcagtgcac	tgttatttct	ggagaaagt g	gtgctggaaa	gactgaaaat	1680
gctcatcttt	tagttcagca	gctgacagt g	cttggaaagg	ctaat aacag	aaccttgcaa	1740
gagaagattt	tacaagt gaa	caatttggta	gaagcctttg	gcaatgcctg	cactattata	1800
aatgacaatt	ctagcagatt	tggaaaat ac	ttagaaatga	aattcacctc	ttctggagcg	1860
gtagtgggag	cacagatttc	tgaatatctc	ctggaaaaat	cccaggttat	ccaccaagct	1920
attggagaaa	aaaattttca	tattttttac	tacatttatg	ctggtttggc	t gaaaagaag	1980
aaactagccc	attacaaact	gcctgaaaat	aagcctccca	ggtagctaca	aaatgaccac	2040
ctcagaacag	tacaagacat	catgaataat	agtttctata	aatcccagta	tgaattaat	2100
gagcaatgtt	tcaaagtcat	aggttttaca	atggagcaac	ttggtagtat	at acagcat a	2160
ctcgctgcaa	tcttgaatgt	tggcaacatt	gaattttctt	ctgtggcaac	tgaacaccag	2220

N3027PCT\_sequ. list . . txt

at t gacaaga gccacat t t c t aat cat aca gccct ggaga act gt gct t c t t t gct t t gc	2280
at t cgggcag at gagct aca agaagct ct c acct cccact gt gt ggt cac t agaggagaa	2340
acaat t at ac gacccaat ac t gt agaaaaa gct accgat g t cagggat gc cat ggct aaa	2400
act t t at at g gacgt ct ct t t agt t ggat a gt caat t gca t t aacagt t t gt t gaagcat	2460
gact cat cac caagt gggaa t ggt gat gag ct gagcat t g gcatt ct t ga t at at t t ggc	2520
t t t gaaaat t t caaaaaaaa t t cct t cgag cagct gt gca t t aacat t gc aaat gaacaa	2580
at t cagt at t at t at aat ca acat gt gt t t gcat gggaac agaat gaat a cct aaat gaa	2640
gat gt ggat g ct agagt t at t gaat at gag gat aact ggc ccct ct t aga t at gt t t ct g	2700
caaaagccaa t ggggt t t act t t ccct act t gat gaagaaa gt agat t t cc caaggccact	2760
gaccagact c t t gt agaaaa at t t gaaggt aacct gaaat cacaat act t ct ggagaccc	2820
aaaagaat gg aact t agt t t t ggaa t t cac cat t at gcag gaaaggt cct ct at aat gca	2880
agt ggat t ct t agccaaaaa cagagacact ct t cct act g acat t gt gct act t t t gagg	2940
t cat ccgaca acagt gt aat t aggcaact a gt caaccacc ct ct gaccaa aacaggt aat	3000
ct gccacat t ct aaaact aa aaat gt t at a aact at caaa t gaggact t c agaaaaat t a	3060
at caacct gg caaagggcga cact ggagaa gccacacgt c at gccagaga gacaaccaac	3120
at gaaaacac aaacggt t gc at cat at t t t agat at t ccc t gat ggat t t gt t gt ct aaa	3180
at ggt ggt gg gccaacct ca t t t t gt ccgt t gcat caaac caaat agt ga gcgt caggca	3240
agaaaaat at g acaaagagaa agt t ct gct a cagct t cggt acacaggaat t ct ggaaaca	3300
gcaagaat t c gaagact agg at t ct cccat cggat act t t t t gct aact t t at aaagcgg	3360
t act acct t c t ct gct acaa gt cgagcgag gagccccgca t gagccct ga cacct gt gcc	3420
accat t t t gg aaaaagct gg t ct cgat aac t gggct ct t g gaaaaacaaa agt gt t cct t	3480
aagt at t at c acgt ggagca gt t aaat ct a at gcgaaagg aagct at t ga caagct t at t	3540
t t gat t caag ct t gt gt cag agcat t ct t g t gt t caagaa gat accaaaa aat acaggag	3600
aaaaggaaaag aaagcgct at aat aat acag t cagct gcaa gaggacacct t gt caggaaa	3660
caaagaaaaag aaat t gt t ga cat gaaaaac acagcagt aa caacct t ca aact t ct gat	3720
caggaat t cg act acaagaa aaact t t gaa aat acaaggg aat ct t t cgt gaagaaacaa	3780
gcagaaaaat g caat ct ct gc t aat gaaaga t t cat t t cag ct ccaaat aa t aaaggaagt	3840
gt at ct gt ag t gaagact t c cact t t caaa cct gaagagg aaaccaccaa t gct gt ggag	3900
agt aacaaca gagt gt at ca gact ccaaaa aaaat gaat a at gt gt at ga ggaagaggt t	3960
aagcaagaat t ct acct t gt agggccagaa gt aagcccca aacagaagt c t gt caaagac	4020
ct ggaagaga acagcaat ct aaggaaagt g gagaaagagg aagct at gat ccagagt t ac	4080
t at cagaggt acacagagga gaggaat t gt gaagagt caa aagcagcat a t ct agaaagg	4140
aaggccat at cagaaaggcc aagct accca gt gcct t ggt t agct gaaaa t gagact t cc	4200
t t t aaaaaaa ct t t ggaacc t aact t agc caaaggt caa t t t at caaaa t gcaaacagc	4260

N3027PCT\_sequ. list . . txt

at ggaaaaag aaaagaagac at ct gt agt t acccagcgt g caccgat at g cagccaggag 4320  
gaaggcagag gccgt ct gag gcat gagaca gt caaagaga ggcaagt t ga accagt gaca 4380  
caggcccagg aggaagaaga t aaagcagcg gt at t cat t c agagcaaat a ccgggggt t ac 4440  
aagagaaggc agcagt t gag gaaggacaag at gt ct t ct t t t aagcat ca gaggat t gt c 4500  
acaacaccaa cagaagt agc aagaaacact cat aat t t gt at t cct at cc cacaaaaacat 4560  
gaggaaat ca at aacat caa gaagaaggat aacaaagact cgaaagcaac t t cagaaaga 4620  
gaagcat gt g g t t t ggcaat t t t t t caaaa cagat at caa agt t at ct ga aga at t t t c 4680  
at t ct gcaga aaaaat t gaa t gaaat gat t t t gt cacagc aact gaagt c act t t at ct g 4740  
gggt gt ct cgc accat aagcc aat t aat aga cgagt t t ct t ct cagcagt g cct ct caggt 4800  
gt ct gt aaag gagaggagcc aaaaat at t g agacccccaa gacgaccccg gaaacccaaa 4860  
acat t aaat a accct gaaga ct ccacat ac t at t at ct ac t t cat aagt c aat ccaagaa 4920  
gaaaaacgaa gaccaaggaa agacagt cag ggaaaat t at t agat t t gga agat t t ct at 4980  
t at aaggaat t t t t gccag t cgt t ct gga ccaaaggaac at agccct ag t t t aagagaa 5040  
cgaagaccac agcaagaact ccagaat caa t gt at t aagg ct aat gaaag gt gct gggcg 5100  
gcgagagagcc ccgagaagga ggaggagaga gagccagcag ccaaccct a cgact t cagg 5160  
aggct cct gc gcaaaacct c ccagcgccgg cgcct cgt cc agcagt cct a accgt t caac 5220  
gaggcagt ca ccgccgt cgg aaggcgct gg agcct gcggg gcagcagggg ccaagcaggc 5280  
act ct ggggc t ggcaccagc aggcact gaa gct gcggccc t gat ct ccgc agaggct gcc 5340  
t gct gcgct c ggccct caag t gcccgggcc ggcct t cgt g ct ccgaaaca agagacct gg 5400  
gagccct cgg gaaacct ccc ccgacgct ct ct ct cggaac t cccgcaccc t cct t t ct ca 5460  
ccagcccgcc agt t gt ggca accct gt cct t gt t cccct a at ct at cact t t gt t ct t t t 5520  
t t t t t gt gac t cct gt ggac t ccact gcgc ct gggat ct c gccaacccct ct ct cat t t g 5580  
gggt gact ga at t cacagat t t t t t t t t at t ggaaacg gct t t t ct t g gccaacagaa 5640  
cact t gct ag cgg t t gaat c t t agagaaaa aagcccggga ggggt gggga gaat t t cgaa 5700  
gat gt at t t c at ct caagct t gct ct t t ct ct t cct t t gg t t at t aaggt cact aaat aa 5760  
aggaagt gcc t t ggaaaacc cgt gaaaaaa aaaaaaaa 5798

<210> 30  
<211> 1616  
<212> PRT  
<213> Homo sapiens

<220>  
<221> M SC\_FEATURE  
<222> (1) . . (1616)  
<223> myosin IIIA (MYO3A)

<400> 30

Met Phe Pro Leu Ile Gly Lys Thr Ile Ile Phe Asp Asn Phe Pro Asp  
1 5 10 15

N3027PCT\_sequ.list.txt

Pro Ser Asp Thr Trp Glu Ile Thr Glu Thr Ile Gly Lys Gly Thr Tyr  
20 25 30

Gly Lys Val Phe Lys Val Leu Asn Lys Lys Asn Gly Gln Lys Ala Ala  
35 40 45

Val Lys Ile Leu Asp Pro Ile His Asp Ile Asp Glu Glu Ile Glu Ala  
50 55 60

Glu Tyr Asn Ile Leu Lys Ala Leu Ser Asp His Pro Asn Val Val Arg  
65 70 75 80

Phe Tyr Gly Ile Tyr Phe Lys Lys Asp Lys Val Asn Gly Asp Lys Leu  
85 90 95

Trp Leu Val Leu Glu Leu Cys Ser Gly Gly Ser Val Thr Asp Leu Val  
100 105 110

Lys Gly Phe Leu Lys Arg Gly Glu Arg Met Ser Glu Pro Leu Ile Ala  
115 120 125

Tyr Ile Leu His Glu Ala Leu Met Gly Leu Gln His Leu His Asn Asn  
130 135 140

Lys Thr Ile His Arg Asp Val Lys Gly Asn Asn Ile Leu Leu Thr Thr  
145 150 155 160

Glu Gly Gly Val Lys Leu Val Asp Phe Gly Val Ser Ala Gln Leu Thr  
165 170 175

Ser Thr Arg His Arg Arg Asn Thr Ser Val Gly Thr Pro Phe Trp Met  
180 185 190

Ala Pro Glu Val Ile Ala Cys Glu Gln Gln Leu Asp Thr Thr Tyr Asp  
195 200 205

Ala Arg Cys Asp Thr Trp Ser Leu Gly Ile Thr Ala Ile Glu Leu Gly  
210 215 220

Asp Gly Asp Pro Pro Leu Ala Asp Leu His Pro Met Arg Ala Leu Phe  
225 230 235 240

Lys Ile Pro Arg Asn Pro Pro Pro Lys Leu Arg Gln Pro Glu Leu Trp  
245 250 255

Ser Ala Glu Phe Asn Asp Phe Ile Ser Lys Cys Leu Thr Lys Asp Tyr  
260 265 270

Glu Lys Arg Pro Thr Val Ser Glu Leu Leu Gln His Lys Phe Ile Thr  
275 280 285

Gln Ile Glu Gly Lys Asp Val Met Leu Gln Lys Gln Leu Thr Glu Phe  
 290 295 300  
 Ile Gly Ile His Gln Cys Met Gly Gly Thr Glu Lys Ala Arg Arg Glu  
 305 310 315 320  
 Arg Ile His Thr Lys Lys Gly Asn Phe Asn Arg Pro Leu Ile Ser Asn  
 325 330 335  
 Leu Lys Asp Val Asp Asp Leu Ala Thr Leu Glu Ile Leu Asp Glu Asn  
 340 345 350  
 Thr Val Ser Glu Gln Leu Glu Lys Cys Tyr Ser Arg Asp Gln Ile Tyr  
 355 360 365  
 Val Tyr Val Gly Asp Ile Leu Ile Ala Leu Asn Pro Phe Gln Ser Leu  
 370 375 380  
 Gly Leu Tyr Ser Thr Lys His Ser Lys Leu Tyr Ile Gly Ser Lys Arg  
 385 390 395 400  
 Thr Ala Ser Pro Pro His Ile Phe Ala Met Ala Asp Leu Gly Tyr Gln  
 405 410 415  
 Ser Met Ile Thr Tyr Asn Ser Asp Gln Cys Ile Val Ile Ser Gly Glu  
 420 425 430  
 Ser Gly Ala Gly Lys Thr Glu Asn Ala His Leu Leu Val Gln Gln Leu  
 435 440 445  
 Thr Val Leu Gly Lys Ala Asn Asn Arg Thr Leu Gln Glu Lys Ile Leu  
 450 455 460  
 Gln Val Asn Asn Leu Val Glu Ala Phe Gly Asn Ala Cys Thr Ile Ile  
 465 470 475 480  
 Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Leu Glu Met Lys Phe Thr  
 485 490 495  
 Ser Ser Gly Ala Val Val Gly Ala Gln Ile Ser Glu Tyr Leu Leu Glu  
 500 505 510  
 Lys Ser Arg Val Ile His Gln Ala Ile Gly Glu Lys Asn Phe His Ile  
 515 520 525  
 Phe Tyr Tyr Ile Tyr Ala Gly Leu Ala Glu Lys Lys Lys Leu Ala His  
 530 535 540  
 Tyr Lys Leu Pro Glu Asn Lys Pro Pro Arg Tyr Leu Gln Asn Asp His  
 545 550 555 560  
 Leu Arg Thr Val Gln Asp Ile Met Asn Asn Ser Phe Tyr Lys Ser Gln  
 Page 111

565

570

575

Tyr Glu Leu Ile Glu Gln Cys Phe Lys Val Ile Gly Phe Thr Met Glu  
 580 585 590  
 Gln Leu Gly Ser Ile Tyr Ser Ile Leu Ala Ala Ile Leu Asn Val Gly  
 595 600 605  
 Asn Ile Glu Phe Ser Ser Val Ala Thr Glu His Gln Ile Asp Lys Ser  
 610 615 620  
 His Ile Ser Asn His Thr Ala Leu Glu Asn Cys Ala Ser Leu Leu Cys  
 625 630 635 640  
 Ile Arg Ala Asp Glu Leu Gln Glu Ala Leu Thr Ser His Cys Val Val  
 645 650 655  
 Thr Arg Gly Glu Thr Ile Ile Arg Pro Asn Thr Val Glu Lys Ala Thr  
 660 665 670  
 Asp Val Arg Asp Ala Met Ala Lys Thr Leu Tyr Gly Arg Leu Phe Ser  
 675 680 685  
 Trp Ile Val Asn Cys Ile Asn Ser Leu Leu Lys His Asp Ser Ser Pro  
 690 695 700  
 Ser Gly Asn Gly Asp Glu Leu Ser Ile Gly Ile Leu Asp Ile Phe Gly  
 705 710 715 720  
 Phe Glu Asn Phe Lys Lys Asn Ser Phe Glu Gln Leu Cys Ile Asn Ile  
 725 730 735  
 Ala Asn Glu Gln Ile Gln Tyr Tyr Tyr Asn Gln His Val Phe Ala Trp  
 740 745 750  
 Glu Gln Asn Glu Tyr Leu Asn Glu Asp Val Asp Ala Arg Val Ile Glu  
 755 760 765  
 Tyr Glu Asp Asn Trp Pro Leu Leu Asp Met Phe Leu Gln Lys Pro Met  
 770 775 780  
 Gly Leu Leu Ser Leu Leu Asp Glu Glu Ser Arg Phe Pro Lys Ala Thr  
 785 790 795 800  
 Asp Gln Thr Leu Val Glu Lys Phe Glu Gly Asn Leu Lys Ser Gln Tyr  
 805 810 815  
 Phe Trp Arg Pro Lys Arg Met Glu Leu Ser Phe Gly Ile His His Tyr  
 820 825 830  
 Ala Gly Lys Val Leu Tyr Asn Ala Ser Gly Phe Leu Ala Lys Asn Arg  
 835 840 845

N3027PCT\_sequ.list.txt

Asp Thr Leu Pro Thr Asp Ile Val Leu Leu Leu Arg Ser Ser Asp Asn  
 850 855 860  
 Ser Val Ile Arg Gln Leu Val Asn His Pro Leu Thr Lys Thr Gly Asn  
 865 870 875 880  
 Leu Pro His Ser Lys Thr Lys Asn Val Ile Asn Tyr Gln Met Arg Thr  
 885 890 895  
 Ser Glu Lys Leu Ile Asn Leu Ala Lys Gly Asp Thr Gly Glu Ala Thr  
 900 905 910  
 Arg His Ala Arg Glu Thr Thr Asn Met Lys Thr Gln Thr Val Ala Ser  
 915 920 925  
 Tyr Phe Arg Tyr Ser Leu Met Asp Leu Leu Ser Lys Met Val Val Gly  
 930 935 940  
 Gln Pro His Phe Val Arg Cys Ile Lys Pro Asn Ser Glu Arg Gln Ala  
 945 950 955 960  
 Arg Lys Tyr Asp Lys Glu Lys Val Leu Leu Gln Leu Arg Tyr Thr Gly  
 965 970 975  
 Ile Leu Glu Thr Ala Arg Ile Arg Arg Leu Gly Phe Ser His Arg Ile  
 980 985 990  
 Leu Phe Ala Asn Phe Ile Lys Arg Tyr Tyr Leu Leu Cys Tyr Lys Ser  
 995 1000 1005  
 Ser Glu Glu Pro Arg Met Ser Pro Asp Thr Cys Ala Thr Ile Leu  
 1010 1015 1020  
 Glu Lys Ala Gly Leu Asp Asn Trp Ala Leu Gly Lys Thr Lys Val  
 1025 1030 1035  
 Phe Leu Lys Tyr Tyr His Val Glu Gln Leu Asn Leu Met Arg Lys  
 1040 1045 1050  
 Glu Ala Ile Asp Lys Leu Ile Leu Ile Gln Ala Cys Val Arg Ala  
 1055 1060 1065  
 Phe Leu Cys Ser Arg Arg Tyr Gln Lys Ile Gln Glu Lys Arg Lys  
 1070 1075 1080  
 Glu Ser Ala Ile Ile Ile Gln Ser Ala Ala Arg Gly His Leu Val  
 1085 1090 1095  
 Arg Lys Gln Arg Lys Glu Ile Val Asp Met Lys Asn Thr Ala Val  
 1100 1105 1110

N3027PCT\_sequ.list.txt

Thr	Thr	Ile	Gln	Thr	Ser	Asp	Gln	Glu	Phe	Asp	Tyr	Lys	Lys	Asn
1115						1120					1125			
Phe	Glu	Asn	Thr	Arg	Glu	Ser	Phe	Val	Lys	Lys	Gln	Ala	Glu	Asn
1130						1135					1140			
Ala	Ile	Ser	Ala	Asn	Glu	Arg	Phe	Ile	Ser	Ala	Pro	Asn	Asn	Lys
1145						1150					1155			
Gly	Ser	Val	Ser	Val	Val	Lys	Thr	Ser	Thr	Phe	Lys	Pro	Glu	Glu
1160						1165					1170			
Glu	Thr	Thr	Asn	Ala	Val	Glu	Ser	Asn	Asn	Arg	Val	Tyr	Gln	Thr
1175						1180					1185			
Pro	Lys	Lys	Met	Asn	Asn	Val	Tyr	Glu	Glu	Glu	Val	Lys	Gln	Glu
1190						1195					1200			
Phe	Tyr	Leu	Val	Gly	Pro	Glu	Val	Ser	Pro	Lys	Gln	Lys	Ser	Val
1205						1210					1215			
Lys	Asp	Leu	Glu	Glu	Asn	Ser	Asn	Leu	Arg	Lys	Val	Glu	Lys	Glu
1220						1225					1230			
Glu	Ala	Met	Ile	Gln	Ser	Tyr	Tyr	Gln	Arg	Tyr	Thr	Glu	Glu	Arg
1235						1240					1245			
Asn	Cys	Glu	Glu	Ser	Lys	Ala	Ala	Tyr	Leu	Glu	Arg	Lys	Ala	Ile
1250						1255					1260			
Ser	Glu	Arg	Pro	Ser	Tyr	Pro	Val	Pro	Trp	Leu	Ala	Glu	Asn	Glu
1265						1270					1275			
Thr	Ser	Phe	Lys	Lys	Thr	Leu	Glu	Pro	Thr	Leu	Ser	Gln	Arg	Ser
1280						1285					1290			
Ile	Tyr	Gln	Asn	Ala	Asn	Ser	Met	Glu	Lys	Glu	Lys	Lys	Thr	Ser
1295						1300					1305			
Val	Val	Thr	Gln	Arg	Ala	Pro	Ile	Cys	Ser	Gln	Glu	Glu	Gly	Arg
1310						1315					1320			
Gly	Arg	Leu	Arg	His	Glu	Thr	Val	Lys	Glu	Arg	Gln	Val	Glu	Pro
1325						1330					1335			
Val	Thr	Gln	Ala	Gln	Glu	Glu	Glu	Asp	Lys	Ala	Ala	Val	Phe	Ile
1340						1345					1350			
Gln	Ser	Lys	Tyr	Arg	Gly	Tyr	Lys	Arg	Arg	Gln	Gln	Leu	Arg	Lys
1355						1360					1365			

Asp Lys Met Ser Ser Phe Lys His Gln Arg Ile Val Thr Thr Pro  
 1370 1375 1380  
 Thr Glu Val Ala Arg Asn Thr His Asn Leu Tyr Ser Tyr Pro Thr  
 1385 1390 1395  
 Lys His Glu Glu Ile Asn Asn Ile Lys Lys Lys Asp Asn Lys Asp  
 1400 1405 1410  
 Ser Lys Ala Thr Ser Glu Arg Glu Ala Cys Gly Leu Ala Ile Phe  
 1415 1420 1425  
 Ser Lys Gln Ile Ser Lys Leu Ser Glu Glu Tyr Phe Ile Leu Gln  
 1430 1435 1440  
 Lys Lys Leu Asn Glu Met Ile Leu Ser Gln Gln Leu Lys Ser Leu  
 1445 1450 1455  
 Tyr Leu Gly Val Ser His His Lys Pro Ile Asn Arg Arg Val Ser  
 1460 1465 1470  
 Ser Gln Gln Cys Leu Ser Gly Val Cys Lys Gly Glu Glu Pro Lys  
 1475 1480 1485  
 Ile Leu Arg Pro Pro Arg Arg Pro Arg Lys Pro Lys Thr Leu Asn  
 1490 1495 1500  
 Asn Pro Glu Asp Ser Thr Tyr Tyr Tyr Leu Leu His Lys Ser Ile  
 1505 1510 1515  
 Gln Glu Glu Lys Arg Arg Pro Arg Lys Asp Ser Gln Gly Lys Leu  
 1520 1525 1530  
 Leu Asp Leu Glu Asp Phe Tyr Tyr Lys Glu Phe Leu Pro Ser Arg  
 1535 1540 1545  
 Ser Gly Pro Lys Glu His Ser Pro Ser Leu Arg Glu Arg Arg Pro  
 1550 1555 1560  
 Gln Gln Glu Leu Gln Asn Gln Cys Ile Lys Ala Asn Glu Arg Cys  
 1565 1570 1575  
 Trp Ala Ala Glu Ser Pro Glu Lys Glu Glu Glu Arg Glu Pro Ala  
 1580 1585 1590  
 Ala Asn Pro Tyr Asp Phe Arg Arg Leu Leu Arg Lys Thr Ser Gln  
 1595 1600 1605  
 Arg Arg Arg Leu Val Gln Gln Ser  
 1610 1615

<211> 5448  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(5448)  
 <223> myosin III B MYO3B transcript variant 1

<400> 31  
 ct agat cgaa agt cct t t gg t aat gat gt g t cat acat t c t agt cat caa agacaccat t 60  
 t t ct gggcct gaagt gt t ct gct ggt t t t t ggaggaat ga gaat ccaat c t ct cat aagc 120  
 cggat t caga aaat aggt ca t cgat gaaac at ct gt at gg at t at t t cac t at aat cct a 180  
 t gat gct t gg act t gaat ca ct t ccagat c ccacagacac ct gggaaat t at agagacca 240  
 t t ggt aaagg cacct at ggc aaagt ct aca aggt aact aa caagagagat gggagcct gg 300  
 ct gcagt gaa aat t ct ggat ccagt cagt g at at ggat ga agaaat t gag gcagaat aca 360  
 acat t t t gca gt t cct t cct aat cat ccca at gt t gt aaa gt t t t at ggg at gt t t t aca 420  
 aagcggat ca ct gt gt aggg ggacagct gt ggct ggt cct ggagct gt gt aat gggggct 480  
 cagt cact ga gct t gt caaa ggt ct act ca gat gt ggcca gcggt t ggat gaagcaat ga 540  
 t ct cat acat ct t gt acggg gccct ct t gg gcct t cagca t t t gcacaac aaccgaat ca 600  
 t ccaccgt ga t gt gaagggg aat aacat t c t t ct gacaac agaaggagga gt t aagct cg 660  
 t t gact t t gg t gt t t cagct caact cacca gt acacgt ct gcggagaaac acat ct gt t g 720  
 gcaccccat t ct ggat ggcc cct gaggt ca t t gcct gt ga gcagcagt at gact ct t cct 780  
 at gacgct cg ct gt gacgt c t ggt cct t gg ggat cacagc t at t gaact g ggggat ggag 840  
 accct cccct ct t t gacat g cat cct gt ga aaacact ct t t aagat t cca agaaat cct c 900  
 cacct act t t act t cat cca gaaaaat ggt gt gaagaat t caaccact t t at t t cacagt 960  
 gt ct t at t aa ggat t t t gaa aggcgacct t ccgt cacaca t ct cct t gac cacccat t t a 1020  
 t t aaaggagt acat ggaaaa gt t ct gt t t c t gcaaaaaca gct ggccaag gt t ct ccaag 1080  
 accagaagca t caaaat cct gt t gct aaaa ccaggcat ga gaggat gcat accagaagac 1140  
 ct t at cat gt ggaagat gct gaaaaat act gcct t gagga t gat t t ggt c aacct agagg 1200  
 t t ct ggat ga ggat acaat t at ccat cagt t gcagaaacg t t at gcagac t t gct aat t t 1260  
 acacat at gt t ggagacat c t t aat t gcct t aaaccct t ccagaat ct a agcat at act 1320  
 ct ccacagt t t t ccagact t t at cat gggg t gaaacgcgc ct ccaat ccc ccccat at 1380  
 t t gcat cagc agat gct gct t accagt gca t ggt t act ct cagcaaagac cagt gcat t g 1440  
 t cat cagcgg agagagt ggc t ct gggaaga cagaaagcgc ccacct gat t gt t caacat t 1500  
 t gact t t ct t gggaaaggcc aat aat caga cct t gagaga gaaaat t ct a caagt caact 1560  
 ccct ggt gga agcct t t ggg aact cat gca ct gccat caa t gacaact cg agccgt t t t g 1620  
 gaaaat at ct ggaaat gat g t t t acaccaa ct ggagt t gt gat gggggca agaat ct ct g 1680  
 aat at ct cct ggaaaaat cc agagt t at aa aacaggcagc gagagagaaa aat t t t cat a 1740

N3027PCT\_sequ. list.txt

t a t t t a c t a t a t t t a t g c t	g g t c t t c a t c a c c a a a a g a a	g c t t t c t g a t t t c a g a c t t c	1800
c t g a g g a a a a a c c t c c t a g g	t a c a t a g c t g a t g a a a c t g g	a a g g g t g a t g c a c g a c a t a a	1860
c t t c c a a g g a g t c t t a c a g a	a g a c a a t t c g a a g c a a t t c a	g c a t t g c t t c a g g a t t a t a g	1920
g g t t c a c g g a c a a a g a g g t g	c a c t c a g t g t a c a g a a t t t t	g g c t g g g a t t t t g a a t a t t g	1980
g g a a c a t t g a g t t c g c a g c t	a t t t c c t c t c a a c a t c a g a c	t g a t a a a a g t g a g g t g c c c a	2040
a t g c t g a a g c t t t g c a a a a t	g c t g c c t c t g t t c t g t g c a t	t a g c c c t g a a g a g c t c c a g g	2100
a g g c c c t c a c c t c c c a c t g t	g t g g t c a c c c g g g g c g a g a c	c a t c a t c c g t g c c a a c a c t g	2160
t a g a c a g g g c t g c g g a c g t t	c g a g a c g c c a t g t c c a a a g c	c c t g t a t g g g a g g c t c t t c a	2220
g c t g g a t t g t g a a t c g c a t t	a a t a c a c t c c t g c a g c c a g a	c g a a a a c a t a t g t a g t g c a g	2280
g a g g t g g a a t g a a t g t g g g g	a t c t t g g a t a t c t t t g g a t t	c g a g a a t t t t c a g a g a a a t t	2340
c a t t t g a g c a g c t c t g c a t a	a a c a t c g c c a a t g a g c a a a t	c c a g t a c t a t t t c a a t c a g c	2400
a t g t t t t t g c t c t t g a g c a g	a t g g a a t a t c a g a a t g a a g g	c a t t g a t g c t g t a c c c g t g g	2460
a a t a t g a g g a c a a c c g c c c g	c t c t t g g a c a t g t t c c t c c a	g a a a c c c c t g g g a c t g c t t g	2520
c a c t t t t g g a t g a g g a a a g t	c g g t t t c c c c a a g c a a c t g a	c c a g a c c c t g g t t g a t a a a t	2580
t t g a a g a t a a t c t a c g a t g c	a a a t a c t t c t g g a g g c c c a a	a g g a g t g g a a c t g t g c t t t g	2640
g c a t t c a g c a t t a t g c t g g a	a a g g t a t t a t a t g a t g c t t c	t g g g g t t c t t g a g a a a a a t a	2700
g a g a c a c t c t c c c t g c c g a t	g t g g t t g t g g t c c t g a g a a c	g t c a g a a a a c a t g c t t c t t c	2760
a g c a g c t c t t c t c a a t c c c t	c t g a c c a a a a c a g g t a a t t t	g g c c c a g a c a a g a g c t a g g a	2820
t a a c a g t g g c c t c a a g t t c t	t t g c c t c c a c a t t t c a g t g c	t g g g a a a g c c a a g g t g g a c a	2880
c t c t g g a g g t g a t a c g g c a t	c c g g a a g a a a c c a c c a a c a t	g a a g a g g c a a a c t g t g g c t t	2940
c t t a c t t c c g g t a t t c t c t g	a t g g a c c t g c t c t c c a a a a t	g g t g g t t g g a c a g c c c c a c t	3000
t t g t g c g c t g c a t t a a a c c c	a a t g a t g a c c g a g a g g c c c t	g c a g t t c t c t c g a g a g a g g g	3060
t g c t g g c c c a g c t c c g c t c c	a c a g g g a t t c t g g a g a c a g t	c a g c a t c c g c c g c c a g g g c t	3120
a t t c c c a c c g c a t c c t t t t t	g a a g a a t t t g t g a a a a g g t a	t t a t t a c t t g g c a t t c a c a g	3180
c a c a t c a a a c a c c t c t t g c t	a g c a a g a g a g c t g t g t g g c	t a t c t t g g a a a g t c c a g a t	3240
t a g a t c a c t g g g t g c t g g g a	a a a c a a a a g g t t t t t c t c a a	a t a t t a c c a t g t t g a g c a a t	3300
t a a a t t t g c t g c t t c g a g a a	g t c a t a g g c a g a g t g g t t g t	g c t g c a g g c a t a t a c c a a g g	3360
g g t g g c t t g g a g c c a g g a g a	t a c a a a a a g g t c a g a g a g a a	g a g a g a g a a g g g a g c c a t t g	3420
c c a t c c a g t c a g g g g a c a c t	t c a a a c c a a a g c a g t g g g c c	a c a t t c c c c c g t c g c a g c a g	3480
g t a c g a g g g g a a g t g c c g a g	g t t c a a g a c t g c a g c g a g c c	t g g t g a c c a t a a a g t t c t c a	3540
g g g g c t c t g t a c a t c g t a g g	a g c c a t t c a c a a g c a g a a t c	c a a c a a t g g c c g t a c a c a g a	3600
c t t c a a g c a a c t c t c c t g c t	g t c a c a g a g a a a a a t g g g c a	t t c a c a a g c c c a g a g t t c t c	3660
c a a a a g g g t g c g a t a t c t t c	g c a g g a c a t g c a a a c a a g c a	c t c g g t t t c t g g g a c t g a t t	3720
t g c t g t c t t c t c g g a t a t g c	c a t c c t g c t c c a g a t c a g c a	a g g a t t g a g t c t c t g g g g a g	3780
c c c c t c a a a a g c c t g g t t c a	g a a a a t g g t c t t g c a c a g a a	g c a t c g a a c a c c t c g c c g a c	3840

N3027PCT\_sequ.list.txt

gat gt cagca gcccaaaat g ct gagt agcc ct gaggacac cat gt act at aaccagt t aa 3900  
at ggaact ct agaat at caa gggagcaaga ggaagccaag aaaact t ggc caaat caaag 3960  
t act t gat gg ggaagat gaa t at t acaaat ct ct gt cacc agt ggact gt at ccct gagg 4020  
agaacaact c agcccaccct t cct t t t t t t ct t cat cct c aaaaggagac t ct t t t gct c 4080  
aacat t aaat t gt gct t cct aaccct aaat ct gt ccagag t aggaacat t cat ggt aat c 4140  
gact gt ct gt cat t gcgt aa gaaagcact g at at ggggt c agct t ct t t g gacat at ggt 4200  
ccat gcct ga acct t act ga accact t gca gat t ccaaaa cat ct t at cc t at cct ct ac 4260  
cact ct ccca cat gt gt t gt gcagcct gag ct gggcgct g cct t cct t t c t cat cccat g 4320  
gggccct gt g ggacact gag aacacct t t a caat agt t t a aacagt cat t cat gccccca 4380  
gt gt ct agga agat aacagc cagt ct cacc ccagt ct aat cat ggaccct gat aat at t g 4440  
ct t gat t t t t cct at caagt t act t t t caa t ccat t caga at ct gccccca gt ggagaccc 4500  
aggagt t cct t t cct gcact ct t ct ccat c ct cccacct t t gct gggct t t t ct at cact 4560  
cccacct ccc ccagagt cag ggct ccat t g ct gagt gccc cat cct ggag gat t ggcccc 4620  
aagat ct cct agaacaggat aat t gcct gt gt t t aggcag at aggcct aa at ct t t caga 4680  
t t ct t t ct ac aaggcaaat a acccct ct ct t gt t aat t at gat gct gaga aagcct ct gt 4740  
ct ct t t at t t cacct t gcc aagaccccac act act t t gg t gat gaaaag aaaggaat ga 4800  
gagggaaaagt t t ggacct gt cact t t ggt g acagggaaaag t ccaggt cac t t t at t ct gt 4860  
aact ct ccat t cact ggt ca aat aact cca t gaggct at c agt ggct aca gt ggaaggac 4920  
ct gat ct t gt ccat ct t t gt gt gcacagag cct agcacag ggct t ggt ag aggggt at at c 4980  
t agt gaat gg agaat acat g gagaaact t a act aagt t ac acaagcat at ct gacaggaa 5040  
t gt t acct t c aat t gt at gt t acat at gat t agt cact t t t cat aact a t aacct ct ga 5100  
t t t t t cact c aagt t t gggc t gat t at at t gt aat gat gt t agat aat ac t caacat gat 5160  
t cagt at gac aaact t t t t t gagcacct ac t t t at at aaa acat gacaaa t t gcagt gt g 5220  
at gt aat caa aaacaaagaa gccct at aag accat t t ct c t agaacagat gt t ct t aat a 5280  
t t t t t ct t ac t ct aaaat at gt ggt agat a gt at gcaaga aaagccgggt gcggt ggct c 5340  
aggcct gt aa t cccagcact t t gggaggcc aagat gggcg gat cat gaag t caggagt t c 5400  
gagaccagcc t gaccaacat ggt gaaaccc cgt ct ct act aaaaaaaa 5448

<210> 32  
<211> 1314  
<212> PRT  
<213> Homo sapi ens

<220>  
<221> M SC FEATURE  
<222> (1)..(1314)  
<223> myosin III B MYO3B transcript variant 1

<400> 32

Met Lys His Leu Tyr Gly Leu Phe His Tyr Asn Pro Met Met Leu Gly  
 1 5 10 15  
 Leu Glu Ser Leu Pro Asp Pro Thr Asp Thr Trp Glu Ile Ile Glu Thr  
 20 25 30  
 Ile Gly Lys Gly Thr Tyr Gly Lys Val Tyr Lys Val Thr Asn Lys Arg  
 35 40 45  
 Asp Gly Ser Leu Ala Ala Val Lys Ile Leu Asp Pro Val Ser Asp Met  
 50 55 60  
 Asp Glu Glu Ile Glu Ala Glu Tyr Asn Ile Leu Gln Phe Leu Pro Asn  
 65 70 75 80  
 His Pro Asn Val Val Lys Phe Tyr Gly Met Phe Tyr Lys Ala Asp His  
 85 90 95  
 Cys Val Gly Gly Gln Leu Trp Leu Val Leu Glu Leu Cys Asn Gly Gly  
 100 105 110  
 Ser Val Thr Glu Leu Val Lys Gly Leu Leu Arg Cys Gly Gln Arg Leu  
 115 120 125  
 Asp Glu Ala Met Ile Ser Tyr Ile Leu Tyr Gly Ala Leu Leu Gly Leu  
 130 135 140  
 Gln His Leu His Asn Asn Arg Ile Ile His Arg Asp Val Lys Gly Asn  
 145 150 155 160  
 Asn Ile Leu Leu Thr Thr Glu Gly Gly Val Lys Leu Val Asp Phe Gly  
 165 170 175  
 Val Ser Ala Gln Leu Thr Ser Thr Arg Leu Arg Arg Asn Thr Ser Val  
 180 185 190  
 Gly Thr Pro Phe Trp Met Ala Pro Glu Val Ile Ala Cys Glu Gln Gln  
 195 200 205  
 Tyr Asp Ser Ser Tyr Asp Ala Arg Cys Asp Val Trp Ser Leu Gly Ile  
 210 215 220  
 Thr Ala Ile Glu Leu Gly Asp Gly Asp Pro Pro Leu Phe Asp Met His  
 225 230 235 240  
 Pro Val Lys Thr Leu Phe Lys Ile Pro Arg Asn Pro Pro Pro Thr Leu  
 245 250 255  
 Leu His Pro Glu Lys Trp Cys Glu Glu Phe Asn His Phe Ile Ser Gln  
 260 265 270  
 Cys Leu Ile Lys Asp Phe Glu Arg Arg Pro Ser Val Thr His Leu Leu  
 Page 119

275

Asp His Pro Phe Ile Lys Gly Val His Gly Lys Val Leu Phe Leu Gln  
290 295 300

Lys Gln Leu Ala Lys Val Leu Gln Asp Gln Lys His Gln Asn Pro Val  
305 310 315 320

Ala Lys Thr Arg His Glu Arg Met His Thr Arg Arg Pro Tyr His Val  
325 330 335

Glu Asp Ala Glu Lys Tyr Cys Leu Glu Asp Asp Leu Val Asn Leu Glu  
340 345 350

Val Leu Asp Glu Asp Thr Ile Ile His Gln Leu Gln Lys Arg Tyr Ala  
355 360 365

Asp Leu Leu Ile Tyr Thr Tyr Val Gly Asp Ile Leu Ile Ala Leu Asn  
370 375 380

Pro Phe Gln Asn Leu Ser Ile Tyr Ser Pro Gln Phe Ser Arg Leu Tyr  
385 390 395 400

His Gly Val Lys Arg Ala Ser Asn Pro Pro His Ile Phe Ala Ser Ala  
405 410 415

Asp Ala Ala Tyr Gln Cys Met Val Thr Leu Ser Lys Asp Gln Cys Ile  
420 425 430

Val Ile Ser Gly Glu Ser Gly Ser Gly Lys Thr Glu Ser Ala His Leu  
435 440 445

Ile Val Gln His Leu Thr Phe Leu Gly Lys Ala Asn Asn Gln Thr Leu  
450 455 460

Arg Glu Lys Ile Leu Gln Val Asn Ser Leu Val Glu Ala Phe Gly Asn  
465 470 475 480

Ser Cys Thr Ala Ile Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Leu  
485 490 495

Glu Met Met Phe Thr Pro Thr Gly Val Val Met Gly Ala Arg Ile Ser  
500 505 510

Glu Tyr Leu Leu Glu Lys Ser Arg Val Ile Lys Gln Ala Ala Arg Glu  
515 520 525

Lys Asn Phe His Ile Phe Tyr Tyr Ile Tyr Ala Gly Leu His His Gln  
530 535 540

Lys Lys Leu Ser Asp Phe Arg Leu Pro Glu Glu Lys Pro Pro Arg Tyr  
545 550 555 560

N3027PCT\_sequ.list.txt

I l e A l a A s p G u T h r G y A r g V a l M e t H i s A s p I l e T h r S e r L y s G u  
565 570 575

S e r T y r A r g A r g G n P h e G u A l a I l e G n H i s C y s P h e A r g I l e I l e  
580 585 590

G y P h e T h r A s p L y s G u V a l H i s S e r V a l T y r A r g I l e L e u A l a G y  
595 600 605

I l e L e u A s n I l e G y A s n I l e G u P h e A l a A l a I l e S e r S e r G n H i s  
610 615 620

G n T h r A s p L y s S e r G u V a l P r o A s n A l a G u A l a L e u G n A s n A l a  
625 630 635 640

A l a S e r V a l L e u C y s I l e S e r P r o G u G u L e u G n G u A l a L e u T h r  
645 650 655

S e r H i s C y s V a l V a l T h r A r g G y G u T h r I l e I l e A r g A l a A s n T h r  
660 665 670

V a l A s p A r g A l a A l a A s p V a l A r g A s p A l a M e t S e r L y s A l a L e u T y r  
675 680 685

G y A r g L e u P h e S e r T r p I l e V a l A s n A r g I l e A s n T h r L e u L e u G n  
690 695 700

P r o A s p G u A s n I l e C y s S e r A l a G y G y G y M e t A s n V a l G y I l e  
705 710 715 720

L e u A s p I l e P h e G y P h e G u A s n P h e G n A r g A s n S e r P h e G u G n  
725 730 735

L e u C y s I l e A s n I l e A l a A s n G u G n I l e G n T y r T y r P h e A s n G n  
740 745 750

H i s V a l P h e A l a L e u G u G n M e t G u T y r G n A s n G u G y I l e A s p  
755 760 765

A l a V a l P r o V a l G u T y r G u A s p A s n A r g P r o L e u L e u A s p M e t P h e  
770 775 780

L e u G n L y s P r o L e u G y L e u L e u A l a L e u L e u A s p G u G u S e r A r g  
785 790 795 800

P h e P r o G n A l a T h r A s p G n T h r L e u V a l A s p L y s P h e G u A s p A s n  
805 810 815

L e u A r g C y s L y s T y r P h e T r p A r g P r o L y s G y V a l G u L e u C y s P h e  
820 825 830

N3027PCT\_sequ.list.txt

Gly Ile Gln His Tyr Ala Gly Lys Val Leu Tyr Asp Ala Ser Gly Val  
 835 840 845  
 Leu Glu Lys Asn Arg Asp Thr Leu Pro Ala Asp Val Val Val Val Leu  
 850 855 860  
 Arg Thr Ser Glu Asn Met Leu Leu Gln Gln Leu Phe Ser Ile Pro Leu  
 865 870 875 880  
 Thr Lys Thr Gly Asn Leu Ala Gln Thr Arg Ala Arg Ile Thr Val Ala  
 885 890 895  
 Ser Ser Ser Leu Pro Pro His Phe Ser Ala Gly Lys Ala Lys Val Asp  
 900 905 910  
 Thr Leu Glu Val Ile Arg His Pro Glu Glu Thr Thr Asn Met Lys Arg  
 915 920 925  
 Gln Thr Val Ala Ser Tyr Phe Arg Tyr Ser Leu Met Asp Leu Leu Ser  
 930 935 940  
 Lys Met Val Val Gly Gln Pro His Phe Val Arg Cys Ile Lys Pro Asn  
 945 950 955 960  
 Asp Asp Arg Glu Ala Leu Gln Phe Ser Arg Glu Arg Val Leu Ala Gln  
 965 970 975  
 Leu Arg Ser Thr Gly Ile Leu Glu Thr Val Ser Ile Arg Arg Gln Gly  
 980 985 990  
 Tyr Ser His Arg Ile Leu Phe Glu Glu Phe Val Lys Arg Tyr Tyr Tyr  
 995 1000 1005  
 Leu Ala Phe Thr Ala His Gln Thr Pro Leu Ala Ser Lys Glu Ser  
 1010 1015 1020  
 Cys Val Ala Ile Leu Glu Lys Ser Arg Leu Asp His Trp Val Leu  
 1025 1030 1035  
 Gly Lys Thr Lys Val Phe Leu Lys Tyr Tyr His Val Glu Gln Leu  
 1040 1045 1050  
 Asn Leu Leu Leu Arg Glu Val Ile Gly Arg Val Val Val Leu Gln  
 1055 1060 1065  
 Ala Tyr Thr Lys Gly Trp Leu Gly Ala Arg Arg Tyr Lys Lys Val  
 1070 1075 1080  
 Arg Glu Lys Arg Glu Lys Gly Ala Ile Ala Ile Gln Ser Gly Asp  
 1085 1090 1095

Thr Ser Asn Gln Ser Ser Gly Pro His Ser Pro Val Ala Ala Gly  
1100 1105 1110

Thr Arg Gly Ser Ala Glu Val Gln Asp Cys Ser Glu Pro Gly Asp  
1115 1120 1125

His Lys Val Leu Arg Gly Ser Val His Arg Arg Ser His Ser Gln  
1130 1135 1140

Ala Glu Ser Asn Asn Gly Arg Thr Gln Thr Ser Ser Asn Ser Pro  
1145 1150 1155

Ala Val Thr Glu Lys Asn Gly His Ser Gln Ala Gln Ser Ser Pro  
1160 1165 1170

Lys Gly Cys Asp Ile Phe Ala Gly His Ala Asn Lys His Ser Val  
1175 1180 1185

Ser Gly Thr Asp Leu Leu Ser Ser Arg Ile Cys His Pro Ala Pro  
1190 1195 1200

Asp Gln Gln Gly Leu Ser Leu Trp Gly Ala Pro Gln Lys Pro Gly  
1205 1210 1215

Ser Glu Asn Gly Leu Ala Gln Lys His Arg Thr Pro Arg Arg Arg  
1220 1225 1230

Cys Gln Gln Pro Lys Met Leu Ser Ser Pro Glu Asp Thr Met Tyr  
1235 1240 1245

Tyr Asn Gln Leu Asn Gly Thr Leu Glu Tyr Gln Gly Ser Lys Arg  
1250 1255 1260

Lys Pro Arg Lys Leu Gly Gln Ile Lys Val Leu Asp Gly Glu Asp  
1265 1270 1275

Glu Tyr Tyr Lys Ser Leu Ser Pro Val Asp Cys Ile Pro Glu Glu  
1280 1285 1290

Asn Asn Ser Ala His Pro Ser Phe Phe Ser Ser Ser Ser Lys Gly  
1295 1300 1305

Asp Ser Phe Ala Gln His  
1310

<210> 33  
<211> 8704  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(8704)

&lt;223&gt; myosin IXA MYO9A

&lt;400&gt; 33

```

gcgcgaccga agcggat aag ggacgcggcg gcggt tggct gtgtctgttg agagagt aca      60
ggacagcccg gactgcgaga ggcggcggcg gaggcagt ag ttgcaccggc agaggcggcc      120
gctggcagcg gttgaggcgg cgggtccaacg cgtgctctct gggcgggggtg cggcggggga      180
tgtgcctgct caggccgggc ggagtctctc tgacagggcg ggggatgcgc cgcggccgct      240
cgcccggacc ctgaggctgc tgggcccacc ctcccgaac cgtccgacc t cgggtggcct      300
cggcctcttc tgccatctcc ggtcctacc tggggcggag ggtggaaggc agcttccgtc      360
gaagaggagg gggctgcggt ggccaccgcg gcggagcccg agttatttta ccaagaaaat      420
ggtttgcacg actttgaaca tat actatcc atgctgatgg gacaggatcc aat atgaat a      480
taaatgatgg aggaagacga cgctttgaag ataatgaaca t acattacgg at at at cct g      540
gggctat ttc agaagggaca atctactgtc cgattcctgc cagaaaaaac tccacagctg      600
ctgaggatgat tgagtctctt ataaacaaac ttcatcttga caaaacaaaa t gttatgttc      660
tagcagaggt aaaggaattt ggtggagaag aatggattct caatccaaca gat t g t ccag      720
ttcagcgaat gatgctgtgg ccccgaatgg ctctggaaaa t cgctt aagt ggagaggact      780
accgctt cct tctgagagag aaaaaccttg atggatcaat ccat t at ggt agcctgcagt      840
catggctacg ggtaacagaa gaacgtcgca ggatgatgga acgggggtttt ct t ccacagc      900
ctcaacagaa agactttgat gat t t at g t a g t t t acct ga t t t gaat gag aaaact ct ct      960
tagaaaacct acgaaatcgc t t t aagcat g aaaaaat t t a t acct at g t t ggcagt at t c      1020
taat agt t at taacccattc aagtttcttc ctat t t at aa ccccaa at at gt caaaat gt      1080
at gat aacca ccaactggga aaacttgagc cccacat t t a t gct gt ggct gat gt agct t      1140
at cat gccat gct t cagcgc aaaaagaat c agt gcat cgt gat t t cagga gagagt ggt t      1200
ctgggaagac tcaaagcaca aact t t c t t a t t caccacct t act gct ct c agt cagaaag      1260
gat t t gccag tggagt agaa cagat t at t c t t ggagct gg accagt act t gaggcct t t g      1320
gaaat gcaaa gacagct cat aat aacaat t caagt cgt t t t gggaagt t t at t caagt aa      1380
at t accagga aacaggcact gt act t ggt g cct at g t t ga aaaat at ct a ct ggagaagt      1440
ccagact cgt t t at caggag cat aat gaac ggaact at ca t gt at t ct at t acct cct gg      1500
caggagcaag tgaagat gag agat cagcat tccat ct t aa gcaaccagag gaat at cat t      1560
at ct caat ca gat acaaag aaaccct ca gacagagct g ggat gat t at t gct at gact      1620
ct gagccgga t t gct t cagc gt ggaaggag aagat t t gag acat gact t t gagcgcct ac      1680
aact t gccat ggaaat ggt a ggat t t ct t c ccaagacacg aagacagat t t t ct ct ct t c      1740
t ct cagccat act acat t t g ggt aat at ct g t t aaaaaa gaagacat ac cgggat gact      1800
ccat t gat at ct gt aat cct gaagt t ct gc ct at t gt ct c agaat t at t a gaggt t aaag      1860
aagagat gct at t t gaagca t t agt t acaa ggaagacggt gacagt ggga gaaaagct t a      1920
t t t t gccat a caagt t ggca gaggct gt ga cagt gaggaa ct ccat ggct aagt ct ct gt      1980

```

N3027PCT\_sequ.list.txt

at agt gccct	gt t t gact gg	at agt t t t t c	gaat t aat ca	t gcact t ct g	aat agt aaag	2040
at t t agagca	t aat accaag	acat t gt ct a	t t ggt gt t ct	t gat at t t t t	gggt t t gaag	2100
at t at gaaaa	t aacagct t t	gaacagt t ct	gt at t aat t t	t gct aat gaa	cgt t t acagc	2160
act act t t aa	t cagcat at c	t t t aaat t gg	aacaagagga	at at agaact	gaaggt at ca	2220
gct ggcacaa	cat agat t ac	at t gat aat a	cct gct gcat	aaat ct t at t	agcaaaaaaac	2280
caacaggact	gct t cat ct t	t t ggat gaag	aaagcaact t	t ccacaggct	acaaat caaa	2340
cat t gct aga	caagt t t aag	cat caacat g	aagat aat t c	t t acat cgaa	t t t ccagccg	2400
t gat ggagcc	t gct t t cat t	at aaaacat t	at gct ggaaa	agt aaaat at	ggggt aaagg	2460
at t t ccggga	aaaaaat aca	gat cat at gc	gcccagacat	t gt agct ct t	ct gagaagca	2520
gcaagaat gc	at t t at ct ct	gggat gat t g	gaat t gat cc	t gt agct gt t	t t ccgat ggg	2580
caat t ct ccg	agct t t t t t c	agagccat gg	t t gct t t cag	ggaagct ggg	aaaagaaaca	2640
t t cacagaaa	aact ggacat	gat gat acag	cgccat gt gc	aat t t t gaaa	agt at ggat a	2700
gt t t t agct t	t ct ccaacac	ccagt ccacc	agaggagct t	agagat t ct g	cagagat gca	2760
aggaagagaa	gt acagt at a	acccggaaaa	at ccagaac	acct ct t t ct	gat ct ccagg	2820
gcat gaat gc	t ct aaat gaa	aaaaaccaac	at gat acat t	t gat at t gcc	t ggaat ggca	2880
gaact gggat	t cgccagagc	agact at caa	gt ggcacct c	ct t gct t gat	aaagat ggaa	2940
t at t t gct aa	t t caact agc	agcaaaact cc	t ggagagagc	ccat ggaat t	ct cagcagaa	3000
acaaaaat t t	caaat ccaag	cct gccct t c	caaagcact t	gct agaagt a	aat t ct t t aa	3060
agcacct gac	aagact gaca	ct acaagat c	gcat t accaa	gt ct ct t ct t	cat t t acaca	3120
agaagaaaaa	acct cccagc	at cagt gcc	agt t t caggc	at cat t aagc	aagct aat gg	3180
aaacact t gg	t caagcagaa	ccat at t t t g	t aaaat gcat	t cgct ct aat	gct gaaaagc	3240
t gccct t aag	gt t cagt gat	gt ct t ggt ac	t t agacagct	t cgat acacc	gggat gct gg	3300
aaacagt t cg	aat t cgccaa	t caggat aca	gct ccaaat a	t t ct t t ccag	gat t t t gt ga	3360
gccact t cca	t gt act t ct t	ccccgaaat a	t t at t ccat c	caaat t t aac	at t caggat t	3420
t ct t caggaa	aat aaat ct t	aat ccagat a	at t at caagt	t ggaaaaacc	at ggt ct t t c	3480
t aaaggagca	ggaacgacag	cact t acaag	at ct gct t ca	ccaagaggt g	ct ccgcagaa	3540
t cat at t gt t	gcagcgat gg	t t cagggt ct	t gct gt gt ag	gcagcat t t c	ct ccat ct ga	3600
gacaagcat c	t gt t at t at c	cagagat t ct	ggaggaat t a	cct aaat cag	aagcaagt ca	3660
gagat gcagc	t gt gcagaag	gat gct t t t g	t t at ggct ag	t gcagct gct	ct t ct ccaag	3720
ct t cct ggcg	t gct cact t a	gagaggcagc	ggg act t gga	gt t acgggct	gcagccat cg	3780
t t at ccagca	gaaat ggaga	gat t act at a	ggcgcaggca	cat ggct gct	at t t gcat ac	3840
aagcaagat g	gaaagcct ac	agggaaagt a	aaaggt acca	agaacaaagg	aaaaaaat t a	3900
t cct t t t gca	at caacat gt	agaggat t ca	gagcaagaca	aagat t t aaa	gct t t t aaaag	3960
aacaaaaggct	aagagaaaca	aagccagaag	t t ggat t ggt	gaat at t aag	ggat at ggat	4020
ct ct ggaaat	t cagggt t ca	gaccct t cag	gat gggagga	t t gt t ct t t t	gacaacagaa	4080

N3027PCT\_sequ. list . . txt

t aaaagccat agaggaat gt aaat ct gt aa t agagagt aa t cgaat t agc cgt gaaagt t	4140
cagt ggact g ct t gaaggag t caccaaaca agcagcagga gagagcccaa agccagagt g	4200
gt gt ggact t gcaggaagat gt gct t gt aa gagagagacc cagat cct t g gaggat ct cc	4260
at cagaaaaa agt aggccgg gct aagagag aaagt aggag aat gagagaa ct agagcaag	4320
ct at at t t ag ct t agaat t g ct gaaagt t c gt t ct ct t gg t ggt at t t ct cct t cagagg	4380
at cgcagat g gt ct acagaa t t ggt gcct g aaggcct t ca gt ct ccacgg ggt acacct g	4440
at agt gagag ct ct caagga agct t ggaac t t ct gagct a t gaggaaagc caaaagagca	4500
aact agagt c t gt cat t t ca gat gaaggag act t gcagt t t ccat cacct aagat at cca	4560
gcagt ccaaa at t t gat t ca cgggacaat g ccct cagt gc ct caaat gag act agcagt g	4620
cagagcat t t gaaggat gga act at gaagg aaat ggt ggt ct gcagt t ct gagt ct at t a	4680
cct gt aaacc acagct gaaa gact cct t ca t t t caaat ag t ct acct act t t t t t t at a	4740
t cccccaaca agaccact g aaaacaaat t cccaact aga cacaagt at c caaagaaaca	4800
aact at t gga aaat gaagac acagcggggg aagct ct t ac t t t ggat at c aacagggaaa	4860
ct agaaggt a t cact gct ca ggaaaagat c agat t gt t cc t t ct t t gaat acagagt ct t	4920
ct aat cct gt gct t aagaag t t agaaaagc t aaacact ga gaaggaagaa aggcaaaaac	4980
agt t gcagca acagaat gaa aaagagat ga t ggaacagat t cgccagcaa acagat at t t	5040
t agagaagga gcgcaaagcc t t caagacaa t t gaaaagcc aagaat t gga gagt gt t t gg	5100
t ggcaccat c t t cct at cag t caaagcaaa gagt agagag gccat cct ct ct cct cagct	5160
t aaat acct c aaat aaggga gaact t aat g t act ggggt c cct at cat t a aaagat gcag	5220
ct ct t gccca aaaagacagt t cct ct gct c act t accccc aaaggaccga cct gt caccg	5280
t gt t ct t t ga aagaaaagga agt ccat gcc aat ct agt ac t gt caaggaa t t at ccaaga	5340
cagacagaat gggcacccag ct gaat gt ag cct gt aaact ct caaat aat cgcat t t caa	5400
aaagagaaca ct t t aggcca act cagt ct t acagccacaa t t ct gat gac ct t t ccagag	5460
agggaaat gc t aggcccat t t ct t cact c caaaggacaa t at gagt at t cccct t gt ca	5520
gcaaagaagc ct t aaacagt aaaaat cct c aact ccat aa agaagat gaa ccagcat gga	5580
aacct gt gaa gt t agct ggg ccaggccaaa gagagacat c acagcgat t t t cgt cagt t g	5640
at gaacaagc aaaact t cat aagact at gt ct caaggaga gat t accaag t t ggcagt ga	5700
gacagaaggc t t cagat t ca gat at aagac ct cagagagc t aagat gaga t t ct gggcca	5760
aagggaaca aggggagaag aagact acca gagt gaaacc t act acccag t cagaggt t t	5820
cgccact ct t t gcaggcaca gat gt gat t c cagct cat ca gt t t ccagat gaat t agct g	5880
cat at cacc aacacct cct t t gagcccag aact gcccg cagt t gccgg aaggaat t ca	5940
aagagaacaa agaacct t ct ccaaaggct a agcgcaagcg aagt gt gaag at t agcaacg	6000
t ggct t t gga t t ct at gcat t ggcaaaat g act ct gt cca gat cat agca agt gt cagt g	6060
at t t aaaaag cat ggat gaa t t t ct t ct ga aaaaggt gaa t gacct agat aat gaagaca	6120

N3027PCT\_sequ. list.txt

gcaagaagga t acact agt g gat gt t gt at t t aaaaaagc cct gaaggaa t t t cggcaga	6180
at at ct t cag ct t t t at t ca t ct gcat t gg cgat ggat ga t gggaaaagc at acggt at a	6240
aagacct ct a t gcact at t t gaacagat t c t gggaaaagac gat gaggct t gagcagcgt g	6300
at t cact ggg t gaat ct cca gt gagagt t t ggg t caacac t t t t aaagt g t t t t agat g	6360
aat at at gaa t gaat t caag act t cagat t gcacagccac aaaggt gcca aaaacagaaa	6420
gaaagaaaag aaggaaaaag gaaact gat t t ggt ggaaga acacaat ggt cacat ct t t a	6480
aagccacca at at agcat c cct acat act gt gaat act g t t ct t ct t t g at at ggat aa	6540
t ggaccgagc ct ct gt t t gc aaat t at gca agt at gct t g ccat aagaag t gct gt ct ga	6600
aaaccacagc caagt gct ct aaaaagt at g at ccagagct gt cat ct cga caat t t gggg	6660
t t gaact gt c ccgt t t gacc agt gaagacc gaact gt t cc t t t agt agt g gaaaagct ca	6720
t aaact acat t gaaat gcat ggact gt at a cagaaggt at t t at cgaaag t ct ggt t cga	6780
ct aat aaaat caaggagct t cggcaggggt c t agat acaga t gct gagagt gt aaat ct ag	6840
at gact at aa cat acacgt c at t gcaagt g t at t caaaca at ggct t cga gat t t gccca	6900
at cct ct cat gacct t t gaa ct ct at gagg aat t t ct t cg agct at gggc ct t caggaga	6960
ggaaggagac aat ccgt ggt gt at act ct g t gat t gat ca act ct cccga act cat ct ca	7020
at acact gga acgcct cat c t t t cat ct ag t caggat t gc t ct gcaggaa gacact aat c	7080
gaat gt ct gc t aat gct t t g gccat t gt gt t t gcgccct g cat t ct ccgc t gccct gaca	7140
ccact gaccc act acaaagt gt acaggaca t cagt aagac t accact t gt gt ggaact ga	7200
t t gt t gt gga acaaat gaat aaat acaagg ct cgt ct caa agat at cagt agct t ggaat	7260
t t gct gagaa t aaggcaaag accaggt t gt cact gat t cg t agat caat g ggaaaggggc	7320
gt at t cgt cg aggaaact at ccaggt ccat cgt ct cct gt t gt agt t cgg t t gcct t ct g	7380
t gt ct gat gt ct cagaggag acct t gact a gt gaggcagc cat ggagact gacat cacag	7440
aacagcagca agcagct at g cagcaggagg agagagt act gact gagcag at t gagaacc	7500
t acagaagga gaaggaggag ct aacat t t g agat gct t gt act ggaaccc cgt gcct ct g	7560
at gat gaaac cct t gagt ct gaggcct cca t t gggact gc t gat agct ca gagaat t t ga	7620
at at ggagt c t gaat at gct at ct ct gaga aat cagaaag aagct t agcc ct t agct ccc	7680
t gaagacagc t ggcaagt ct gaacct t cca gcaagt t gcg aaagcaact t aaaaagcagc	7740
aagact ct t t agat gt cgt g gact ct t cgg t ct cct ct t t at gt ct gt ct aacacggcat	7800
cat ct cat gg gaccagaaaa ct at t t caga t t t at t ccaa at ct ccat t c t accgagct g	7860
cct caggt aa t gaggccct g ggaat ggaag gaccat t ggg ccagacaaaa t t cct ggaag	7920
acaagcct ca gt t cat cagc agaggaacct t caaccggga aaagggcaaa caaaaat t aa	7980
agaat gt gaa aaact cacct cagaaaacca aagagacccc agaggggaca gt cat gt ct g	8040
gccgcagaaa aact gt ggac ccagact gca cct ccaacca acagct agca ct ct t t ggaa	8100
at aat gaat t t at ggt ct ga accggcagat gt gt gt ccct ccgt ggct ac agagt ggt aa	8160
acaaat ct ca cct t t ggggc t gcgt t t cat cacct cgt cc acaat agt ca at cct aat t g	8220

N3027PCT\_sequ.list.txt

t ggt cct gcc t c t t t t c t a a g c a t a t g g c t a a g a c t g t a t g t g c t g a a t t c c t g g g c c t c 8280  
c t g c a g a a g c a g a a a g c c t g c t g g g g a t g g t g c c a g c t g t g c c t t g g c t g t t g t a t t t g a 8340  
a t t g a g a t t t t t a c t a t a c a a a g c c a c c t a g g g c c t g g g g a t t t g g g t c a g t t g t a g t t g 8400  
c c t c t c c c c c a c c c t c t t t t c c c t t c c c a a a g g t g g g t g t t g a a c t a g g g g g g a t a t t g c 8460  
t g t c c t g a g g g a c c c t c t c a t t t c t g a c a t t t g a a g a a a a c g t a t a a a t c t t t c t t a a c c 8520  
g t g a a a g c a a a a g c c t t t g g g t t t a t t t t g g g a t a g t t a g g a g c t a g g g t a g a a t a t a a t 8580  
t t t t t t c c a a a a a c t t a c t t a c a a a c a a a a a g c c t a a t c c c t c t a t t t t a a g a t t t c t g a 8640  
a a a a a c a c t c c a t g t t a t a t t c t g g g g a a a g c a a a a c a 8700  
a a a a 8704

<210> 34  
<211> 2548  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(2548)  
<223> myosin IXA MYO9A

<400> 34

Met Asn Ile Asn Asp Gly Gly Arg Arg Arg Phe Glu Asp Asn Glu His  
1 5 10 15

Thr Leu Arg Ile Tyr Pro Gly Ala Ile Ser Glu Gly Thr Ile Tyr Cys  
20 25 30

Pro Ile Pro Ala Arg Lys Asn Ser Thr Ala Ala Glu Val Ile Glu Ser  
35 40 45

Leu Ile Asn Lys Leu His Leu Asp Lys Thr Lys Cys Tyr Val Leu Ala  
50 55 60

Glu Val Lys Glu Phe Gly Gly Glu Glu Trp Ile Leu Asn Pro Thr Asp  
65 70 75 80

Cys Pro Val Gln Arg Met Met Leu Trp Pro Arg Met Ala Leu Glu Asn  
85 90 95

Arg Leu Ser Gly Glu Asp Tyr Arg Phe Leu Leu Arg Glu Lys Asn Leu  
100 105 110

Asp Gly Ser Ile His Tyr Gly Ser Leu Gln Ser Trp Leu Arg Val Thr  
115 120 125

Glu Glu Arg Arg Arg Met Met Glu Arg Gly Phe Leu Pro Gln Pro Gln  
130 135 140

N3027PCT\_sequ.list.txt

Gln Lys Asp Phe Asp Asp Leu Cys Ser Leu Pro Asp Leu Asn Glu Lys  
145 150 155 160

Thr Leu Leu Glu Asn Leu Arg Asn Arg Phe Lys His Glu Lys Ile Tyr  
165 170 175

Thr Tyr Val Gly Ser Ile Leu Ile Val Ile Asn Pro Phe Lys Phe Leu  
180 185 190

Pro Ile Tyr Asn Pro Lys Tyr Val Lys Met Tyr Asp Asn His Gln Leu  
195 200 205

Gly Lys Leu Glu Pro His Ile Tyr Ala Val Ala Asp Val Ala Tyr His  
210 215 220

Ala Met Leu Gln Arg Lys Lys Asn Gln Cys Ile Val Ile Ser Gly Glu  
225 230 235 240

Ser Gly Ser Gly Lys Thr Gln Ser Thr Asn Phe Leu Ile His His Leu  
245 250 255

Thr Ala Leu Ser Gln Lys Gly Phe Ala Ser Gly Val Glu Gln Ile Ile  
260 265 270

Leu Gly Ala Gly Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Ala  
275 280 285

His Asn Asn Asn Ser Ser Arg Phe Gly Lys Phe Ile Gln Val Asn Tyr  
290 295 300

Gln Glu Thr Gly Thr Val Leu Gly Ala Tyr Val Glu Lys Tyr Leu Leu  
305 310 315 320

Glu Lys Ser Arg Leu Val Tyr Gln Glu His Asn Glu Arg Asn Tyr His  
325 330 335

Val Phe Tyr Tyr Leu Leu Ala Gly Ala Ser Glu Asp Glu Arg Ser Ala  
340 345 350

Phe His Leu Lys Gln Pro Glu Glu Tyr His Tyr Leu Asn Gln Ile Thr  
355 360 365

Lys Lys Pro Leu Arg Gln Ser Trp Asp Asp Tyr Cys Tyr Asp Ser Glu  
370 375 380

Pro Asp Cys Phe Thr Val Glu Gly Glu Asp Leu Arg His Asp Phe Glu  
385 390 395 400

Arg Leu Gln Leu Ala Met Glu Met Val Gly Phe Leu Pro Lys Thr Arg  
405 410 415

Arg Gln Ile Phe Ser Leu Leu Ser Ala Ile Leu His Leu Gly Asn Ile

420

425

430

Cys Tyr Lys<sub>435</sub> Lys Lys Thr Tyr Arg<sub>440</sub> Asp Asp Ser Ile Asp<sub>445</sub> Ile Cys Asn  
 Pro Glu<sub>450</sub> Val Leu Pro Ile Val<sub>455</sub> Ser Glu Leu Leu Glu<sub>460</sub> Val Lys Glu Glu  
 Met<sub>465</sub> Leu Phe Glu Ala Leu<sub>470</sub> Val Thr Arg Lys Thr<sub>475</sub> Val Thr Val Gly Glu<sub>480</sub>  
 Lys Leu Ile Leu Pro<sub>485</sub> Tyr Lys Leu Ala Glu<sub>490</sub> Ala Val Thr Val Arg<sub>495</sub> Asn  
 Ser Met Ala Lys<sub>500</sub> Ser Leu Tyr Ser Ala<sub>505</sub> Leu Phe Asp Trp Ile<sub>510</sub> Val Phe  
 Arg Ile Asn<sub>515</sub> His Ala Leu Leu Asn<sub>520</sub> Ser Lys Asp Leu Glu<sub>525</sub> His Asn Thr  
 Lys Thr<sub>530</sub> Leu Ser Ile Gly Val<sub>535</sub> Leu Asp Ile Phe Gly<sub>540</sub> Phe Glu Asp Tyr  
 Glu<sub>545</sub> Asn Asn Ser Phe Glu<sub>550</sub> Gln Phe Cys Ile Asn<sub>555</sub> Phe Ala Asn Glu Arg<sub>560</sub>  
 Leu Gln His Tyr Phe<sub>565</sub> Asn Gln His Ile Phe<sub>570</sub> Lys Leu Glu Gln Glu<sub>575</sub> Glu  
 Tyr Arg Thr Glu<sub>580</sub> Gly Ile Ser Trp His<sub>585</sub> Asn Ile Asp Tyr Ile<sub>590</sub> Asp Asn  
 Thr Cys Cys<sub>595</sub> Ile Asn Leu Ile Ser<sub>600</sub> Lys Lys Pro Thr Gly<sub>605</sub> Leu Leu His  
 Leu Leu<sub>610</sub> Asp Glu Glu Ser Asn<sub>615</sub> Phe Pro Gln Ala Thr<sub>620</sub> Asn Gln Thr Leu  
 Leu<sub>625</sub> Asp Lys Phe Lys His<sub>630</sub> Gln His Glu Asp Asn<sub>635</sub> Ser Tyr Ile Glu Phe<sub>640</sub>  
 Pro Ala Val Met Glu<sub>645</sub> Pro Ala Phe Ile Ile<sub>650</sub> Lys His Tyr Ala Gly<sub>655</sub> Lys  
 Val Lys Tyr Gly<sub>660</sub> Val Lys Asp Phe Arg<sub>665</sub> Glu Lys Asn Thr Asp<sub>670</sub> His Met  
 Arg Pro Asp<sub>675</sub> Ile Val Ala Leu Leu Arg Ser Ser Lys Asn<sub>685</sub> Ala Phe Ile  
 Ser Gly<sub>690</sub> Met Ile Gly Ile Asp<sub>695</sub> Pro Val Ala Val Phe<sub>700</sub> Arg Trp Ala Ile

N3027PCT\_sequ.list.txt

```

Leu Arg Ala Phe Phe Arg Ala Met Val Ala Phe Arg Glu Ala Gly Lys
705      710      715

Arg Asn Ile His Arg Lys Thr Gly His Asp Asp Thr Ala Pro Cys Ala
      725      730      735

Ile Leu Lys Ser Met Asp Ser Phe Ser Phe Leu Glu His Pro Val His
      740      745

Glu Arg Ser Leu Glu Ile Leu Glu Arg Cys Lys Glu Glu Lys Tyr Ser
      755      760

Ile Thr Arg Lys Asn Pro Arg Thr Pro Leu Ser Asp Leu Glu Gly Met
      770      775      780

Asn Ala Leu Asn Glu Lys Asn Glu His Asp Thr Phe Asp Ile Ala Trp
785      790      795      800

Asn Gly Arg Thr Gly Ile Arg Glu Ser Arg Leu Ser Ser Gly Thr Ser
      805      810      815

Leu Leu Asp Lys Asp Gly Ile Phe Ala Asn Ser Thr Ser Ser Lys Leu
      820      825

Leu Glu Arg Ala His Gly Ile Leu Thr Arg Asn Lys Asn Phe Lys Ser
      835      840      845

Lys Pro Ala Leu Pro Lys His Leu Leu Glu Val Asn Ser Leu Lys His
      850      855      860

Leu Thr Arg Leu Thr Leu Glu Asp Arg Ile Thr Lys Ser Leu Leu His
865      870      875      880

Leu His Lys Lys Lys Lys Pro Pro Ser Ile Ser Ala Glu Phe Glu Ala
      885      890      895

Ser Leu Ser Lys Leu Met Glu Thr Leu Gly Glu Ala Glu Pro Tyr Phe
      900      905      910

Val Lys Cys Ile Arg Ser Asn Ala Glu Lys Leu Pro Leu Arg Phe Ser
      915      920      925

Asp Val Leu Val Leu Arg Glu Leu Arg Tyr Thr Gly Met Leu Glu Thr
930      935      940

Val Arg Ile Arg Glu Ser Gly Tyr Ser Ser Lys Tyr Ser Phe Glu Asp
945      950      955      960

Phe Val Ser His Phe His Val Leu Leu Pro Arg Asn Ile Ile Pro Ser
      965      970      975

```

N3027PCT\_sequ.list.txt

Lys Phe Asn Ile Gln Asp Phe Phe Arg Lys Ile Asn Leu Asn Pro Asp  
 980 985 990  
 Asn Tyr Gln Val Gly Lys Thr Met Val Phe Leu Lys Glu Gln Glu Arg  
 995 1000 1005  
 Gln His Leu Gln Asp Leu Leu His Gln Glu Val Leu Arg Arg Ile  
 1010 1015 1020  
 Ile Leu Leu Gln Arg Trp Phe Arg Val Leu Leu Cys Arg Gln His  
 1025 1030 1035  
 Phe Leu His Leu Arg Gln Ala Ser Val Ile Ile Gln Arg Phe Trp  
 1040 1045 1050  
 Arg Asn Tyr Leu Asn Gln Lys Gln Val Arg Asp Ala Ala Val Gln  
 1055 1060 1065  
 Lys Asp Ala Phe Val Met Ala Ser Ala Ala Ala Leu Leu Gln Ala  
 1070 1075 1080  
 Ser Trp Arg Ala His Leu Glu Arg Gln Arg Tyr Leu Glu Leu Arg  
 1085 1090 1095  
 Ala Ala Ala Ile Val Ile Gln Gln Lys Trp Arg Asp Tyr Tyr Arg  
 1100 1105 1110  
 Arg Arg His Met Ala Ala Ile Cys Ile Gln Ala Arg Trp Lys Ala  
 1115 1120 1125  
 Tyr Arg Glu Ser Lys Arg Tyr Gln Glu Gln Arg Lys Lys Ile Ile  
 1130 1135 1140  
 Leu Leu Gln Ser Thr Cys Arg Gly Phe Arg Ala Arg Gln Arg Phe  
 1145 1150 1155  
 Lys Ala Leu Lys Glu Gln Arg Leu Arg Glu Thr Lys Pro Glu Val  
 1160 1165 1170  
 Gly Leu Val Asn Ile Lys Gly Tyr Gly Ser Leu Glu Ile Gln Gly  
 1175 1180 1185  
 Ser Asp Pro Ser Gly Trp Glu Asp Cys Ser Phe Asp Asn Arg Ile  
 1190 1195 1200  
 Lys Ala Ile Glu Glu Cys Lys Ser Val Ile Glu Ser Asn Arg Ile  
 1205 1210 1215  
 Ser Arg Glu Ser Ser Val Asp Cys Leu Lys Glu Ser Pro Asn Lys  
 1220 1225 1230

G n G n G u Arg Ala G n Ser G n Ser Gly Val Asp Leu G n G u  
 1235 1240 1245  
 Asp Val Leu Val Arg G u Arg Pro Arg Ser Leu G u Asp Leu Hi s  
 1250 1255 1260  
 G n Lys Lys Val Gly Arg Ala Lys Arg G u Ser Arg Arg Met Arg  
 1265 1270 1275  
 G u Leu G u G n Ala Ile Phe Ser Leu G u Leu Leu Lys Val Arg  
 1280 1285 1290  
 Ser Leu Gly Gly Ile Ser Pro Ser G u Asp Arg Arg Trp Ser Thr  
 1295 1300 1305  
 G u Leu Val Pro G u Gly Leu G n Ser Pro Arg Gly Thr Pro Asp  
 1310 1315 1320  
 Ser G u Ser Ser G n Gly Ser Leu G u Leu Leu Ser Tyr G u G u  
 1325 1330 1335  
 Ser G n Lys Ser Lys Leu G u Ser Val Ile Ser Asp G u Gly Asp  
 1340 1345 1350  
 Leu G n Phe Pro Ser Pro Lys Ile Ser Ser Ser Pro Lys Phe Asp  
 1355 1360 1365  
 Ser Arg Asp Asn Ala Leu Ser Ala Ser Asn G u Thr Ser Ser Ala  
 1370 1375 1380  
 G u Hi s Leu Lys Asp Gly Thr Met Lys G u Met Val Val Oys Ser  
 1385 1390 1395  
 Ser G u Ser Ile Thr Oys Lys Pro G n Leu Lys Asp Ser Phe Ile  
 1400 1405 1410  
 Ser Asn Ser Leu Pro Thr Phe Phe Tyr Ile Pro G n G n Asp Pro  
 1415 1420 1425  
 Leu Lys Thr Asn Ser G n Leu Asp Thr Ser Ile G n Arg Asn Lys  
 1430 1435 1440  
 Leu Leu G u Asn G u Asp Thr Ala Gly G u Ala Leu Thr Leu Asp  
 1445 1450 1455  
 Ile Asn Arg G u Thr Arg Arg Tyr Hi s Oys Ser Gly Lys Asp G n  
 1460 1465 1470  
 Ile Val Pro Ser Leu Asn Thr G u Ser Ser Asn Pro Val Leu Lys  
 1475 1480 1485  
 Lys Leu G u Lys Leu Asn Thr G u Lys G u G u Arg G n Lys G n  
 1490 1495

Leu 1505	Gln	Gln	Asn	Glu	Lys 1510	Glu	Met	Met	Glu	Gln 1515	Ile	Arg	Gln	
Gln 1520	Thr	Asp	Ile	Leu	Glu	Lys 1525	Glu	Arg	Lys	Ala	Phe 1530	Lys	Thr	Ile
Glu 1535	Lys	Pro	Arg	Ile	Gly	Glu 1540	Cys	Leu	Val	Ala	Pro 1545	Ser	Ser	Tyr
Gln 1550	Ser	Lys	Gln	Arg	Val	Glu 1555	Arg	Pro	Ser	Ser	Leu 1560	Leu	Ser	Leu
Asn 1565	Thr	Ser	Asn	Lys	Gly	Glu 1570	Leu	Asn	Val	Leu	Gly 1575	Ser	Leu	Ser
Leu 1580	Lys	Asp	Ala	Ala	Leu	Ala 1585	Gln	Lys	Asp	Ser	Ser 1590	Ser	Ala	His
Leu 1595	Pro	Pro	Lys	Asp	Arg	Pro 1600	Val	Thr	Val	Phe	Phe 1605	Glu	Arg	Lys
Gly 1610	Ser	Pro	Cys	Gln	Ser	Ser 1615	Thr	Val	Lys	Glu	Leu 1620	Ser	Lys	Thr
Asp 1625	Arg	Met	Gly	Thr	Gln	Leu 1630	Asn	Val	Ala	Cys	Lys 1635	Leu	Ser	Asn
Asn 1640	Arg	Ile	Ser	Lys	Arg	Glu 1645	His	Phe	Arg	Pro	Thr 1650	Gln	Ser	Tyr
Ser 1655	His	Asn	Ser	Asp	Asp	Leu 1660	Ser	Arg	Glu	Gly	Asn 1665	Ala	Arg	Pro
Ile 1670	Phe	Phe	Thr	Pro	Lys	Asp 1675	Asn	Met	Ser	Ile	Pro 1680	Leu	Val	Ser
Lys 1685	Glu	Ala	Leu	Asn	Ser	Lys 1690	Asn	Pro	Gln	Leu	His 1695	Lys	Glu	Asp
Glu 1700	Pro	Ala	Trp	Lys	Pro	Val 1705	Lys	Leu	Ala	Gly	Pro 1710	Gly	Gln	Arg
Glu 1715	Thr	Ser	Gln	Arg	Phe	Ser 1720	Ser	Val	Asp	Glu	Gln 1725	Ala	Lys	Leu
His 1730	Lys	Thr	Met	Ser	Gln	Gly 1735	Glu	Ile	Thr	Lys	Leu 1740	Ala	Val	Arg
Gln 1745	Lys	Ala	Ser	Asp	Ser	Asp 1750	Ile	Arg	Pro	Gln	Arg 1755	Ala	Lys	Met

N3027PCT\_sequ.list.txt

Arg	Phe 1760	Trp	Ala	Lys	Gly	Lys 1765	Gln	Gly	Glu	Lys	Lys 1770	Thr	Thr	Arg
Val	Lys 1775	Pro	Thr	Thr	Gln	Ser 1780	Glu	Val	Ser	Pro	Leu 1785	Phe	Ala	Gly
Thr	Asp 1790	Val	Ile	Pro	Ala	His 1795	Gln	Phe	Pro	Asp	Glu 1800	Leu	Ala	Ala
Tyr	His 1805	Pro	Thr	Pro	Pro	Leu 1810	Ser	Pro	Glu	Leu	Pro 1815	Gly	Ser	Cys
Arg	Lys 1820	Glu	Phe	Lys	Glu	Asn 1825	Lys	Glu	Pro	Ser	Pro 1830	Lys	Ala	Lys
Arg	Lys 1835	Arg	Ser	Val	Lys	Ile 1840	Ser	Asn	Val	Ala	Leu 1845	Asp	Ser	Met
His	Trp 1850	Gln	Asn	Asp	Ser	Val 1855	Gln	Ile	Ile	Ala	Ser 1860	Val	Ser	Asp
Leu	Lys 1865	Ser	Met	Asp	Glu	Phe 1870	Leu	Leu	Lys	Lys	Val 1875	Asn	Asp	Leu
Asp	Asn 1880	Glu	Asp	Ser	Lys	Lys 1885	Asp	Thr	Leu	Val	Asp 1890	Val	Val	Phe
Lys	Lys 1895	Ala	Leu	Lys	Glu	Phe 1900	Arg	Gln	Asn	Ile	Phe 1905	Ser	Phe	Tyr
Ser	Ser 1910	Ala	Leu	Ala	Met	Asp 1915	Asp	Gly	Lys	Ser	Ile 1920	Arg	Tyr	Lys
Asp	Leu 1925	Tyr	Ala	Leu	Phe	Glu 1930	Gln	Ile	Leu	Glu	Lys 1935	Thr	Met	Arg
Leu	Glu 1940	Gln	Arg	Asp	Ser	Leu 1945	Gly	Glu	Ser	Pro	Val 1950	Arg	Val	Trp
Val	Asn 1955	Thr	Phe	Lys	Val	Phe 1960	Leu	Asp	Glu	Tyr	Met 1965	Asn	Glu	Phe
Lys	Thr 1970	Ser	Asp	Cys	Thr	Ala 1975	Thr	Lys	Val	Pro	Lys 1980	Thr	Glu	Arg
Lys	Lys 1985	Arg	Arg	Lys	Lys	Glu 1990	Thr	Asp	Leu	Val	Glu 1995	Glu	His	Asn
Gly	His 2000	Ile	Phe	Lys	Ala	Thr 2005	Gln	Tyr	Ser	Ile	Pro 2010	Thr	Tyr	Cys

N3027PCT\_sequ.list.txt

Glu	Tyr	Oys	Ser	Ser	Leu	Ile	Trp	Ile	Met	Asp	Arg	Ala	Ser	Val
2015						2020					2025			
Oys	Lys	Leu	Oys	Lys	Tyr	Ala	Oys	His	Lys	Lys	Oys	Oys	Leu	Lys
2030						2035					2040			
Thr	Thr	Ala	Lys	Oys	Ser	Lys	Lys	Tyr	Asp	Pro	Glu	Leu	Ser	Ser
2045						2050					2055			
Arg	Gln	Phe	Gly	Val	Glu	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Arg
2060						2065					2070			
Thr	Val	Pro	Leu	Val	Val	Glu	Lys	Leu	Ile	Asn	Tyr	Ile	Glu	Met
2075						2080					2085			
His	Gly	Leu	Tyr	Thr	Glu	Gly	Ile	Tyr	Arg	Lys	Ser	Gly	Ser	Thr
2090						2095					2100			
Asn	Lys	Ile	Lys	Glu	Leu	Arg	Gln	Gly	Leu	Asp	Thr	Asp	Ala	Glu
2105						2110					2115			
Ser	Val	Asn	Leu	Asp	Asp	Tyr	Asn	Ile	His	Val	Ile	Ala	Ser	Val
2120						2125					2130			
Phe	Lys	Gln	Trp	Leu	Arg	Asp	Leu	Pro	Asn	Pro	Leu	Met	Thr	Phe
2135						2140					2145			
Glu	Leu	Tyr	Glu	Glu	Phe	Leu	Arg	Ala	Met	Gly	Leu	Gln	Glu	Arg
2150						2155					2160			
Lys	Glu	Thr	Ile	Arg	Gly	Val	Tyr	Ser	Val	Ile	Asp	Gln	Leu	Ser
2165						2170					2175			
Arg	Thr	His	Leu	Asn	Thr	Leu	Glu	Arg	Leu	Ile	Phe	His	Leu	Val
2180						2185					2190			
Arg	Ile	Ala	Leu	Gln	Glu	Asp	Thr	Asn	Arg	Met	Ser	Ala	Asn	Ala
2195						2200					2205			
Leu	Ala	Ile	Val	Phe	Ala	Pro	Oys	Ile	Leu	Arg	Oys	Pro	Asp	Thr
2210						2215					2220			
Thr	Asp	Pro	Leu	Gln	Ser	Val	Gln	Asp	Ile	Ser	Lys	Thr	Thr	Thr
2225						2230					2235			
Oys	Val	Glu	Leu	Ile	Val	Val	Glu	Gln	Met	Asn	Lys	Tyr	Lys	Ala
2240						2245					2250			
Arg	Leu	Lys	Asp	Ile	Ser	Ser	Leu	Glu	Phe	Ala	Glu	Asn	Lys	Ala
2255						2260					2265			

Lys Thr 2270	Arg Leu Ser Leu	Ile Arg Arg Ser Met Gly 2275 2280	Lys Gly Arg
Ile Arg 2285	Arg Gly Asn Tyr	Pro Gly Pro Ser Ser 2290 2295	Val Val Val
Arg Leu 2300	Pro Ser Val Ser	Asp Val Ser Glu Glu Thr 2305 2310	Leu Thr Ser
Glu Ala 2315	Ala Met Glu Thr	Asp Ile Thr Glu Gln Gln 2320 2325	Gln Ala Ala
Met Gln 2330	Gln Glu Glu Arg	Val Leu Thr Glu Gln Ile 2335 2340	Glu Asn Leu
Gln Lys 2345	Glu Lys Glu Glu	Leu Thr Phe Glu Met 2350 2355	Val Leu Glu
Pro Arg 2360	Ala Ser Asp Asp	Glu Thr Leu Glu Ser 2365 2370	Ala Ser Ile
Gly Thr 2375	Ala Asp Ser Ser	Glu Asn Leu Asn Met 2380 2385	Ser Glu Tyr
Ala Ile 2390	Ser Glu Lys Ser	Glu Arg Ser Leu Ala 2395 2400	Ser Ser Leu
Lys Thr 2405	Ala Gly Lys Ser	Glu Pro Ser Ser Lys 2410 2415	Arg Lys Gln
Leu Lys 2420	Lys Gln Gln Asp	Ser Leu Asp Val Val 2425 2430	Ser Ser Val
Ser Ser 2435	Leu Cys Leu Ser	Asn Thr Ala Ser Ser 2440 2445	His Gly Thr Arg
Lys Leu 2450	Phe Gln Ile Tyr	Ser Lys Ser Pro Phe 2455 2460	Tyr Arg Ala Ala
Ser Gly 2465	Asn Glu Ala Leu	Gly Met Glu Gly Pro 2470 2475	Leu Gly Gln Thr
Lys Phe 2480	Leu Glu Asp Lys	Pro Gln Phe Ile Ser 2485 2490	Arg Gly Thr Phe
Asn Pro 2495	Glu Lys Gly Lys	Gln Lys Leu Lys Asn 2500 2505	Val Lys Asn Ser
Pro Gln 2510	Lys Thr Lys Glu	Thr Pro Glu Gly Thr 2515 2520	Val Met Ser Gly
Arg Arg	Lys Thr Val Asp	Pro Asp Cys Thr Ser	Asn Gln Gln Leu

2525

N3027PCT\_sequ.list.txt  
2530 2535Ala Leu Phe Gly Asn Asn Glu Phe Met Val  
2540 2545<210> 35  
<211> 7488  
<212> DNA  
<213> Homo sapiens<220>  
<221> mi sc\_f e a t u r e  
<222> (1)..(7488)  
<223> myosi n I X B MYO9B

```

<400> 35
at g a g t g t g a a a g a g g c a g g c a g c t c g g g c c g c c g g g a g c a g g c g g c c t a c c a c c t g c a c 60
a t c t a c c c c c a g c t g t c c a c c a c c g a g a g c c a g g c c t c g t g c c g c g t g a c t g c c a c c a a g 120
g a c a g c a c c a c c t c g g a c g t c a t c a a g g a c g c c a t t g c c a g c c t g c g g c t g g a c g g c a c c 180
a a a t g t t a t g t g c t g g t g g a g g t c a a a g a g t c g g g a g g c g a g g a a t g g g t g c t g g a c g c c 240
a a c g a c t c g c c t g t g c a c c g g g t g c t g c t a t g g c c c c g g c g g g c a c a g g a c g a g c a c c c t 300
c a g g a g g a t g g c t a c t a c t t c c t g c t g c a g g a g c g c a a c g c a g a t g g a a c c a t c a a g t a c 360
g t g c a t a t g c a g c t g g t g g c g c a g g c c a c a g c c a c c c g g c g c c t a g t g g a g c g t g g c c t c 420
c t g c c a c g g c a g c a g g c g g a c t t t g a t g a c c t g t g t a a c c t c c c c g a g c t a a c c g a g g g c 480
a a c c t c c t g a a g a a c c t c a a g c a c c g c t t c c t g c a a c a a a a g a t c t a c a c g t a c g c g g g g 540
a g c a t c c t g g t g g c c a t c a a c c c t t t a a g t t c c t g c c c a t c t a c a a c c c c a a g t a c g t g 600
a a g a t g t a t g a g a a c c a g c a g c t g g g c a a g c t g g a g c c a c a c g t c t t c g c g c t g g c c g a c 660
g t g g c c t a c t a c a c c a t g c t c a g g a a g c g c g t g a a c c a g t g c a t c g t g a t c t c g g g t g a g 720
a g c g g c t c c g g c a a g a c c c a g a g c a c a a c t t c c t c a t c c a c t g c c t c a c c g c c c t c a g c 780
c a g a a g g g c t a c g c c a g c g g c g t c g a g a g g a c c a t c c t g g g t g c t g g c c c t g t g c t g g a g 840
g c t t t t g g a a t g c c a a g a c a g c c c a c a a c a a c a a c t c c a g c g g t t t g g g a a t t c a t c 900
c a a g t c a g c t a c c t a g a g a g t g g c a t c g t g a g a g a g c t g t c g t c g a g a a t a t c t g c t t 960
g a a a a g t c t c g c c t g g t g t c t c a g g a g a a g g a t g a g a g g a a c t a c c a t g t g t t t a t t a t 1020
t t g t t a c t t g g g g t c a g c g a g g a a g a g c g c c a a g a a t t t c a g c t c a a g c a g c c t g a a g a t 1080
t a t t t c t a c c t c a a c c a g c a t a a c t t g a a g a t t g a a g a t g g g g a g g a c c t g a a g c a t g a c 1140
t t t g a g a g g c t c a a g c a g g c a t g g a g a t g g t g g g c t t c c t c c c c g c c a c c a a g a a g c a g 1200
a t t t t t g c c g t c c t c t c g g c c a t c c t g t a c c t g g g c a a c g t c a c t t a t a a g a a g a g a g c t 1260
a c a g g c c g a g a g g a a g g g t t g g a g g t c g g g c c a c c c g a g g t g c t g g a c a c c c t g t c g c a g 1320
c t t c t g a a g g t g a a g c g a g a a a t c t t g g t g g a g g t t c t g a c c a a a a g a a a a a c g g t g a c c 1380
g t c a a c g a c a a g c t t a t c c t t c c c t a c a g c c t c a g c g a g g c c a t c a c t g c c c g c g a c t c c 1440
a t g g c c a a g t c t c t g t a c a g c g c c c t g t t c g a c t g g a t t g t g c t g c g g a t c a a c c a c g c a 1500

```

N3027PCT\_sequ. list .txt

ct cct caaca agaaggacgt ggaagaggca gt ct cgt gcc t gt ccat t gg ggt cct ggac	1560
at ct t cgggt t t gaagact t cgagaggaac agct t t gagg agt t ct gcat caact acgcc	1620
aat gagcagc t gcagt at t a ct t caaccag cacat ct t ca agct ggagca ggaggaat at	1680
cagggcgagg ggat cacgt g gcacaacat c ggct acacag acaat gt cgg ct gcat ccat	1740
ct cat cagca agaaacccac gggcct ct t c t acct gct gg acgaggagag caact t cccc	1800
cacgccacga gccagaccct gct ggccaag t t caaacagc aacat gagga caat aagt ac	1860
t t cct gggca ccccggt cat ggagccagct t t cat cat cc agcact t cgc aggggaaggt g	1920
aaat at caga t caaggact t ccgggagaag aacat ggact acat gcggcc agacat cgt g	1980
gccct gct gc ggggcagt ga cagct cct ac gt gcgggagc t cat cggcat ggaccccgt g	2040
gccgt gt t cc gct gggccgt gct ccgggct gct at ccggg ccat ggcagt gct t cgggag	2100
gccggacgcc t gcggggccga gagggccgaa aaggct gcag gt at gagcag ccct ggt gcc	2160
caaagt cacc cagaagagct gccaagagga gccagcacc ct t cgaaaaa act t t accgc	2220
gat t t gcat a accaaat gat caagagcat c aaaggat t gc cct ggcaggg cgaggacccc	2280
cgt agcct t c t ccagt ccct cagt cggct c cagaaacccc gcgcct t cat cct gaaaagt	2340
aaaggat at ca aacaaaagca gat cat t cca aagaacct ac t ggact ccaa gt ccct gaaa	2400
ct cat cat ca gcat gact ct gcacgaccgc accaccaagt ccct act gca cct gcacaag	2460
aagaaaaagc caccaagcat cagcgcaccag t t ccagacat ccct t aacaa gct ct t ggag	2520
gcact gggga aggcggagcc ct t ct t t at c cgct gcat cc gt t ccaat gc t gaaaagaaa	2580
gagct gt gct t t gacgacga gct ggt cct g cagcagct gc gct acaccgg cat gct ggag	2640
accgt gcgca t ccggaggt c agggat acagc gccagat aca cgt t ccagga t t t caccgag	2700
cagt t ccagg t gct cct gcc caaggat gcc cagccct gca gggaggt cat ct ccaccct c	2760
ct ggagaaaa t gaagat aga caagaggaac t accagat cg ggaagaccaa ggt ct t cct g	2820
aaggagacgg agcggcaagc cct gcaggag acgct gcacc gggaggt ggt gcggaaaat c	2880
ct gct gct gc agagct ggt t ccggat ggt g ct ggagcgt c ggcact t cct gcagat gaag	2940
cgggcccgg t caccat cca ggcct gct gg cgggt cct acc ggggt ccggag ggcgct ggag	3000
aggacgcagg ct gccgt gt a cct ccaggcc t cat ggaggg gct act ggca gcggaagct c	3060
t accggcacc agaaacagag cat cat ccgc ct gcagagcc t gt gt cgggg gcacct gcag	3120
cgcaagagct t cagccagat gat ct cggag aagcagaagg cagaagagaa ggagagggaa	3180
gccct ggaag ccgcaagagc aggt gct gag gagggcggac agggat caggc ggct ggaggg	3240
cagcaggt ag ct gagcaggg gccggagcca gcggaggat g gcgggcacct ggcct cggag	3300
cct gaggt gc agccaagt ga caggt ccccc ct agagcact cct cacct ga gaaggaggcc	3360
ccaagcccag agaagact ct cccaccccag aaaaccgt gg cggct gaaag t caccagaaa	3420
gt ccccagca gccggggagaa gcgt gact cg cgt cggcaaa gagggct gga gcacgt caag	3480
t t ccagaaca aacacat cca gt cct gcaag gaggagagt g ccct cagaga acct t ccaga	3540
agggt ccccc aggagcaagg ggt gact ct c ct ggaagaca aaaaggagag cagagaagat	3600

N3027PCT\_sequ. list . . txt

gaaaccct t c	t agt cgt aga	gacggaggct	gagaacacat	ct caaaagca	gcccacagag	3660
caaccccagg	ccat ggcagt	t ggcaaggt c	t ct gaagaaa	ct gagaagac	gct gcccagt	3720
gggagcccca	ggcct ggcca	gt t ggagcgg	ccgaccagcc	t ggccct gga	cagcagggt c	3780
agcccaccgg	cccct ggtag	cgcccccgag	acccccgagg	acaagagcaa	accat gt ggc	3840
agcccaagg	t t caggaaaa	gccccgacagc	cccggaggct	ccacgcagat	ccagcggt ac	3900
ct ggacgccg	agcggct ggc	cagcgccgt g	gaact gt ggc	ggggcaagaa	gct ggt ggcc	3960
gccgccagcc	ct agt gccat	gct cagccag	t ccct ggacc	t cagcgacag	acaccgggccc	4020
acagggggccg	ccct cagccc	cacagaggag	aggcgcacct	cct t ct ccac	gagcgacgt c	4080
t ccaagct cc	t cccgt cctt	ggccaaggct	cagcct gcag	cagaaaccac	ggacggagag	4140
cgaagt gcca	aaaagccagc	t gt ccagaag	aagaagccag	gcgacgcac c	ct ccct ccca	4200
gacgcagggc	t gt ccccg	ct ct caggt c	gact ct aaat	ccacgt t t aa	gaggct t t t t	4260
ct gcat aaaa	ccaaggat aa	aaaat acagc	ct ggagggcg	cagaggagct	ggagaat gca	4320
gt gt ccgggc	acgt ggt gct	ggaagccacc	accat gaaga	agggcct gga	agccccct cc	4380
ggacagcagc	at cgccacgc	t gcaggt gag	aagcgcacca	aggaaccagg	aggcaaagg	4440
aagaagaacc	gaaat gt caa	gat t gggaag	at cacagt gt	cagagaagt g	gcgggaat cg	4500
gt gt t ccgcc	agat caccaa	cgccaat gag	ct caagt acc	t ggacgagt t	cct gct caac	4560
aagat aaat g	acct ccgt t c	ccagaagacg	cccat t gaga	gct t gt t t at	cgaagccacc	4620
gagaagt t ca	ggagcaacat	caaaacgat g	t act ct gt cc	cgaacgggaa	gat ccacgt g	4680
ggct acaagg	at ct gat gga	gaact accag	at cgt cgt ca	gcaacct ggc	cact gagcgt	4740
ggccagaagg	acaccaacct	ggt cct caac	ct ct t ccagt	cact gct aga	t gagt t cacc	4800
cgt ggct aca	ccaagaacga	ct t cgagcca	gt gaagcaga	gcaaagct ca	gaagaagaag	4860
cggaagcagg	agcgt gct gt	ccaggagcac	aacgggcacg	t gt t cgccag	ct accaggt t	4920
agcat cccgc	agt cgt gcga	gcagt gcct c	t cct at at ct	ggct cat gga	caaggccct g	4980
ct ct gcagcg	t gt gcaagat	gacct gccac	aagaagt gcg	t gcacaagat	t cagagccac	5040
t gct cct aca	cct acgggag	gaagggcgag	ccaggcgt t g	agcct ggcca	ct t cggcgt g	5100
t gcgt agaca	gcct gaccag	cgacaaggcc	t cgggt gccca	t cgt gct gga	gaagct cct g	5160
gaacacgt gg	agat gcacgg	cct gt acacc	gagggcct ct	accgcaagt c	gggt gct gcc	5220
aaccgcact c	gggagct ccg	gcaggcgct g	cagacagacc	ccgcagcagt	caagct ggag	5280
aact t ccca	t ccacgccat	cacaggggt g	ct gaagcagt	ggct gcggga	gct gcccag	5340
cccct cat ga	cct t cgcaca	gt acggcgac	t t cct ccgag	ccgt cgagct	gccggagaag	5400
caggagcagc	t ggct gccat	ct at gccgt c	ct ggagcacc	t t ccagaagc	caaccacaac	5460
t ccct ggaga	gact cat ct t	ccacct t gt c	aaggt ggccc	t gct cgagga	t gt caaccgc	5520
at gt cacct g	gggcgct ggc	cat t at ct t c	gcacct gcc	t cct gcgct g	ccct gacaac	5580
t cggacccgc	t gaccagcat	gaaggacgt c	ct caagat ca	ccacgt gcgt	ggagat gct g	5640

N3027PCT\_sequ. list.txt

at caaggagc agat gaggaa at acaaagt g aagat ggagg agat cagcca act ggaggct	5700
gcagagagt a t cgcct t ccg caggct t t cg ct cct gcgac aaaat gct cc at ggcct ct c	5760
aaact ggggt t t t cgt ct cc ct at gagggg gt cct gaaca agagcccca gacccgggac	5820
at ccaggagg aggagct gga ggt gct gct g gaggaggagg cagccggcgg cgat gaggac	5880
cgggaaaagg agat t ct cat t gaacggat c cagt ccat ca aggaggagaa ggaggacat c	5940
acct accggc t gccggagct ggaccaagg ggct cggacg aggagaacct ggact cggag	6000
acgt cggcca gcaccgagag cct gct ggag gagcggggccg ggcgggggggc ct cggaaggg	6060
ccccct gcgc ct gct ct ccc t t gccccggc gcgcccaccc cgagccccct cccaccgt g	6120
gccgccccct c cagcagcaag gccgt cgt cc t t cgt aacgg t cagagt gaa gaccccccg	6180
cggaccccca t cat gccac ggccaacat c aagct cccac caggcct gcc ct cccacct g	6240
cct cgct ggg caccgggt gc ccgggaggcg gct gccccag t gcggcgccg ggagccacct	6300
gcccggccgc cggaaccagat acat t ccgt g t acat cagc ccggggcaga cct gccagt g	6360
cagggcgccc t ggagcccc agaagaggat ggccagccac ct ggggcca gcgagggt ac	6420
t cggat cccc caacgt act g cct gcccccc gcct cgggcc agaccaat gg ct gagagcca	6480
cagct gacaa agt ct gcat g t ccgaggacg gcccct gcac t ggagct ggg cgccagagct	6540
gcagagct ag t gt t cggccc t cagagaagg at ccagaat c aaaagct caa gagt gacgt g	6600
agggt gggcac cggccccaag t gcagagt ca aggcaggagg aggccggct g gagccaggcc	6660
ccct cgcacg cagccccaat at cat ggacg cacct gt ggg gagcaccaca t ct ccacct g	6720
cggcct caca t ct cccact cccct t t t t g t acgt t t aac t gt t t ct t t g t acgt ggt t t	6780
acgt aact t t aaact gt aac agcct t aat g gaagacaaaa t ggt t t t t a t at gt gt at g	6840
t acaaagt t t t ct at t aacg ct gcccgct ct ccct t at aac ct ggacgt ga gct gt cagag	6900
cagaagccac t aggccact g cgcgt ct gag gct cagaccc t gct gt ggt t ggct t ggggt	6960
ggccaat ggg ct gggacct ccat gagagt t t t ggacact t ggggt cacct gacctgt gcc	7020
t ct ct gacac at gt ct ccgg ggggcagcca cct ggccaat gt gcat t t t t gcacat gct g	7080
gaacct t cca t ggggggt ct g ggct at t ggc t ggagccagg acat gagt ca ggggcacct	7140
ggacct cag t gccaggagg act t gaat gt ggct gt cact ct t ccggacg ccaagggt g	7200
caggaggct g ct t t t ggcac t acccaccct gt gt gacaga at aggagcca gcgact cagg	7260
act gct cag ggt caggagg gcaacgcct g aagt cagacc t ccct at agg t caacaggga	7320
caacct gggg at ct ct ggag cagggccct c ct ct ct cagg ct t gggccac t cccccagac	7380
acct ggacac gt ggccacaa at ct gggaca agggggccccc gcacagcat g aaat aaaaag	7440
t gcct gagaa gt gt gt gcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	7488

<210> 36  
 <211> 2157  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; M SC\_FEATURE

&lt;222&gt; (1)..(2157)

&lt;223&gt; myosin I XB MYO9B

&lt;400&gt; 36

Met Ser Val Lys Glu Ala Gly Ser Ser Gly Arg Arg Glu Gln Ala Ala  
1 5 10 15Tyr His Leu His Ile Tyr Pro Gln Leu Ser Thr Thr Glu Ser Gln Ala  
20 25 30Ser Cys Arg Val Thr Ala Thr Lys Asp Ser Thr Thr Ser Asp Val Ile  
35 40 45Lys Asp Ala Ile Ala Ser Leu Arg Leu Asp Gly Thr Lys Cys Tyr Val  
50 55 60Leu Val Glu Val Lys Glu Ser Gly Gly Glu Glu Trp Val Leu Asp Ala  
65 70 75 80Asn Asp Ser Pro Val His Arg Val Leu Leu Trp Pro Arg Arg Ala Gln  
85 90 95Asp Glu His Pro Gln Glu Asp Gly Tyr Tyr Phe Leu Leu Gln Glu Arg  
100 105 110Asn Ala Asp Gly Thr Ile Lys Tyr Val His Met Gln Leu Val Ala Gln  
115 120 125Ala Thr Ala Thr Arg Arg Leu Val Glu Arg Gly Leu Leu Pro Arg Gln  
130 135 140Gln Ala Asp Phe Asp Asp Leu Cys Asn Leu Pro Glu Leu Thr Glu Gly  
145 150 155 160Asn Leu Leu Lys Asn Leu Lys His Arg Phe Leu Gln Gln Lys Ile Tyr  
165 170 175Thr Tyr Ala Gly Ser Ile Leu Val Ala Ile Asn Pro Phe Lys Phe Leu  
180 185 190Pro Ile Tyr Asn Pro Lys Tyr Val Lys Met Tyr Glu Asn Gln Gln Leu  
195 200 205Gly Lys Leu Glu Pro His Val Phe Ala Leu Ala Asp Val Ala Tyr Tyr  
210 215 220Thr Met Leu Arg Lys Arg Val Asn Gln Cys Ile Val Ile Ser Gly Glu  
225 230 235 240Ser Gly Ser Gly Lys Thr Gln Ser Thr Asn Phe Leu Ile His Cys Leu  
245 250 255

N3027PCT\_sequ.list.txt

Thr Ala Leu Ser 260 Gln Lys Gly Tyr Ala 265 Ser Gly Val Glu Arg 270 Thr Ile

Leu Gly Ala 275 Gly Pro Val Leu Glu 280 Ala Phe Gly Asn 285 Lys Thr Ala

His Asn 290 Asn Asn Ser Ser Arg 295 Phe Gly Lys Phe Ile 300 Gln Val Ser Tyr

Leu Glu 305 Ser Gly Ile Val 310 Arg Gly Ala Val Val 315 Glu Lys Tyr Leu Leu 320

Glu Lys Ser Arg 325 Leu Val Ser Gln Glu Lys 330 Asp Glu Arg Asn Tyr 335 His

Val Phe Tyr Tyr 340 Leu Leu Leu Gly Val 345 Ser Glu Glu Glu Arg 350 Gln Glu

Phe Gln 355 Leu Lys Gln Pro Glu Asp 360 Tyr Phe Tyr Leu Asn 365 Gln His Asn

Leu Lys 370 Ile Glu Asp Gly Glu 375 Asp Leu Lys His Asp 380 Phe Glu Arg Leu

Lys Gln 385 Ala Met Glu Met 390 Val Gly Phe Leu Pro 395 Ala Thr Lys Lys Gln 400

Ile Phe Ala Val 405 Leu Ser Ala Ile Leu Tyr 410 Leu Gly Asn Val Thr 415 Tyr

Lys Lys Arg 420 Ala Thr Gly Arg Glu Glu 425 Gly Leu Glu Val Gly 430 Pro Pro

Glu Val 435 Leu Asp Thr Leu Ser Gln 440 Leu Leu Lys Val Lys 445 Arg Glu Ile

Leu Val 450 Glu Val Leu Thr Lys 455 Arg Lys Thr Val Thr 460 Val Asn Asp Lys

Leu Ile 465 Leu Pro Tyr Ser 470 Leu Ser Glu Ala Ile 475 Thr Ala Arg Asp Ser 480

Met Ala Lys Ser 485 Leu Tyr Ser Ala Leu Phe 490 Asp Trp Ile Val Leu Arg 495

Ile Asn His 500 Ala Leu Leu Asn Lys Lys 505 Asp Val Glu Glu Ala 510 Val Ser

Cys Leu 515 Ser Ile Gly Val Leu Asp 520 Ile Phe Gly Phe Glu 525 Asp Phe Glu

N3027PCT\_sequ.list.txt

Arg Asn Ser Phe Glu Gln Phe Cys Ile Asn Tyr Ala Asn Glu Gln Leu  
 530 535 540  
 Gln Tyr Tyr Phe Asn Gln His Ile Phe Lys Leu Glu Gln Glu Glu Tyr  
 545 550 555 560  
 Gln Gly Glu Gly Ile Thr Trp His Asn Ile Gly Tyr Thr Asp Asn Val  
 565 570 575  
 Gly Cys Ile His Leu Ile Ser Lys Lys Pro Thr Gly Leu Phe Tyr Leu  
 580 585 590  
 Leu Asp Glu Glu Ser Asn Phe Pro His Ala Thr Ser Gln Thr Leu Leu  
 595 600 605  
 Ala Lys Phe Lys Gln Gln His Glu Asp Asn Lys Tyr Phe Leu Gly Thr  
 610 615 620  
 Pro Val Met Glu Pro Ala Phe Ile Ile Gln His Phe Ala Gly Lys Val  
 625 630 635 640  
 Lys Tyr Gln Ile Lys Asp Phe Arg Glu Lys Asn Met Asp Tyr Met Arg  
 645 650 655  
 Pro Asp Ile Val Ala Leu Leu Arg Gly Ser Asp Ser Ser Tyr Val Arg  
 660 665 670  
 Glu Leu Ile Gly Met Asp Pro Val Ala Val Phe Arg Trp Ala Val Leu  
 675 680 685  
 Arg Ala Ala Ile Arg Ala Met Ala Val Leu Arg Glu Ala Gly Arg Leu  
 690 695 700  
 Arg Ala Glu Arg Ala Glu Lys Ala Ala Gly Met Ser Ser Pro Gly Ala  
 705 710 715 720  
 Gln Ser His Pro Glu Glu Leu Pro Arg Gly Ala Ser Thr Pro Ser Glu  
 725 730 735  
 Lys Leu Tyr Arg Asp Leu His Asn Gln Met Ile Lys Ser Ile Lys Gly  
 740 745 750  
 Leu Pro Trp Gln Gly Glu Asp Pro Arg Ser Leu Leu Gln Ser Leu Ser  
 755 760 765  
 Arg Leu Gln Lys Pro Arg Ala Phe Ile Leu Lys Ser Lys Gly Ile Lys  
 770 775 780  
 Gln Lys Gln Ile Ile Pro Lys Asn Leu Leu Asp Ser Lys Ser Leu Lys  
 785 790 795 800

N3027PCT\_sequ.list.txt

Leu Ile Ile Ser Met Thr Leu His Asp Arg Thr Thr Lys Ser Leu Leu  
805 810 815

His Leu His Lys Lys Lys Lys Pro Pro Ser Ile Ser Ala Gln Phe Gln  
820 825 830

Thr Ser Leu Asn Lys Leu Leu Gu Ala Leu Gly Lys Ala Gu Pro Phe  
835 840 845

Phe Ile Arg Cys Ile Arg Ser Asn Ala Gu Lys Lys Gu Leu Cys Phe  
850 855 860

Asp Asp Gu Leu Val Leu Gln Gln Leu Arg Tyr Thr Gly Met Leu Gu  
865 870 875 880

Thr Val Arg Ile Arg Arg Ser Gly Tyr Ser Ala Lys Tyr Thr Phe Gln  
885 890 895

Asp Phe Thr Gu Gln Phe Gln Val Leu Leu Pro Lys Asp Ala Gln Pro  
900 905 910

Cys Arg Gu Val Ile Ser Thr Leu Leu Gu Lys Met Lys Ile Asp Lys  
915 920 925

Arg Asn Tyr Gln Ile Gly Lys Thr Lys Val Phe Leu Lys Gu Thr Gu  
930 935 940

Arg Gln Ala Leu Gln Gu Thr Leu His Arg Gu Val Val Arg Lys Ile  
945 950 955 960

Leu Leu Leu Gln Ser Trp Phe Arg Met Val Leu Gu Arg Arg His Phe  
965 970 975

Leu Gln Met Lys Arg Ala Ala Val Thr Ile Gln Ala Cys Trp Arg Ser  
980 985 990

Tyr Arg Val Arg Arg Ala Leu Gu Arg Thr Gln Ala Ala Val Tyr Leu  
995 1000 1005

Gln Ala Ser Trp Arg Gly Tyr Trp Gln Arg Lys Leu Tyr Arg His  
1010 1015 1020

Gln Lys Gln Ser Ile Ile Arg Leu Gln Ser Leu Cys Arg Gly His  
1025 1030 1035

Leu Gln Arg Lys Ser Phe Ser Gln Met Ile Ser Gu Lys Gln Lys  
1040 1045 1050

Ala Gu Gu Lys Gu Arg Gu Ala Leu Gu Ala Ala Arg Ala Gly  
1055 1060 1065

Ala Gu Gu Gly Gly Gln Gly Gln Ala Ala Gly Gly Gln Gln Val

1070

1075

1080

Ala	Glu	Gln	Gly	Pro	Glu	Pro	Ala	Glu	Asp	Gly	Gly	His	Leu	Ala
1085						1090					1095			
Ser	Glu	Pro	Glu	Val	Gln	Pro	Ser	Asp	Arg	Ser	Pro	Leu	Glu	His
1100						1105					1110			
Ser	Ser	Pro	Glu	Lys	Glu	Ala	Pro	Ser	Pro	Glu	Lys	Thr	Leu	Pro
1115						1120					1125			
Pro	Gln	Lys	Thr	Val	Ala	Ala	Glu	Ser	His	Glu	Lys	Val	Pro	Ser
1130						1135					1140			
Ser	Arg	Glu	Lys	Arg	Glu	Ser	Arg	Arg	Gln	Arg	Gly	Leu	Glu	His
1145						1150					1155			
Val	Lys	Phe	Gln	Asn	Lys	His	Ile	Gln	Ser	Cys	Lys	Glu	Glu	Ser
1160						1165					1170			
Ala	Leu	Arg	Glu	Pro	Ser	Arg	Arg	Val	Thr	Gln	Glu	Gln	Gly	Val
1175						1180					1185			
Ser	Leu	Leu	Glu	Asp	Lys	Lys	Glu	Ser	Arg	Glu	Asp	Glu	Thr	Leu
1190						1195					1200			
Leu	Val	Val	Glu	Thr	Glu	Ala	Glu	Asn	Thr	Ser	Gln	Lys	Gln	Pro
1205						1210					1215			
Thr	Glu	Gln	Pro	Gln	Ala	Met	Ala	Val	Gly	Lys	Val	Ser	Glu	Glu
1220						1225					1230			
Thr	Glu	Lys	Thr	Leu	Pro	Ser	Gly	Ser	Pro	Arg	Pro	Gly	Gln	Leu
1235						1240					1245			
Glu	Arg	Pro	Thr	Ser	Leu	Ala	Leu	Asp	Ser	Arg	Val	Ser	Pro	Pro
1250						1255					1260			
Ala	Pro	Gly	Ser	Ala	Pro	Glu	Thr	Pro	Glu	Asp	Lys	Ser	Lys	Pro
1265						1270					1275			
Cys	Gly	Ser	Pro	Arg	Val	Gln	Glu	Lys	Pro	Asp	Ser	Pro	Gly	Gly
1280						1285					1290			
Ser	Thr	Gln	Ile	Gln	Arg	Tyr	Leu	Asp	Ala	Glu	Arg	Leu	Ala	Ser
1295						1300					1305			
Ala	Val	Glu	Leu	Trp	Arg	Gly	Lys	Lys	Leu	Val	Ala	Ala	Ala	Ser
1310						1315					1320			
Pro	Ser	Ala	Met	Leu	Ser	Gln	Ser	Leu	Asp	Leu	Ser	Asp	Arg	His
1325						1330					1335			

N3027PCT\_sequ.list.txt

Arg	Ala	Thr	Gly	Ala	Ala	Leu	Thr	Pro	Thr	Glu	Glu	Arg	Arg	Thr
	1340					1345					1350			
Ser	Phe	Ser	Thr	Ser	Asp	Val	Ser	Lys	Leu	Leu	Pro	Ser	Leu	Ala
	1355					1360					1365			
Lys	Ala	Gln	Pro	Ala	Ala	Glu	Thr	Thr	Asp	Gly	Glu	Arg	Ser	Ala
	1370					1375					1380			
Lys	Lys	Pro	Ala	Val	Gln	Lys	Lys	Lys	Pro	Gly	Asp	Ala	Ser	Ser
	1385					1390					1395			
Leu	Pro	Asp	Ala	Gly	Leu	Ser	Pro	Gly	Ser	Gln	Val	Asp	Ser	Lys
	1400					1405					1410			
Ser	Thr	Phe	Lys	Arg	Leu	Phe	Leu	His	Lys	Thr	Lys	Asp	Lys	Lys
	1415					1420					1425			
Tyr	Ser	Leu	Glu	Gly	Ala	Glu	Glu	Leu	Glu	Asn	Ala	Val	Ser	Gly
	1430					1435					1440			
His	Val	Val	Leu	Glu	Ala	Thr	Thr	Met	Lys	Lys	Gly	Leu	Glu	Ala
	1445					1450					1455			
Pro	Ser	Gly	Gln	Gln	His	Arg	His	Ala	Ala	Gly	Glu	Lys	Arg	Thr
	1460					1465					1470			
Lys	Glu	Pro	Gly	Gly	Lys	Gly	Lys	Lys	Asn	Arg	Asn	Val	Lys	Ile
	1475					1480					1485			
Gly	Lys	Ile	Thr	Val	Ser	Glu	Lys	Trp	Arg	Glu	Ser	Val	Phe	Arg
	1490					1495					1500			
Gln	Ile	Thr	Asn	Ala	Asn	Glu	Leu	Lys	Tyr	Leu	Asp	Glu	Phe	Leu
	1505					1510					1515			
Leu	Asn	Lys	Ile	Asn	Asp	Leu	Arg	Ser	Gln	Lys	Thr	Pro	Ile	Glu
	1520					1525					1530			
Ser	Leu	Phe	Ile	Glu	Ala	Thr	Glu	Lys	Phe	Arg	Ser	Asn	Ile	Lys
	1535					1540					1545			
Thr	Met	Tyr	Ser	Val	Pro	Asn	Gly	Lys	Ile	His	Val	Gly	Tyr	Lys
	1550					1555					1560			
Asp	Leu	Met	Glu	Asn	Tyr	Gln	Ile	Val	Val	Ser	Asn	Leu	Ala	Thr
	1565					1570					1575			
Glu	Arg	Gly	Gln	Lys	Asp	Thr	Asn	Leu	Val	Leu	Asn	Leu	Phe	Gln
	1580					1585					1590			

## N3027PCT\_sequ.list.txt

Ser	Leu	Leu	Asp	Glu	Phe	Thr	Arg	Gly	Tyr	Thr	Lys	Asn	Asp	Phe
1595						1600					1605			
Glu	Pro	Val	Lys	Gln	Ser	Lys	Ala	Gln	Lys	Lys	Lys	Arg	Lys	Gln
1610						1615					1620			
Glu	Arg	Ala	Val	Gln	Glu	His	Asn	Gly	His	Val	Phe	Ala	Ser	Tyr
1625						1630					1635			
Gln	Val	Ser	Ile	Pro	Gln	Ser	Cys	Glu	Gln	Cys	Leu	Ser	Tyr	Ile
1640						1645					1650			
Trp	Leu	Met	Asp	Lys	Ala	Leu	Leu	Cys	Ser	Val	Cys	Lys	Met	Thr
1655						1660					1665			
Cys	His	Lys	Lys	Cys	Val	His	Lys	Ile	Gln	Ser	His	Cys	Ser	Tyr
1670						1675					1680			
Thr	Tyr	Gly	Arg	Lys	Gly	Glu	Pro	Gly	Val	Glu	Pro	Gly	His	Phe
1685						1690					1695			
Gly	Val	Cys	Val	Asp	Ser	Leu	Thr	Ser	Asp	Lys	Ala	Ser	Val	Pro
1700						1705					1710			
Ile	Val	Leu	Glu	Lys	Leu	Leu	Glu	His	Val	Glu	Met	His	Gly	Leu
1715						1720					1725			
Tyr	Thr	Glu	Gly	Leu	Tyr	Arg	Lys	Ser	Gly	Ala	Ala	Asn	Arg	Thr
1730						1735					1740			
Arg	Glu	Leu	Arg	Gln	Ala	Leu	Gln	Thr	Asp	Pro	Ala	Ala	Val	Lys
1745						1750					1755			
Leu	Glu	Asn	Phe	Pro	Ile	His	Ala	Ile	Thr	Gly	Val	Leu	Lys	Gln
1760						1765					1770			
Trp	Leu	Arg	Glu	Leu	Pro	Glu	Pro	Leu	Met	Thr	Phe	Ala	Gln	Tyr
1775						1780					1785			
Gly	Asp	Phe	Leu	Arg	Ala	Val	Glu	Leu	Pro	Glu	Lys	Gln	Glu	Gln
1790						1795					1800			
Leu	Ala	Ala	Ile	Tyr	Ala	Val	Leu	Glu	His	Leu	Pro	Glu	Ala	Asn
1805						1810					1815			
His	Asn	Ser	Leu	Glu	Arg	Leu	Ile	Phe	His	Leu	Val	Lys	Val	Ala
1820						1825					1830			
Leu	Leu	Glu	Asp	Val	Asn	Arg	Met	Ser	Pro	Gly	Ala	Leu	Ala	Ile
1835						1840					1845			

I l e	P h e	A l a	P r o	C y s	L e u	L e u	A r g	C y s	P r o	A s p	A s n	S e r	A s p	P r o
1850						1855					1860			
L e u	T h r	S e r	M e t	L y s	A s p	V a l	L e u	L y s	I l e	T h r	T h r	C y s	V a l	G l u
1865						1870					1875			
M e t	L e u	I l e	L y s	G l u	G n	M e t	A r g	L y s	T y r	L y s	V a l	L y s	M e t	G l u
1880						1885					1890			
G l u	I l e	S e r	G n	L e u	G l u	A l a	A l a	G l u	S e r	I l e	A l a	P h e	A r g	A r g
1895						1900					1905			
L e u	S e r	L e u	L e u	A r g	G n	A s n	A l a	P r o	T r p	P r o	L e u	L y s	L e u	G l y
1910						1915					1920			
P h e	S e r	S e r	P r o	T y r	G l u	G l y	V a l	L e u	A s n	L y s	S e r	P r o	L y s	T h r
1925						1930					1935			
A r g	A s p	I l e	G n	G l u	G l u	G l u	L e u	G l u	V a l	L e u	L e u	G l u	G l u	G l u
1940						1945					1950			
A l a	A l a	G l y	G l y	A s p	G l u	A s p	A r g	G l u	L y s	G l u	I l e	L e u	I l e	G l u
1955						1960					1965			
A r g	I l e	G n	S e r	I l e	L y s	G l u	G l u	L y s	G l u	A s p	I l e	T h r	T y r	A r g
1970						1975					1980			
L e u	P r o	G l u	L e u	A s p	P r o	A r g	G l y	S e r	A s p	G l u	G l u	A s n	L e u	A s p
1985						1990					1995			
S e r	G l u	T h r	S e r	A l a	S e r	T h r	G l u	S e r	L e u	L e u	G l u	G l u	A r g	A l a
2000						2005					2010			
G l y	A r g	G l y	A l a	S e r	G l u	G l y	P r o	P r o	A l a	P r o	A l a	L e u	P r o	C y s
2015						2020					2025			
P r o	G l y	A l a	P r o	T h r	P r o	S e r	P r o	L e u	P r o	T h r	V a l	A l a	A l a	P r o
2030						2035					2040			
P r o	A r g	A r g	A r g	P r o	S e r	S e r	P h e	V a l	T h r	V a l	A r g	V a l	L y s	T h r
2045						2050					2055			
P r o	A r g	A r g	T h r	P r o	I l e	M e t	P r o	T h r	A l a	A s n	I l e	L y s	L e u	P r o
2060						2065					2070			
P r o	G l y	L e u	P r o	S e r	H i s	L e u	P r o	A r g	T r p	A l a	P r o	G l y	A l a	A r g
2075						2080					2085			
G l u	A l a	A l a	A l a	P r o	V a l	A r g	A r g	A r g	G l u	P r o	P r o	A l a	A r g	A r g
2090						2095					2100			
P r o	A s p	G n	I l e	H i s	S e r	V a l	T y r	I l e	T h r	P r o	G l y	A l a	A s p	L e u

2105

2110

2115

Pro Val Gln Gly Ala Leu Gu Pro Leu Gu Gu Asp Gly Gln Pro  
 2120 2125 2130

Pro Gly Ala Lys Arg Arg Tyr Ser Asp Pro Pro Thr Tyr Oys Leu  
 2135 2140 2145

Pro Pro Ala Ser Gly Gln Thr Asn Gly  
 2150 2155

<210> 37  
 <211> 9508  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(9508)  
 <223> myosin VB MYO5B

<400> 37  
 gt ccggccgt agctgcgccg ccgcgccggg agt aaaggt c gcgccgccgg gagcgagccg 60  
 gccgcggcgc ctgcgggaag ccggcggggc aggt cggaga agagcgagaa gat cgagaaa 120  
 ct ccaggcca gcccgggaac atggcgccag gcggggccagc cgccggact ga gagccgcggg 180  
 gcagccagga gccggggccc gagccccgcc cggccccgggc cat gt cggg g ggcgagct ct 240  
 acagccagt g cacaaggt c tggat ccct g accct gat ga ggt at ggcgc t cagct gagt 300  
 taaccaagga ct acaaagaa ggagacaaga gcct acagct cagact ggag gat gaaacga 360  
 ttct ggaat a cccaat t gat gt acaacgca accagct gcc ct t ct t acgg aat ccagat a 420  
 t ct t ggt ggg agaaaat gac ct gact gccc t t agct at ct t cat gaggct gcagt t t t gc 480  
 at aat t t gaa ggt ccgt t t c ct ggagt cca accat at ct a cact t act gt ggt at cgt ac 540  
 t t gt t gccat t aat cct t at gaacagt t gc caat ct at gg acaagat gt c at ct at acct 600  
 acagt ggcca aaacat ggga gacat ggacc cccacat ct t t gct gt ggca gaagaagcct 660  
 acaagcagat ggccagagat gagaagaat c agt ccat cat agt cagt ggg gagt ct ggag 720  
 ccgggaagac ggt at cagcc aagt at gcca t gcgct at t t cgccaccgt t ggt ggct cgg 780  
 ccagt gaaac caacat cgaa gagaaggt gc tggcat ccag t cccat cat g gaggccat t g 840  
 gaaat gccaa gaccacccgc aat gacaaca gcagccgt t t t ggcaagt ac at ccagat t g 900  
 gct t t gacaa aaggt accac at cat cgggg ccaacat gag gact t acct c t t ggagaagt 960  
 ccagagt ggt ct t ccaggca gat gat gaga ggaat t acca cat ct t t t ac cagct ct gt g 1020  
 ct gct gccgg t ct t ccagaa t t t aaagagc t t gcact aac aagt gcagag gact t t t t ct 1080  
 at acat caca gggaggagac act t ccat cg aggggt gt gga cgat gct gag gact t t gaga 1140  
 agact cgaca agcct t caca ct cct cgag t gaaagagt c ccat cagat g agcat t t t t a 1200  
 agat aat t gc t t ct at ct t g cacct t ggaa gt gt ggcgat t caggct gag cgt gat ggt g 1260

N3027PCT\_sequ. list .txt

at t cct gt ag t at at cacc	caggat gt at acct aagcaa	ct t ct gccga	ct gct agggg	1320
t ggagcacag t cagat ggag	cact ggct gt gt cat cgcaa	gct ggt cacc	acct cggaga	1380
cct acgt caa gaccat gt cc	ct gcagcagg t gat caat gc	gcgcaacgcc	ct ggccaagc	1440
acat ct at gc ccagt t gt t c	ggct ggat t g t ggagcacat	caacaaggcc	ct gcacacct	1500
ccct caagca gcact cct t c	at cgggggt cc t ggacat ct a	t ggggt t t gag	acat t t gagg	1560
t aaacagct t t gagcagt t c	t gt at caact at gcaaat ga	aaagct ccag	cagcagt t ca	1620
act cgcat gt t t t caaact g	gagcaagaag aat acat gaa	ggaacagat c	cct t ggaccc	1680
t gat t gat t t t t at gat aac	caacct t gt a t cgacct cat	t gaagccaag	ct ggggt at ct	1740
t ggacct gt t ggat gaagaa	t gt aagggt cc ccaaaggaac	t gaccagaac	t gggct caga	1800
agct ct at ga ccggcact cc	agcagccagc act t ccagaa	gccccgcat g	t ccaacacgg	1860
cct t cat cat cgt ccact t t	gcagacaagg t ggagt acct	ct ct gat ggt	t t t ct ggaga	1920
aaaacagaga cacggt gt at	gaagagcaga t caat at cct	gaaggccagc	aagt t cccac	1980
t agt ggct ga ct t gt t t cat	gat gacaagg accct gt t cc	t gccaccacc	cct gggaagg	2040
gggt cat ct t c gaagat cagc	gt ccgt t ct g ccagaccccc	cat gaaagt c	t ccaacaagg	2100
agcacaagaa aaccgt t ggc	caccagt t cc gt acct ccct	gcat ct gct c	at ggagaccc	2160
t gaat gccac gacacct cac	t at gt ccgct gcat caagcc	caacgat gag	aagct cccct	2220
t t cact t t ga cccaaagaga	gcagt gcagc aact cagagc	ct gcgggggt g	t t ggagacga	2280
t t cgaat cag t gcagct ggc	t acccat cca ggt gggcct a	ccat gact t t	t t caaccggt	2340
at cgggt gct ggt caagaag	agagagct cg ccaacacaga	caaaaaggcc	at ct gcaggt	2400
ct gt cct gga gaacct cat c	aaggaccccg acaagt t cca	gt t t ggccgc	accaagat ct	2460
t ct t t cgagc aggccaggt g	gcct acct gg agaagct gcg	ggct gacaag	t t ccggacag	2520
ccacct cat gat ccagaaa	act gt ccggg gat ggct gca	gaaggt gaaa	t at cacaggc	2580
t gaagggggc t acct t aacc	ct gcagaggt act gccgggg	acacct ggcc	cgcaggct gg	2640
ct gagcacct gcggaggat c	agagcggct g t ggt gct cca	gaaacat t ac	cgcat gcaga	2700
gggcccggca ggct accag	agggt ccgca gagct gccgt	t gt t at ccag	gcct t cacc	2760
gggcat gt t t gt gcggaga	acct accgcc aggt cct cat	ggagcacaag	gccaccacca	2820
t ccagaagca cgt gcggggc	t ggat ggcac gcaggcact t	ccagcggct g	cgggat gcag	2880
ccat t gt cat ccagt gt gcc	t t ccggat gc t caaggccag	gcgggagct g	aaggccct ca	2940
ggat t gaggc ccgct cagca	gagcat ct ga aacgt ct caa	cgt gggcat g	gagaacaagg	3000
t ggt ccagct gcagcggaag	at cgat gagc agaacaaaga	gt t caagaca	ct t t cagagc	3060
agt t gt ccgt gaccacct ca	acat acacca t ggaggt aga	gcggct gaag	aaggagct gg	3120
t gcact acca gcagagccca	gggt gaggaca ccagcct cag	gct gcaggag	gaggt ggaga	3180
gcct gcgcac agagct gcag	agggccact cggagcgcaa	gat ct t ggag	gacgcccaca	3240
gcagggagaa agat gagct g	aggaagcgag t t gcagacct	ggagcaagaa	aat gct ct ct	3300
t gaaagat ga gaaagaacag	ct caacaacc aaat cct gt g	ccagt ct aaa	gat gaat t t g	3360

N3027PCT\_sequ. list . . txt

cccagaact c t gt gaaggaa aat ct cat ga agaaagaact ggaggaggag cgat cccggt	3420
accagaacct t gt gaaggaa t at t cacagt t ggagcagag at acgacaac ct t cgggat g	3480
aaat gaccat cat aaagcaa act ccaggt c at aggcggaa cccat caaac caaagt agct	3540
t agaat ct ga ct ccaat t ac ccct ccat ct ccacat ct ga gat cggagac act gaggat g	3600
ccct ccagca ggt ggaggaa at t ggcct gg agaaggcagc cat ggacat g acggt ct t cc	3660
t gaagct gca gaagagagt a cgggagct gg agcaggagag gaaaaagct g caagt gcagc	3720
t ggagaagag agaacagcag gacagcaaga aagt ccaggc ggaaccacca cagact gaca	3780
t agat t t gga cccgaat gca gat ct ggcct acaat agt ct gaagaggcaa gagct ggagt	3840
cagagaacaa aaagct gaag aat gacct ga at gagct gag gaaagccgt g gccgaccaag	3900
ccacgcagaa t aact ccagc cacggct ccc cagat agct a cagcct cct g ct gaaccagc	3960
t caagct ggc ccacgaggag ct cgaggt gc gcaaggagga ggt gct cat c ct caggaccc	4020
agat cgt gag cgccgaccag cggcgact cg ccggcaggaa cgcgagccg aacat t aat g	4080
ccagat caag t t ggcct aac agt gaaaagc at gt t gacca ggaggat gcc at t gaggcct	4140
at cacggggt ct gccagaca aacagcaaga ct gaggat t g gggat at t t a aat gaagat g	4200
gagaact cgg ct t ggcct ac caaggcct aa agcaagt t gc caggct gct g gaggct cagc	4260
t gcaggccca gagcct ggag cat gaggagg aggt ggagca t ct caaggct cagct cgagg	4320
ccct gaagga ggagat ggac aaacagcagc agacct t ct g ccagacgct a ct gct ct ccc	4380
cagaggccca ggt ggaat t c ggcgt t cagc aggaaat at c ccggct gacc aacgagaat c	4440
t ggacct t aa agaact ggt a gaaaagct gg aaaagaat ga gaggaagct c aaaaagcaac	4500
t gaagat t t a cat gaagaaa gcccaggacc t agaagct gc ccaggcat t g gcccagagt g	4560
agaggaagcg ccat gagct c aacaggcagg t cacgggt cca gcggaaagag aaggat t t cc	4620
agggcat gct ggagt accac aaagaggacg aggccct cct cat ccggaac ct ggt gacag	4680
act t gaagcc ccagat gct g t cgggcacag t gccct gt ct cccgcct ac at cct ct aca	4740
t gt gcat ccg gcacgcggac t acaccaacg acgat ct caa ggt gact cc ct gct gacct	4800
ccaccat caa cggcat t aag aaagt cct ga aaaagcacia t gat gact t t gagat gacgt	4860
cat t ct ggt t at ccaacacc t gccgcct t c t t cact gt ct gaagcagt ac agcggggat g	4920
agggct t cat gact cagaac act gcaaagc agaat gaaca ct gt ct t aag aat t t t gacc	4980
t caccgaat a ccgt caggt g ct gagt gacc t t t ccat t ca gat ct accag cagct cat t a	5040
aaat t gccga gggcgt gt t a cagccgat ga t agt t t ct gc cat gt t ggaa aat gagagca	5100
t t cagggt ct at ct ggt gt g aagcccaccg gct accggaa gcgct cct cc agcat ggcag	5160
at ggggat aa ct cat act gc ct ggaagct a t cat ccgcca gat gaat gcc t t t cat acag	5220
t cat gt gt ga ccagggt t g gaccct gaga t cat cct gca ggt at t caaa cagct ct t ct	5280
acat gat caa cgcagt gact ct t aacaacc t gct ct t gcg gaaggacgt c t gct ct t gga	5340
gcacaggcat gcaact cagg t acaat at aa gt cagct t ga ggagt ggct t cggggaagaa	5400

N3027PCT\_sequ. list.txt

acctt cacca	gagt ggagca	gtt cagacca	t ggaacct ct	gat ccaagca	gcccagct cc	5460
t gcaatt aaa	gaagaaaacc	caggaggacg	cagaggct at	ct gct ccct g	t gt acct ccc	5520
t cagcaccca	gcagatt gtc	aaaatttt aa	accttt at ac	t cccct gaat	gaattt gaag	5580
aacgggt aac	agt ggccttt	at acgaacaa	t ccaggcaca	act acaagag	cggaat gacc	5640
ct cagcaact	gct att agat	gccaagcaca	t gttt cct gt	ttt gttt cca	ttt aat ccat	5700
ctt ct ct aac	cat ggact ca	at ccacat cc	cagcgt gt ct	caat ct ggaa	tt cct caat g	5760
aagt ct gaag	at gcat gttt	ccagcat tag	ttt gat tccc	aat gt gagca	agaaggaagt	5820
at at acagt a	aagt aaatt c	aaggat ct gt	t aaat ct ggt	aaaagt agat	caaat cagag	5880
att gacagcc	t gt ggagggt	gct gaact at	acagaatt ag	acacaact at	gt catt attt	5940
ttt gt acct a	ct gct cagaa	t aaaaacact	t gaaat at gg	aagatttt aa	gttt gat ttc	6000
agt ccaacac	at at acat aa	ttt at agaca	ccaagcagt c	cccat agaca	t at aaaaggt	6060
gt caatt ct a	t aaaacgaag	ct gcct agtt	tt gat cttt g	cat agaact a	gagaat gt cc	6120
aaatt aaaat	accaaatt at a	t at aagt cac	at aaatt gcc	tt caaagggc	ttt acaaat	6180
aat ggt act a	at aaccat ga	t aat ggcat a	t act gacatt	t cccaaagt t	t gcaaaccat	6240
aggt gt ggt t	gagttt gt gg	t gagat gttt	t aagaacaaa	aat at gggga	t gagact t ct	6300
gagaaat att	cccaaaat at	ttttt aat gg	ct gatt at ac	acagacagt g	gt gt aact ga	6360
cct ccagacc	agacatttt g	agt act ggt t	t ct gaagcaa	aat t agaagt	gccagt cct c	6420
agt gt gct ca	aacgctttt g	t gtt at ctt g	attt aat gga	agagatt at t	aaaat gct gc	6480
t at cccaaac	t ccaagt gag	aaagat ggaa	aaat atttt g	ttt ct gat gc	t agt ccat ac	6540
acttt ccaag	t cccacaaaa	cttt cacaaa	aat gt at at a	agct aaat at	t agaaacgga	6600
t aacaaactt	gtttt attt a	tagat gt aaa	aaccaaacaa	gt caat at ga	aagctttt aa	6660
t ct ct t aat a	ccatt aagct	t ccagt aaga	gcat cacat a	at gct ct act	gt t ccagaaa	6720
ccaaat agt a	aaacaaact a	aagt t cgcac	at cagat cat	ct gaaaaacc	tt caaaaat a	6780
at cagtt cag	ggat att at a	caaaagttt g	ggtttttttt	tttt aagaga	at aaaat ggc	6840
tt aggt caac	ttt cctttt	caggtt attt	t caacgtttt	t caaattt ag	cacacaaaaa	6900
att gt aaat a	t ct ct cccac	aaaat aagga	tttt aaaaaa	gt aat t cagt	aat at aacag	6960
gctt agat gt	tt gct gct ct	tagaattttt	ttt aactt gt	tttt ggttt c	tt caaaagca	7020
agcat t caat	t ggaaaccca	t att cttt cc	acactttttt	tt act gt ctt	tt ct gt attt	7080
ctt gat agca	gt at gct gtt	cccat aagaa	aaaaat ggt a	ttt gcaaat c	at ggaagaac	7140
agcct ct gt a	tt acatt gag	aaaat aagat	tt at ccat ga	att ggaagt a	gaacagcct g	7200
cctt caccct	ctttt act ca	accaccaac	tt aaaaggct	ctt ggaaaca	cagcacact c	7260
cacgct acct	t ct gcact gt	gccct tagag	cacagct t cc	t cagt t gt t c	t ct gcat ct c	7320
ct ggggctt a	ggccagt ctt	agcct ggggt	aaggct gct g	acatt gt gtt	ccaat cagt t	7380
gt cat gggca	tt at cccct c	t acat ccaca	tt aaacat gc	cggct t ct ct	t gggcat cgg	7440
cagagct gt g	ccttttt ctt	t cagtt acag	tt acat aat c	act gacgt cc	at gacact t a	7500

N3027PCT\_sequ.list.txt

cccat ggat c	cat gt gct ga	ct t cat t t ag	aaggccaat c	t aaaacaact	gggt t t gt gg	7560
ct acct ct t t	aaagt t gt t t	gt gaaggat a	at t t gt t t t t	t aat gcact t	t agt t t gaaa	7620
gt gagt ct ct	t at gt aagga	ccat cct t aa	aagacaaaaa	at gcct t gt t	agagt gt t aa	7680
ggagt t t t ga	cat gcagt gg	t t ccacaaac	acagt ggct t	act at cct t a	t aact gt ct	7740
t at accat ca	t t ct ct ccat	ct ct ct t ggt	cact act ct c	t gct gt cact	gggt t aat cac	7800
t aggt gccaa	gagct t act g	aat aaaagct	t ggcaat t ag	aat aaat ggg	gaggggaagga	7860
cct t at gaat	agt ccat t t a	gcct aagaaa	t ggcagat t t	agt t ct t ct c	t t ccaaaaga	7920
t aaaggt at a	t cct ggaat t	gt act t aaaa	ct t acagat g	act aacaaat	at at act t t a	7980
t at gt agt t a	at at t t agat	ct gt ct t at t	t aat act t gg	aggct agaag	aagcat ct t t	8040
aggggaact a	t at aat ct t t	t gt t agcat t	t t ct ct gcat	t t t aaaaaat	cat t t caat t	8100
caaacat t t a	t cagt gt cat	gaaat cagt a	at gact ct t t	aacaat t cag	gt t t gaact c	8160
t gcat t agat	gt ct ct t t aa	t t t t t aat a	t t t aaaaat t t	agt t gacat t	t t t t t cacca	8220
gggt gcct t t a	gcggt t act a	agat aact ga	cat cagt t gt	t t ct ct gaaa	t aagt gt t gc	8280
t gt gggaat a	at t t t aat gt	t caaggt gat	at cat ggggg	agt t t t gt ct	t t t aaaacat	8340
t agaagcat t	t t aaat at t a	agaat caaat	at t t at agat	caaaact t gt	gt t t t aagt a	8400
t t at acggga	cct gt t t act	t at agt aaat	gt gaat gt ac	acat gagt t g	t t gct gaagc	8460
t gacaagcat	at t acat aca	t gcat t t t cc	ct gt gccct c	at agt t gcag	t t agagt t cc	8520
agt acct gt a	ggct cacct g	ggaggcagat	t agacccaaa	gggt agat gt t	t t t cccct t t	8580
ccat gaagca	t gt cagt ggg	agt t gct t cc	t t t gat t t cc	ct agt act aa	at t t t aaggc	8640
t t t t gt aaaa	acaaaacaaa	act aggagct	t ggaacagt t	aaaaat caac	act gct acca	8700
t caat t cat c	aaat at t t ac	t t agagct t t	cat acat t aa	gat t ccagt a	accaat aaat	8760
t agaat t cat	t t ct t ct gca	t aaagt aaat	t t t cat acac	t t gacct act	aagacagcaa	8820
gggt gt cct a	aat t gaggca	t t t gt at aat	gcct gcat aa	ct aaat ggt c	act aaaaat gg	8880
gacagcat gg	ggcaagacct	t gt agt t ct t	cacagaat at	t t gt ggt cag	t t t ct ccaat	8940
t aat t t gct g	cat gagccaa	at aacct aa	t t cact t t t t	at acccact g	gt gccat aat	9000
t agagaat t a	gaggt gt ag	acagaggt t a	at gccaat ga	gaaacacagg	acaggggt t t t	9060
t t t t at t at a	aaggt cat t a	gat acaaaaag	at t gt t t t t c	aaaaaat t t c	t aat t ct aac	9120
aaaggggat c	aat cagaaat	gaaact aagc	t act t t ct aa	agt gacact g	t at cagaat a	9180
at ccagat t t	gaat at aaca	t t t t gccacc	aact gacat t	t agat gaagg	act gcct ct c	9240
t gaaagagt t	cagat cat at	t caggggt ga	at ccaacacc	at ggaagaaa	gact act gat	9300
gaaaaat at t t	t cccact t t g	cacaaat ct g	t aaact acac	ct t t gt t t at	agaaaaat gc	9360
t t gt aat agt	cact gt aat a	t t t agct gt g	gat aaaaat t	t gt ggaaat a	aat act t t t g	9420
aat aaagagg	t gt gccaaat	ct aaat gaaa	t t t aaaact c	t gcagct aca	gggt t gacaaa	9480
gt t t ct t t gt	aat gct ct ct	t gagaagc				9508

N3027PCT\_sequ.list.txt

<210> 38  
 <211> 1848  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1848)  
 <223> myosin VB MYO5B

<400> 38

Met Ser Val Gly Glu Leu Tyr Ser Gln Cys Thr Arg Val Trp Ile Pro  
 1 5 10 15

Asp Pro Asp Glu Val Trp Arg Ser Ala Glu Leu Thr Lys Asp Tyr Lys  
 20 25 30

Glu Gly Asp Lys Ser Leu Gln Leu Arg Leu Glu Asp Glu Thr Ile Leu  
 35 40 45

Glu Tyr Pro Ile Asp Val Gln Arg Asn Gln Leu Pro Phe Leu Arg Asn  
 50 55 60

Pro Asp Ile Leu Val Gly Glu Asn Asp Leu Thr Ala Leu Ser Tyr Leu  
 65 70 75 80

His Glu Pro Ala Val Leu His Asn Leu Lys Val Arg Phe Leu Glu Ser  
 85 90 95

Asn His Ile Tyr Thr Tyr Cys Gly Ile Val Leu Val Ala Ile Asn Pro  
 100 105 110

Tyr Glu Gln Leu Pro Ile Tyr Gly Gln Asp Val Ile Tyr Thr Tyr Ser  
 115 120 125

Gly Gln Asn Met Gly Asp Met Asp Pro His Ile Phe Ala Val Ala Glu  
 130 135 140

Glu Ala Tyr Lys Gln Met Ala Arg Asp Glu Lys Asn Gln Ser Ile Ile  
 145 150 155 160

Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Val Ser Ala Lys Tyr Ala  
 165 170 175

Met Arg Tyr Phe Ala Thr Val Gly Gly Ser Ala Ser Glu Thr Asn Ile  
 180 185 190

Glu Glu Lys Val Leu Ala Ser Ser Pro Ile Met Glu Ala Ile Gly Asn  
 195 200 205

Ala Lys Thr Thr Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Ile  
 210 215 220

N3027PCT\_sequ.list.txt

Gln Ile Gly Phe Asp Lys Arg Tyr His Ile Ile Gly Ala Asn Met Arg  
 225 230 235 240  
 Thr Tyr Leu Leu Gu Lys Ser Arg Val Val Phe Gln Ala Asp Asp Gu  
 245 250 255  
 Arg Asn Tyr His Ile Phe Tyr Gln Leu Cys Ala Ala Ala Gly Leu Pro  
 260 265 270  
 Gu Phe Lys Gu Leu Ala Leu Thr Ser Ala Gu Asp Phe Phe Tyr Thr  
 275 280 285  
 Ser Gln Gly Gly Asp Thr Ser Ile Gu Gly Val Asp Asp Ala Gu Asp  
 290 295 300  
 Phe Gu Lys Thr Arg Gln Ala Phe Thr Leu Leu Gly Val Lys Gu Ser  
 305 310 315 320  
 His Gln Met Ser Ile Phe Lys Ile Ile Ala Ser Ile Leu His Leu Gly  
 325 330 335  
 Ser Val Ala Ile Gln Ala Gu Arg Asp Gly Asp Ser Cys Ser Ile Ser  
 340 345 350  
 Pro Gln Asp Val Tyr Leu Ser Asn Phe Cys Arg Leu Leu Gly Val Gu  
 355 360 365  
 His Ser Gln Met Gu His Trp Leu Cys His Arg Lys Leu Val Thr Thr  
 370 375 380  
 Ser Gu Thr Tyr Val Lys Thr Met Ser Leu Gln Gln Val Ile Asn Ala  
 385 390 395 400  
 Arg Asn Ala Leu Ala Lys His Ile Tyr Ala Gln Leu Phe Gly Trp Ile  
 405 410 415  
 Val Gu His Ile Asn Lys Ala Leu His Thr Ser Leu Lys Gln His Ser  
 420 425 430  
 Phe Ile Gly Val Leu Asp Ile Tyr Gly Phe Gu Thr Phe Gu Val Asn  
 435 440 445  
 Ser Phe Gu Gln Phe Cys Ile Asn Tyr Ala Asn Gu Lys Leu Gln Gln  
 450 455 460  
 Gln Phe Asn Ser His Val Phe Lys Leu Gu Gln Gu Gu Tyr Met Lys  
 465 470 475 480  
 Gu Gln Ile Pro Trp Thr Leu Ile Asp Phe Tyr Asp Asn Gln Pro Cys  
 485 490 495

Ile Asp Leu Ile Glu Ala Lys Leu Gly Ile Leu Asp Leu Leu Asp Glu  
 500 505 510  
 Glu Cys Lys Val Pro Lys Gly Thr Asp Glu Asn Trp Ala Glu Lys Leu  
 515 520 525  
 Tyr Asp Arg His Ser Ser Ser Glu His Phe Glu Lys Pro Arg Met Ser  
 530 535 540  
 Asn Thr Ala Phe Ile Ile Val His Phe Ala Asp Lys Val Glu Tyr Leu  
 545 550 555 560  
 Ser Asp Gly Phe Leu Glu Lys Asn Arg Asp Thr Val Tyr Glu Glu Glu  
 565 570 575  
 Ile Asn Ile Leu Lys Ala Ser Lys Phe Pro Leu Val Ala Asp Leu Phe  
 580 585 590  
 His Asp Asp Lys Asp Pro Val Pro Ala Thr Thr Pro Gly Lys Gly Ser  
 595 600 605  
 Ser Ser Lys Ile Ser Val Arg Ser Ala Arg Pro Pro Met Lys Val Ser  
 610 615 620  
 Asn Lys Glu His Lys Lys Thr Val Gly His Glu Phe Arg Thr Ser Leu  
 625 630 635 640  
 His Leu Leu Met Glu Thr Leu Asn Ala Thr Thr Pro His Tyr Val Arg  
 645 650 655  
 Cys Ile Lys Pro Asn Asp Glu Lys Leu Pro Phe His Phe Asp Pro Lys  
 660 665 670  
 Arg Ala Val Glu Glu Leu Arg Ala Cys Gly Val Leu Glu Thr Ile Arg  
 675 680 685  
 Ile Ser Ala Ala Gly Tyr Pro Ser Arg Trp Ala Tyr His Asp Phe Phe  
 690 695 700  
 Asn Arg Tyr Arg Val Leu Val Lys Lys Arg Glu Leu Ala Asn Thr Asp  
 705 710 715 720  
 Lys Lys Ala Ile Cys Arg Ser Val Leu Glu Asn Leu Ile Lys Asp Pro  
 725 730 735  
 Asp Lys Phe Glu Phe Gly Arg Thr Lys Ile Phe Phe Arg Ala Gly Glu  
 740 745 750  
 Val Ala Tyr Leu Glu Lys Leu Arg Ala Asp Lys Phe Arg Thr Ala Thr  
 755 760 765  
 Ile Met Ile Glu Lys Thr Val Arg Gly Trp Leu Glu Lys Val Lys Tyr  
 770 775 780 785 790 795

770

775

780

His Arg Leu Lys Gly Ala Thr Leu Thr Leu Gln Arg Tyr Cys Arg Gly  
 785 790 795 800  
 His Leu Ala Arg Arg Leu Ala Glu His Leu Arg Arg Ile Arg Ala Ala  
 805 810 815  
 Val Val Leu Gln Lys His Tyr Arg Met Gln Arg Ala Arg Gln Ala Tyr  
 820 825 830  
 Gln Arg Val Arg Arg Ala Ala Val Val Ile Gln Ala Phe Thr Arg Ala  
 835 840 845  
 Met Phe Val Arg Arg Thr Tyr Arg Gln Val Leu Met Glu His Lys Ala  
 850 855 860  
 Thr Thr Ile Gln Lys His Val Arg Gly Trp Met Ala Arg Arg His Phe  
 865 870 875 880  
 Gln Arg Leu Arg Asp Ala Ala Ile Val Ile Gln Cys Ala Phe Arg Met  
 885 890 895  
 Leu Lys Ala Arg Arg Glu Leu Lys Ala Leu Arg Ile Glu Ala Arg Ser  
 900 905 910  
 Ala Glu His Leu Lys Arg Leu Asn Val Gly Met Glu Asn Lys Val Val  
 915 920 925  
 Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys Glu Phe Lys Thr Leu  
 930 935 940  
 Ser Glu Gln Leu Ser Val Thr Thr Ser Thr Tyr Thr Met Glu Val Glu  
 945 950 955 960  
 Arg Leu Lys Lys Glu Leu Val His Tyr Gln Gln Ser Pro Gly Glu Asp  
 965 970 975  
 Thr Ser Leu Arg Leu Gln Glu Glu Val Glu Ser Leu Arg Thr Glu Leu  
 980 985 990  
 Gln Arg Ala His Ser Glu Arg Lys Ile Leu Glu Asp Ala His Ser Arg  
 995 1000 1005  
 Glu Lys Asp Glu Leu Arg Lys Arg Val Ala Asp Leu Glu Gln Glu  
 1010 1015 1020  
 Asn Ala Leu Leu Lys Asp Glu Lys Glu Gln Leu Asn Asn Gln Ile  
 1025 1030 1035  
 Leu Cys Gln Ser Lys Asp Glu Phe Ala Gln Asn Ser Val Lys Glu  
 1040 1045 1050

N3027PCT\_sequ.list.txt

Asn	Leu	Met	Lys	Lys	Glu	Leu	Glu	Glu	Glu	Arg	Ser	Arg	Tyr	Gln
1055						1060					1065			
Asn	Leu	Val	Lys	Glu	Tyr	Ser	Gln	Leu	Glu	Gln	Arg	Tyr	Asp	Asn
1070						1075					1080			
Leu	Arg	Asp	Glu	Met	Thr	Ile	Ile	Lys	Gln	Thr	Pro	Gly	His	Arg
1085						1090					1095			
Arg	Asn	Pro	Ser	Asn	Gln	Ser	Ser	Leu	Glu	Ser	Asp	Ser	Asn	Tyr
1100						1105					1110			
Pro	Ser	Ile	Ser	Thr	Ser	Glu	Ile	Gly	Asp	Thr	Glu	Asp	Ala	Leu
1115						1120					1125			
Gln	Gln	Val	Glu	Glu	Ile	Gly	Leu	Glu	Lys	Ala	Ala	Met	Asp	Met
1130						1135					1140			
Thr	Val	Phe	Leu	Lys	Leu	Gln	Lys	Arg	Val	Arg	Glu	Leu	Glu	Gln
1145						1150					1155			
Glu	Arg	Lys	Lys	Leu	Gln	Val	Gln	Leu	Glu	Lys	Arg	Glu	Gln	Gln
1160						1165					1170			
Asp	Ser	Lys	Lys	Val	Gln	Ala	Glu	Pro	Pro	Gln	Thr	Asp	Ile	Asp
1175						1180					1185			
Leu	Asp	Pro	Asn	Ala	Asp	Leu	Ala	Tyr	Asn	Ser	Leu	Lys	Arg	Gln
1190						1195					1200			
Glu	Leu	Glu	Ser	Glu	Asn	Lys	Lys	Leu	Lys	Asn	Asp	Leu	Asn	Glu
1205						1210					1215			
Leu	Arg	Lys	Ala	Val	Ala	Asp	Gln	Ala	Thr	Gln	Asn	Asn	Ser	Ser
1220						1225					1230			
His	Gly	Ser	Pro	Asp	Ser	Tyr	Ser	Leu	Leu	Leu	Asn	Gln	Leu	Lys
1235						1240					1245			
Leu	Ala	His	Glu	Glu	Leu	Glu	Val	Arg	Lys	Glu	Glu	Val	Leu	Ile
1250						1255					1260			
Leu	Arg	Thr	Gln	Ile	Val	Ser	Ala	Asp	Gln	Arg	Arg	Leu	Ala	Gly
1265						1270					1275			
Arg	Asn	Ala	Glu	Pro	Asn	Ile	Asn	Ala	Arg	Ser	Ser	Trp	Pro	Asn
1280						1285					1290			
Ser	Glu	Lys	His	Val	Asp	Gln	Glu	Asp	Ala	Ile	Glu	Ala	Tyr	His
1295						1300					1305			

N3027PCT\_sequ.list.txt

Gly	Val	Oys	Gln	Thr	Asn	Ser	Lys	Thr	Glu	Asp	Trp	Gly	Tyr	Leu
	1310					1315					1320			
Asn	Glu	Asp	Gly	Glu	Leu	Gly	Leu	Ala	Tyr	Gln	Gly	Leu	Lys	Gln
	1325					1330					1335			
Val	Ala	Arg	Leu	Leu	Glu	Ala	Gln	Leu	Gln	Ala	Gln	Ser	Leu	Glu
	1340					1345					1350			
His	Glu	Glu	Glu	Val	Glu	His	Leu	Lys	Ala	Gln	Leu	Glu	Ala	Leu
	1355					1360					1365			
Lys	Glu	Glu	Met	Asp	Lys	Gln	Gln	Gln	Thr	Phe	Oys	Gln	Thr	Leu
	1370					1375					1380			
Leu	Leu	Ser	Pro	Glu	Ala	Gln	Val	Glu	Phe	Gly	Val	Gln	Gln	Glu
	1385					1390					1395			
Ile	Ser	Arg	Leu	Thr	Asn	Glu	Asn	Leu	Asp	Leu	Lys	Glu	Leu	Val
	1400					1405					1410			
Glu	Lys	Leu	Glu	Lys	Asn	Glu	Arg	Lys	Leu	Lys	Lys	Gln	Leu	Lys
	1415					1420					1425			
Ile	Tyr	Met	Lys	Lys	Ala	Gln	Asp	Leu	Glu	Ala	Ala	Gln	Ala	Leu
	1430					1435					1440			
Ala	Gln	Ser	Glu	Arg	Lys	Arg	His	Glu	Leu	Asn	Arg	Gln	Val	Thr
	1445					1450					1455			
Val	Gln	Arg	Lys	Glu	Lys	Asp	Phe	Gln	Gly	Met	Leu	Glu	Tyr	His
	1460					1465					1470			
Lys	Glu	Asp	Glu	Ala	Leu	Leu	Ile	Arg	Asn	Leu	Val	Thr	Asp	Leu
	1475					1480					1485			
Lys	Pro	Gln	Met	Leu	Ser	Gly	Thr	Val	Pro	Oys	Leu	Pro	Ala	Tyr
	1490					1495					1500			
Ile	Leu	Tyr	Met	Oys	Ile	Arg	His	Ala	Asp	Tyr	Thr	Asn	Asp	Asp
	1505					1510					1515			
Leu	Lys	Val	His	Ser	Leu	Leu	Thr	Ser	Thr	Ile	Asn	Gly	Ile	Lys
	1520					1525					1530			
Lys	Val	Leu	Lys	Lys	His	Asn	Asp	Asp	Phe	Glu	Met	Thr	Ser	Phe
	1535					1540					1545			
Trp	Leu	Ser	Asn	Thr	Oys	Arg	Leu	Leu	His	Oys	Leu	Lys	Gln	Tyr
	1550					1555					1560			

Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Thr Ala Lys Gln Asn  
 1565 1570 1575  
 Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val  
 1580 1585 1590  
 Leu Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Ile  
 1595 1600 1605  
 Ala Glu Gly Val Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu  
 1610 1615 1620  
 Asn Glu Ser Ile Gln Gly Leu Ser Gly Val Lys Pro Thr Gly Tyr  
 1625 1630 1635  
 Arg Lys Arg Ser Ser Ser Met Ala Asp Gly Asp Asn Ser Tyr Cys  
 1640 1645 1650  
 Leu Glu Ala Ile Ile Arg Gln Met Asn Ala Phe His Thr Val Met  
 1655 1660 1665  
 Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys  
 1670 1675 1680  
 Gln Leu Phe Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu  
 1685 1690 1695  
 Leu Arg Lys Asp Val Cys Ser Trp Ser Thr Gly Met Gln Leu Arg  
 1700 1705 1710  
 Tyr Asn Ile Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg Asn Leu  
 1715 1720 1725  
 His Gln Ser Gly Ala Val Gln Thr Met Glu Pro Leu Ile Gln Ala  
 1730 1735 1740  
 Ala Gln Leu Leu Gln Leu Lys Lys Lys Thr Gln Glu Asp Ala Glu  
 1745 1750 1755  
 Ala Ile Cys Ser Leu Cys Thr Ser Leu Ser Thr Gln Gln Ile Val  
 1760 1765 1770  
 Lys Ile Leu Asn Leu Tyr Thr Pro Leu Asn Glu Phe Glu Glu Arg  
 1775 1780 1785  
 Val Thr Val Ala Phe Ile Arg Thr Ile Gln Ala Gln Leu Gln Glu  
 1790 1795 1800  
 Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ala Lys His Met Phe  
 1805 1810 1815  
 Pro Val Leu Phe Pro Phe Asn Pro Ser Ser Leu Thr Met Asp Ser

1820

I l e H i s I l e P r o A l a C y s L e u A s n L e u G l u P h e L e u A s n G l u V a l  
1835 1840 1845

<210> 39  
<211> 8662  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_f e a t u r e  
<222> ( 1 ) . . ( 8662)  
<223> myosi n VI M Y O 6

```

<400> 39
gtgcacgccg cagt gccggg gact cggcgg ggcgccggcc ggcgggcgga gaccgact cg      60
ggat ct gt cc gagcaggaag ccagcct cag cccggccgct gt cgccgccc t gt cct ggt g      120
cccgt ccgcg t cgt cgccct ct t cact ggc cct cat cact t ct caccgcg ccct ccagct      180
t caccctgt ac aggt agcccc gccgccgcgc acct gcct t c gct ccgcac cggg gacagt      240
ggat agt gga aacaggagat cgt ggat cct cct t caaaaa t ggaggat gg aaagcccgt t      300
t gggcgccac accct acaga t ggat t t cag at gggcaat a t t gt ggat at t ggccccgac      360
agct t aacaa t t gaaccct t gaat cagaaa ggcaagacat t t t t ggct ct cat aaaccaa      420
gt gt t t cct g cagaagagga cagt aaaaaa gat gt ggaag at aact gt t c act aat gt at      480
t t aaat gaag ccacact gct ccat aat at c aaagt t cgat at agt aaaga cagaat t t at      540
acat at gt cg ccaacat t ct gat t gcagt g aat ccat act t t gacat acc t aaaat at at      600
t ct t cagaag caat aaagt c at at caagga aaat ct ct t g ggacaagacc acct cat gt c      660
t t t gcaat t g ct gat aaagc t t t t cgagac at gaaggt gc t caagat gag t cagt ct at c      720
at t gt at ct g gagaat cagg agccggcaaa acagaaaat a caaaat t t gt t ct aagat ac      780
ct gact gaat cct at ggaac aggt caagat at t gat gaca gaat t gt t ga agct aaccca      840
ct cct agaag cct t t ggaaa t gcgaagact gt t cgcaaca at aat agcag t cgat t t ggg      900
aaat t t gt ag aaat acat t t t aat gaaaag agct cagt t g t t ggaggat t t gt t t cacat      960
t at ct cct ag agaaat ct ag gat ct gt gt t caaggcaaag aggaaagaaa t t at cat at c      1020
t t t t at aggt t gt gt gct gg t gct t ct gaa gat at t agag aaaaact t ca t t t gagt t ca      1080
ccagat aat t t t cggt at t t aaaccgaggc t gcact agat act t t gct aa caaagaaact      1140
gacaaacaga t t t t acagaa ccgcaaaagt cct gagt acc t t aaggcagg t t ct at gaaa      1200
gat cct ct gc t agat gacca t ggt gat t t t at t agaat gt gcacggct at gaaaaaaat t      1260
ggg t t ggat g at gaagaaaa gct t gat ct c t t ccgggt ag t agct ggcgt cct gcacct t      1320
ggaaat at t g at t t t gagga agct ggcagc act t caggt g gt t gt aat ct gaagaat aaa      1380
t ct gct cagt ct t t ggaat a t t gt gct gaa t t act ggggt t t ggaccaaga t gat ct t cga      1440
gt aagt t t ga ccacaagagt cat gct aaca acagcagggg gcaccaaagg aacagt t at a      1500

```

N3027PCT\_sequ. list.txt

aaggt acct c t gaaagt gga gcaagcaaac aat gct cgt g at gccct ggc aaagacagt g	1560
t at agccat c t t t t t gat ca t gt ggt aaac agagt aaat c agt gt t t t cc t t t t gaaaca	1620
t cat cct at t t t at t ggagt cct agat at t gct ggt t t t g agt act t t ga gcat aacagt	1680
t t t gaacaat t t t gcat caa ct at t gcaat gaaaaact t c aacaat t t t t t aat gaaagg	1740
at t ct gaagg aggaacaaga act ct at caa aaagaagg t t aggt gt t aa t gaagt gcat	1800
t at gt ggat a at caggact g t at agat t t a at t gaagcca aat t agt ggg aat act ggat	1860
at t t t ggat g aagaaaat cg cct t ccccag ccaagt gat c aacact t t ac at ct gcagt t	1920
cacaaaaagc acaaggat ca t t t t cgact c act at t ccca gaaaat ct aa gct ggcagt t	1980
cat aggaat a t cagagacga cgaaggct t c at t at caggc at t t t gcggg ggcagt gt gc	2040
t at gaaaca cccagt t t gt ggagaaaaat aat gat gct t t acat at gt c t ct t gaat cc	2100
t t aat at gt g aat ccagaga t aagt t t at a cggaat t at t t gaat cat c cacaat aac	2160
aacaaagat a ct aaacaaaa agcaggaaaa ct t agct t ca t cagcgt ggg aaacaagt t t	2220
aagacacagt t aaat t t gct t ct ggat aaa ct t cgaagt a ct ggagcaag ct t t at t cgt	2280
t gcat caaac ct aact t aaa gat gacaagc caccact t t g aaggt gct ca aat t ct gt ct	2340
cagct t cagt gt t cagggat ggt gt ct gt t t t ggact t ga t gcagggg gg t t acccat ca	2400
cgagct t cat t t cat gaact ct acaacat g t acaaaaaagt at at gccaga t aaact t gca	2460
agat t ggat c caagact at t t t gt aaggct t t gt t t aaag ct t t gggct t aaat gaaaat	2520
gact acaagt t t ggg t t aac caaagt at t t t t agacct g gcaagt t t gc agaat t t gat	2580
cagat cat ga agt ct gacct t gaccact t a gcagagt t gg t t aaaagagt caat cact gg	2640
ct cacat gca gt cgct ggaa gaaagt t cag t ggt gct cac t ct cagt cat caaat t gaaa	2700
aacaaaaat aa aat at cgagc t gaagcct gc at t aaaat gc aaaaaact at t cgaat gt gg	2760
ct t t gcaaga ggagacacaa acct cgcat t gat ggt ct gg t t aaggt ggg cact gaaa	2820
aaacgact t g at aaat t t aa t gaggt agt c agt gt gt t ga aagat ggaaa acccgagat g	2880
aat aaacaga t caagaat ct ggaaat t t ct at t gat act t t gat ggccaa aat t aagt cc	2940
act at gat ga cgcaggaaca aat ccagaaa gaat at gat g cact ggt t aa aagct cagag	3000
gaact cct ca gt gcat t aca gaaaaaaaaa cagcaggaag aggaagcaga aaggct gagg	3060
cgt at t caag aagaaat gga aaaggaaaga aaaagacgt g aagaagacga aaaacgt cga	3120
agaaaggaag aggaggaaag gcggat gaaa ct t gagat gg aagcaaagag aaaacaagaa	3180
gaagaagaga gaaagaaaag ggaagat gat gaaaaacgca t t caagct ga agt ggaggca	3240
cagct ggccc gacagaagga ggaggaat cc caacagcaag cagt t ct gga gcaggagcgc	3300
agggaccggg agct ggccct gaggat t gcc cagagt gaag ccgagct cat cagt gat gag	3360
gcccaggccg acct ggcgct gcggagaaat gat ggaaca gacccaaaat gacaccggaa	3420
caaat ggcca aagaaat gt c agaat t t t t g agt agaggt c ct gct gt act agccacaaaa	3480
gcagct gct g gt act aagaa at at gat ct t agt aaat gga aat at gcaga act acgt gat	3540
accat caat a ct t ct t gt ga t at t gagct c ct ggcagct t gcagagaaga at t t cat agg	3600

N3027PCT\_sequ.list.txt

agactaaaag	tgtatcatgc	ttggaaatct	aagaacaaga	agagaaat ac	t gaaacagag	3660
caacgtgctc	caaagtctgt	tactgattat	gattttgcac	catttttgaa	caattcacct	3720
cagcaaaacc	cagcagctca	gattcctgcc	aggcagcggg	agattgaaat	gaaccgacag	3780
caacgtttct	tccgcatccc	attcatccgc	cctgccgacc	agtacaaaga	ccctcagagt	3840
aagaaaaaag	gctggaggga	tgcccatttt	gatggacat	ggattgcccg	gcaaatggaa	3900
ctccatcctg	acaagccacc	catcctactt	gtggctggta	aggacgacat	ggagatgtgt	3960
gagctgaatc	ttgaggagac	tggcctgact	cggaaagcgtg	gtgctgagat	cttgccaaga	4020
cagtttgaag	aaatctggga	acgctgtgga	ggcatccagt	accttcagaa	tgcgattgag	4080
agcagacagg	ctcgccccac	ctatgcaaca	gccatgctgc	agagtctgtt	aaagt agat g	4140
ttgcacacca	gccttacagc	tgggagcctt	tgccatggta	cttaggtagg	gtgtgtgcc	4200
ccagatttaa	ccattccata	atcatgttag	agttacttct	ataaagt gaa	cagattttat	4260
taatcacggc	ttttggtgaa	tttgtttaag	gttaattatg	gtagcaaat t	ttggacctaa	4320
acattatfff	tctgtatccc	gctgtaatfc	ccaaaactct	catatatctc	t aactattac	4380
acatgggcat	attctgatgt	ttctcatcct	ttgccagaag	actaccttac	atccatcgt a	4440
attgttctct	aggaaaagag	aacttttttc	aaaattcaaa	atacttttta	aggatggcac	4500
agtaccat at	aactggagt a	ataaaacat g	agctt acatt	cttacaat aa	ctaaaccact	4560
taaaat gat c	aaggcactaa	tgttttggct	t gaaaagct g	tgtactttat	agacattttc	4620
agacattttt	ggaaattttcc	attaaagggtg	gaaaatctat	ttttttcctc	ctttgcagt g	4680
tcttagtttg	aatgaaacac	ttcgaagtfc	tagaattcta	gaaagagcct	t aatgtat tt	4740
gatgtattct	gtgat aagag	gtactaat ag	tatccagcac	agatttgctt	ttctttgct a	4800
gcacaatgtg	tgttgctgtc	agaatattct	ttttatattc	tgtggaaaaa	t aaaggaaat	4860
tcagattgtt	t aaatgccta	aaagttttga	gat aagtttt	gtttcaatt a	gaaaaggaaa	4920
taggttttag	gtggcatagt	ggcttaactg	gactgaattc	aaatattctt	t caacttcat	4980
ctcaatagt g	atttttgtat	cagaatcttg	tccaagttgt	ttcattgatt	t agt aagt gt	5040
tctgcttcca	acatctttct	ttttaagaaa	ttcctagtgt	cttttttggc	ctttgaggt t	5100
ttggtaattg	tagacctgtt	tcat aagctt	tgt aattcag	aaatccttgt	attt agt aag	5160
tgttgtttt	acataactga	t aattttaaa	atgttttctt	tgtgtgctgt	t agt attgat	5220
tcaaatgtca	gcagctttaa	gcctaatatt	tatgactttc	acatttggaa	ttt aaagaca	5280
aaaat acat c	aaggagt tat	gctgacataa	ttct aaggag	ttttgttgt a	tttt agaat a	5340
aaattataaa	gtaaaatgat	tctctgtact	gctttttccc	ccagttttta	gagaccctaa	5400
cctttgaaat	gaaattccag	t gatttcttt	tttccctaga	aagattacct	cagtt aggga	5460
agtatttccc	agctgactag	tgtttgtgag	ccacagacac	tgtcttcaga	attgcttctc	5520
tcatgtctta	gtagagaaat	atttatttat	tatgat acat	tcaaatgatt	gt caagt taa	5580
attaaatggg	tgtgtctgtg	ctattgagaa	t gcaaatgtg	attatctttt	gaaggctgt a	5640

N3027PCT\_sequ. list . . txt

t t a c t g c a t a g c t t c a c c c a c c c t c g g g t c a t t t c g t c c c t g t g a t t g g g g a c a g a a g g t	5700
g t a g c t a c t g a a g t a a t g a c c t a t t c t c t c t c t t c c a t c t c t c g c c t t t a a c t g g t g t t	5760
t t t a t t t g t g t a g g a t a g t g a a t g a t a a g c t t t t t t c c t a a c c a g t a g t g a g t a a g t t c	5820
t t g a a c a a a a t t t a g t a g c c a a a t t g t t t t t t a a t g a c a t g t c t c t t t a g t a c a a t a g t t	5880
t t g t g t a t c t t t t a g a t a c a t t t a a t a g g c a c t a g a t g g a a a a t t a a a g a g t t a a a c a t a t	5940
t t a a a t g a g a g a a t c t a a t g t t t c a g a a a t t t g t a a g a a a t g t a t c a c a g c a a a g g g t t g	6000
t t a t a a g t c c t t a g t t t t t g a c t c t a a t a g t t a a t a c a a t t a t a g t t a a t c t t a a g c c a t	6060
a a t g t t t c t a a t c a t g t c a c a c a g c t g t c c t a g a a c t t a t c t a t t t a a a a t a g t t t c c t g	6120
a g t t a a t t t t g g c c a g c a g g g c a a c t g c c c t a a t t c a g a t a g a t t t a c a g t a a c c t a c g t	6180
a c a g t a g a t g c a c a t a c a c a c a g a c a c c c c t t t g c t g g a g a a a c t t a g g a c c c t g t c a g c	6240
c t t t t a a a g g a a a c a g c a g g a g t g g t g t c c t a a a t g a t g t t c a t g c a g c t g c t t t a c c a t	6300
g t t c a c a g t c a a g c c c a t g c a t g c c a g g t t a a a a c t g t g g a a a t c a a a a g t a a a t t c a c t	6360
c a t a t t t t a a t c a t t t t a a c t g a g a t t t a a a a t t a g a a g t t t a a a c c a c t a t a t a t a a a g	6420
a a c t a a t c t t t t c t t a a t a c c a g t t c t t t c c a t a g c a t a t g c t t t g c a a a g g c a g c a t g c	6480
a t a a a a t a t t t a a a a t g a g a g g a c a g a a t g t t t t c a c a t t t g a t t c a a t t t t a a t a t a a t	6540
t c c t a a t t g t g g t a a c a c a g t t g a g a t a t g t a t t a t a g a t t a t g g g a a c t a a t t g a g a a a	6600
a g g a a g t t a c t c t a a t c c a c g t a t g t t a a g a g a a t a t g a g t t t t c t t a g t t g t a a a g t t	6660
g g g g a g a t g g c a c c t t c t c a g a g g a t t g t g a a a a t a t g a g g a a g a a a a a a a c a g t g c a t	6720
g t a g g a g c a c a g g g c c a c a c a a a g g c a t t c t a t t g t t a t g c t c a t t c t g c t t c t g t a a t g	6780
a c t t t t c a t a g g t c a t t c t t g t g a a c c a t t t t g t t t t g c a a g c a a c c a a g g a a g a a c a t	6840
c t t a a g t g g a a a a t c a g t g g t g g t t g t g a a c a c t t a g a g a t a g c a a t c c a c a g g c a a g a	6900
a t a a t g g t a t t g t t t g t a g a g c t t t a t t a a t t g g a t a t t t t t a a a a g a c a t t t t c a t t c	6960
a c a g g t c a t t a c t a t g g t t c t c a g c g a t c c a a a t a t g t a g a t c a t t g g t t t t t t t t t a	7020
c c t g a a g t a g c t t a a g a g t a c t t g g a t c a g t a g a a t a a a t t t a t t g a a t c a a t c a g t c	7080
a g c c a a t t a a t a t g a t g t t a g t g a t a g a c c t g c c t c c t t t t a t g g a a g a g t a a c a g a t c	7140
c a g a g a g g t c a a g t a a t t t a g t t g t a g a c t g a a a a t a t a t c a a a g c c t t t g c t g c a a t c	7200
a t a t g t a a c a a a a g a a c c a a a a c a a a c a c t t t t t a g t g g c a c c t g t g g a t t t a c a a a g g	7260
g t t g c c t c t c t g t c a t t c c a c a a c t t c a g a a g g t g t g a c a g g t t t t c c c t a t t t a t c a t t	7320
a c c a a t a a t a a c a a g t a t t g a g a g t t t t a a a a t t t c t c c c a g a a g a t a a a c t a a c a a g g a	7380
t g g a a g g g g a g g g c a a a g g a t a t c t a a c a t g a g a a t a a g g a c a t g t t a g a g g g g g g g a a	7440
a c a g t t g t a a c a a t a a g g a a a g a g a a g a g c a a c a g t g g a a g a g a c a g g t t g t g t g c c c c t	7500
a a a g a t t c t g c a c c c c c a g t t t g g a a a c a c t g a t a c a t t t t a g g a c a c a g a g c a c t c c t a	7560
g a t c t c t a c g a a a t t t t a g a a t g a a t a a t g t g t a a t t t a t a g g a t c a g a a c g t a t g g t t a	7620
t t a a a a c t t g g a t c a a g a t a t g c c c g g t g t a t a c a t t c t t a g c a c a t a g g a a t g g c a c t g	7680
c c a t a c t g g a g a a g g t c a g c a g t a a a t a g g c a t t c t g t a c a t a a g c c t c a t g g a a g g g t a	7740

N3027PCT\_sequ.list.txt

```

agatggagag actggcagaa gt agcacct a ct ct gct ggg agcact t ct c t gagt acgct 7800
t t agt t caat t caaat cact gt at t c t t t c cccat t gct a acct aat at a t gaaacaagc 7860
t t agct gt ct cagaagt t t t t caagagat g at caggaaaa att aat gcac att caaaagg 7920
agaat ct t ca gt acaaatt t gt t t t t t t aa aaat agat t t agggct gggc gcggt ggct c 7980
acgcct gt aa t cccagcact t t gggaggcc gaggcgggt g gat cagcagg t caagact t c 8040
gagaccagcc t ggccaacat ggt gaaaccc t gt ct ct act aaaaat acaa aacat t agcc 8100
aggcgt ggt a gt ggg t gcct gt aat ccct g ct act t ggga ggct gaggca ggagaat cac 8160
t t gaacgcgg gaggcagagg t t gcaggag ccgagat ggc gccat t gcac t ccat cct gg 8220
gcaacaagag cgaaat t cca t ct caaaaaa t aaaat agat t t agggggt a caagt gcagt 8280
t t t gt t acat ggg t at at t g cat agt ggt a aaat gt gggc t t t t agt gt a cct aacaccc 8340
agagaagcat acat t gt gcc cagt aggt aa t t t t t cat cc ct aaacct t t t ct cagcct c 8400
ccact t t ct g gagt ct ccaa t gt cgg t t at t ccact ct t t at gt ccat at ct acacat t c 8460
aat cct aat t t gt accaagt agcat ct cac ct t t aaat ca caggct t at t agt t ggg t gt 8520
t t t ct t t t t a ct t at gaaaa t t cat ct agt caaact gt ca att aat t t t t cct cat t t ca 8580
t t aaaagt gt at at ct aat g ct t t ct ct aa aaat t gat gt act ggaaat a caaat aaat a 8640
aat gct ccct gt gt agaat t t c 8662

```

<210> 40  
 <211> 1285  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1285)  
 <223> myosin VI MYO6  
 <400> 40

Met Glu Asp Gly Lys Pro Val Trp Ala Pro His Pro Thr Asp Gly Phe  
1 5 10 15

Gln Met Gly Asn Ile Val Asp Ile Gly Pro Asp Ser Leu Thr Ile Glu  
20 25 30

Pro Leu Asn Gln Lys Gly Lys Thr Phe Leu Ala Leu Ile Asn Gln Val  
35 40 45

Phe Pro Ala Glu Glu Asp Ser Lys Lys Asp Val Glu Asp Asn Oys Ser  
50 55 60

Leu Met Tyr Leu Asn Glu Ala Thr Leu Leu His Asn Ile Lys Val Arg  
65 70 75 80

Tyr Ser Lys Asp Arg Ile Tyr Thr Tyr Val Ala Asn Ile Leu Ile Ala  
85 90 95

N3027PCT\_sequ.list.txt

Val Asn Pro Tyr Phe Asp Ile Pro Lys Ile Tyr Ser Ser Glu Ala Ile  
100 105 110

Lys Ser Tyr Gln Gly Lys Ser Leu Gly Thr Arg Pro Pro His Val Phe  
115 120 125

Ala Ile Ala Asp Lys Ala Phe Arg Asp Met Lys Val Leu Lys Met Ser  
130 135 140

Gln Ser Ile Ile Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn  
145 150 155 160

Thr Lys Phe Val Leu Arg Tyr Leu Thr Glu Ser Tyr Gly Thr Gly Gln  
165 170 175

Asp Ile Asp Asp Arg Ile Val Glu Ala Asn Pro Leu Leu Glu Ala Phe  
180 185 190

Gly Asn Ala Lys Thr Val Arg Asn Asn Asn Ser Ser Arg Phe Gly Lys  
195 200 205

Phe Val Glu Ile His Phe Asn Glu Lys Ser Ser Val Val Gly Gly Phe  
210 215 220

Val Ser His Tyr Leu Leu Glu Lys Ser Arg Ile Cys Val Gln Gly Lys  
225 230 235 240

Glu Glu Arg Asn Tyr His Ile Phe Tyr Arg Leu Cys Ala Gly Ala Ser  
245 250 255

Glu Asp Ile Arg Glu Lys Leu His Leu Ser Ser Pro Asp Asn Phe Arg  
260 265 270

Tyr Leu Asn Arg Gly Cys Thr Arg Tyr Phe Ala Asn Lys Glu Thr Asp  
275 280 285

Lys Gln Ile Leu Gln Asn Arg Lys Ser Pro Glu Tyr Leu Lys Ala Gly  
290 295 300

Ser Met Lys Asp Pro Leu Leu Asp Asp His Gly Asp Phe Ile Arg Met  
305 310 315 320

Cys Thr Ala Met Lys Lys Ile Gly Leu Asp Asp Glu Glu Lys Leu Asp  
325 330 335

Leu Phe Arg Val Val Ala Gly Val Leu His Leu Gly Asn Ile Asp Phe  
340 345 350

Glu Glu Ala Gly Ser Thr Ser Gly Gly Cys Asn Leu Lys Asn Lys Ser  
355 360 365

N3027PCT\_sequ.list.txt

Ala Gln Ser Leu Glu Tyr Cys Ala Glu Leu Leu Gly Leu Asp Gln Asp  
370 375 380

Asp Leu Arg Val Ser Leu Thr Thr Arg Val Met Leu Thr Thr Ala Gly  
385 390 395 400

Gly Thr Lys Gly Thr Val Ile Lys Val Pro Leu Lys Val Glu Gln Ala  
405 410 415

Asn Asn Ala Arg Asp Ala Leu Ala Lys Thr Val Tyr Ser His Leu Phe  
420 425 430

Asp His Val Val Asn Arg Val Asn Gln Cys Phe Pro Phe Glu Thr Ser  
435 440 445

Ser Tyr Phe Ile Gly Val Leu Asp Ile Ala Gly Phe Glu Tyr Phe Glu  
450 455 460

His Asn Ser Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu  
465 470 475 480

Gln Gln Phe Phe Asn Glu Arg Ile Leu Lys Glu Glu Gln Glu Leu Tyr  
485 490 495

Gln Lys Glu Gly Leu Gly Val Asn Glu Val His Tyr Val Asp Asn Gln  
500 505 510

Asp Cys Ile Asp Leu Ile Glu Ala Lys Leu Val Gly Ile Leu Asp Ile  
515 520 525

Leu Asp Glu Glu Asn Arg Leu Pro Gln Pro Ser Asp Gln His Phe Thr  
530 535 540

Ser Ala Val His Gln Lys His Lys Asp His Phe Arg Leu Thr Ile Pro  
545 550 555 560

Arg Lys Ser Lys Leu Ala Val His Arg Asn Ile Arg Asp Asp Glu Gly  
565 570 575

Phe Ile Ile Arg His Phe Ala Gly Ala Val Cys Tyr Glu Thr Thr Gln  
580 585 590

Phe Val Glu Lys Asn Asn Asp Ala Leu His Met Ser Leu Glu Ser Leu  
595 600 605

Ile Cys Glu Ser Arg Asp Lys Phe Ile Arg Glu Leu Phe Glu Ser Ser  
610 615 620

Thr Asn Asn Asn Lys Asp Thr Lys Gln Lys Ala Gly Lys Leu Ser Phe  
625 630 635 640

N3027PCT\_sequ.list.txt

I l e S e r V a l G l y A s n L y s P h e L y s T h r G l n L e u A s n L e u L e u L e u A s p  
645 650 655

L y s L e u A r g S e r T h r G l y A l a S e r P h e I l e A r g C y s I l e L y s P r o A s n  
660 665 670

L e u L y s M e t T h r S e r H i s H i s P h e G l u G l y A l a G l n I l e L e u S e r G l n  
675 680 685

L e u G l n C y s S e r G l y M e t V a l S e r V a l L e u A s p L e u M e t G l n G l y G l y  
690 700

T y r P r o S e r A r g A l a S e r P h e H i s G l u L e u T y r A s n M e t T y r L y s L y s  
705 710 715 720

T y r M e t P r o A s p L y s L e u A l a A r g L e u A s p P r o A r g L e u P h e C y s L y s  
725 730 735

A l a L e u P h e L y s A l a L e u G l y L e u A s n G l u A s n A s p T y r L y s P h e G l y  
740 745

L e u T h r L y s V a l P h e P h e A r g P r o G l y L y s P h e A l a G l u P h e A s p G l n  
755 760 765

I l e M e t L y s S e r A s p P r o A s p H i s L e u A l a G l u L e u V a l L y s A r g V a l  
770 775 780

A s n H i s T r p L e u T h r C y s S e r A r g T r p L y s L y s V a l G l n T r p C y s S e r  
785 790 800

L e u S e r V a l I l e L y s L e u L y s A s n L y s I l e L y s T y r A r g A l a G l u A l a  
805 810 815

C y s I l e L y s M e t G l n L y s T h r I l e A r g M e t T r p L e u C y s L y s A r g A r g  
820 825 830

H i s L y s P r o A r g I l e A s p G l y L e u V a l L y s V a l G l y T h r L e u L y s L y s  
835 840 845

A r g L e u A s p L y s P h e A s n G l u V a l V a l S e r V a l L e u L y s A s p G l y L y s  
850 855 860

P r o G l u M e t A s n L y s G l n I l e L y s A s n L e u G l u I l e S e r I l e A s p T h r  
865 870 875 880

L e u M e t A l a L y s I l e L y s S e r T h r M e t M e t T h r G l n G l u G l n I l e G l n  
885 890 895

L y s G l u T y r A s p A l a L e u V a l L y s S e r S e r G l u G l u L e u L e u S e r A l a  
900 905 910

L e u G l n L y s L y s L y s G l n G l n G l u G l u G l u A l a G l u A r g L e u A r g A r g  
Page 169

915

I l e G n G u G u M e t G u L y s G u A r g L y s A r g A r g G u G u A s p G u  
930 935 940

L y s A r g A r g A r g L y s G u G u G u G u A r g A r g M e t L y s L e u G u M e t  
945 950 955 960

G u A l a L y s A r g L y s G n G u G u G u G u A r g L y s L y s A r g G u A s p  
965 970 975

A s p G u L y s A r g I l e G n A l a G u V a l G u A l a G n L e u A l a A r g G n  
980 985 990

L y s G u G u G u S e r G n G n G n A l a V a l L e u G u G n G u A r g A r g  
995 1000 1005

A s p A r g G u L e u A l a L e u A r g I l e A l a G n S e r G u A l a G u L e u  
1010 1015 1020

I l e S e r A s p G u A l a G n A l a A s p L e u A l a L e u A r g A r g A s n A s p  
1025 1030 1035

G y T h r A r g P r o L y s M e t T h r P r o G u G n M e t A l a L y s G u M e t  
1040 1045 1050

S e r G u P h e L e u S e r A r g G y P r o A l a V a l L e u A l a T h r L y s A l a  
1055 1060 1065

A l a A l a G y T h r L y s L y s T y r A s p L e u S e r L y s T r p L y s T y r A l a  
1070 1075 1080

G u L e u A r g A s p T h r I l e A s n T h r S e r C y s A s p I l e G u L e u L e u  
1085 1090 1095

A l a A l a C y s A r g G u G u P h e H i s A r g A r g L e u L y s V a l T y r H i s  
1100 1105 1110

A l a T r p L y s S e r L y s A s n L y s L y s A r g A s n T h r G u T h r G u G n  
1115 1120 1125

A r g A l a P r o L y s S e r V a l T h r A s p T y r A s p P h e A l a P r o P h e L e u  
1130 1135 1140

A s n A s n S e r P r o G n G n A s n P r o A l a A l a G n I l e P r o A l a A r g  
1145 1150 1155

G n A r g G u I l e G u M e t A s n A r g G n G n A r g P h e P h e A r g I l e  
1160 1165 1170

P r o P h e I l e A r g P r o A l a A s p G n T y r L y s A s p P r o G n S e r L y s  
1175 1180 1185

# N3027PCT\_sequ.list.txt

Lys Lys Gly Trp Trp Tyr Ala His Phe Asp Gly Pro Trp Ile Ala  
1190 1195 1200

Arg Gln Met Glu Leu His Pro Asp Lys Pro Pro Ile Leu Leu Val  
1205 1210 1215

Ala Gly Lys Asp Asp Met Glu Met Cys Glu Leu Asn Leu Glu Glu  
1220 1225 1230

Thr Gly Leu Thr Arg Lys Arg Gly Ala Glu Ile Leu Pro Arg Gln  
1235 1240 1245

Phe Glu Glu Ile Trp Glu Arg Cys Gly Gly Ile Gln Tyr Leu Gln  
1250 1255 1260

Asn Ala Ile Glu Ser Arg Gln Ala Arg Pro Thr Tyr Ala Thr Ala  
1265 1270 1275

Met Leu Gln Ser Leu Leu Lys  
1280 1285

<210> 41  
<211> 7367  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(7367)  
<223> myosin VIIA MYO7A

<400> 41  
ggcaggagag agagggagag acaagagaca cacacagaga gacggcgagg aagggaaaga 60  
cccagagggga cgcctagaac gagacttggg gccagacaga ggaagagggg acgtgtgttt 120  
gcagactggc tgggcccgtg acccagcttc ctgagtcctc cgtgcaggtg gcagctgtac 180  
caggctggca ggtcactgag agtgggcagc tgggccccag aactgtgcct ggcccagtgg 240  
gcagcaggag ctctgactt gggaccatgg tgatcttca gcagggggac catgtgtgga 300  
tggacctgag attggggcag gagttcgacg tggccatcgg ggcgggtggtg aagctctgcg 360  
actctgggca ggtccagggtg gtggatgatg aagacaatga aactggatc tctccgcaga 420  
acgcaacgca catcaagcct atgcaccca cgtcgggtcca cggcgtggag gacatgatcc 480  
gcctggggga cctcaacgag gcgggcatct tgcgcaacct gcttatccgc taccgggacc 540  
acctcatcta cacgtatcgg ggctccatcc tgggtggctgt gaaccctac cagctgctct 600  
ccatctactc gccagagcac atccgccagt ataccaaca gaagattggg gagatgcccc 660  
cccacatctt tgccattgct gacaactgct acttcaacat gaaacgcaac agccgagacc 720  
agtgtgcat catcagtggt gaatctgggg ccgggaagac ggagagcaca aagctgatcc 780  
tgcagttcct ggcagccatc agtgggcagc actcgtggat tgagcagcag gtcttggagg 840

N3027PCT\_sequ. list . . txt

ccacccccat	tctggaagca	tttgggaatg	ccaagaccat	ccgcaatgac	aactcaagcc	900
gtttcgga	gtacatcgac	atccacttca	acaagcgggg	cgccatcgag	ggcgcggaaga	960
ttgagcagta	cctgctggaa	aagtacagt	gtctgtcgcca	ggccctggat	gaaaggaact	1020
accacgtgtt	ctactgcatg	ctggagggtg	tgagttagga	tcagaagaag	aagctgggct	1080
tgggccaggc	ctctgactac	aactacttgg	ccatgggtaa	ctgcataac	tgtgagggcc	1140
gggtggacag	ccaggagtac	gccaacatcc	gctcggccat	gaagggtgctc	atgttcactg	1200
acaccgagaa	ctgggagatc	tgaagctcc	tggctgccat	cctgcacctg	ggcaacctgc	1260
agtatgaggc	acgcacattt	gaaaacctgg	atgcctgtga	gggttctcttc	tccccatcgc	1320
tggccacagc	tgcattcctg	cttgagggtga	acccccaga	cctgatgagc	tgcctgacta	1380
gccgcaccct	catcacccgc	ggggagacgg	tgtccacccc	actgagcagg	gaacaggcac	1440
tggacgtgcg	cgacgccttc	gtaaagggga	tctacgggcg	gctgttcgtg	tggattgtgg	1500
acaagatcaa	cgcagcaatt	tacaagcctc	cctcccagga	tgtgaagaac	tctcgcaggt	1560
ccatcggcct	cctggacatc	tttgggtttg	agaactttgc	tgtgaacagc	tttgagcagc	1620
tctgcatcaa	cttcgccaat	gagcacctgc	agcagttctt	tgtgcggcac	gtgttcaagc	1680
tggagcagga	ggaatagac	ctggagagca	ttgactggct	gcacatcgag	ttcactgaca	1740
accaggatgc	cctggacatg	attgccaaca	agcccatgaa	catcatctcc	ctcatcgatg	1800
aggagagcaa	gttcccgaag	ggcacagaca	ccaccatgtt	acacaagctg	aactcccagc	1860
acaagctcaa	cgccaactac	atcccccca	agaacaacca	tgagaccag	tttggcatca	1920
accattttgc	aggcatcgtc	tactatgaga	cccaaggctt	cctggagaag	aaccgagaca	1980
ccctgcatgg	ggacattatc	cagctgggtcc	actcctccag	gaacaagttc	atcaagcaga	2040
tcttccaggc	cgatgtcgcc	atggcgccg	agaccaggaa	gcgctcgccc	acacttagca	2100
gccagttcaa	gcggtcactg	gagctgctga	tgcgcacgct	gggtgcctgc	cagcccttct	2160
ttgtgcgatg	catcaagccc	aatgagttca	agaagcccat	gctgttcgac	cggcacctgt	2220
gcgtgcgcca	gctgcggtac	tcaggaatga	tggagaccat	ccgaatccgc	cgagctggct	2280
accccatccg	ctacagcttc	gtagagtttg	tggagcggta	ccgtgtgctg	ctgccaggtg	2340
tgaagccggc	ctacaagcag	ggcgacctcc	gcgggacttg	ccagcgcatg	gctgaggctg	2400
tgctgggcac	ccacgatgac	tggcagatag	gcaaaaccaa	gatctttctg	aaggaccacc	2460
atgacatgct	gctggaagtg	gagcgggaca	aagccatcac	cgacagagtc	atcctccttc	2520
agaaagtcat	ccggggattc	aaagacaggt	ctaactttct	gaagctgaag	aacgctgcca	2580
cactgatcca	gaggcactgg	cggggtcaca	actgtaggaa	gaactacggg	ctgatgcgtc	2640
tgggcttcct	gcggctgcag	gccctgcacc	gctcccggaa	gctgcaccag	cagtaccgcc	2700
tggcccggcca	gcgcatcatc	cagttccagg	cccgtgccg	cgcctatctg	gtgcgcaagg	2760
ccttccggcca	ccgcctctgg	gctgtgctca	ccgtgcaggc	ctatgcccg	ggcatgatcg	2820
cccgcaggct	gcaccaacgc	ctcagggtg	agtatctgtg	gcgcctcgag	gctgagaaaa	2880

N3027PCT\_sequ. list . txt

t gcggt ggc	ggaggaagag	aagct t cgga	aggagat gag	cgccaagaag	gccaaggagg	2940
aggccgagcg	caagcat cag	gagcgcct gg	cccagct ggc	t cgt gaggac	gct gagcggg	3000
agct gaagga	gaaggaggcc	gct cggcgga	agaaggagct	cct ggagcag	at ggaaaggg	3060
cccgccat ga	gcct gt caat	cact cagaca	t ggt ggacaa	gat gt t t ggc	t t cct gggga	3120
ct t caggt gg	cct gccaggc	caggaggggc	aggcacct ag	t ggct t t gag	gacct ggagc	3180
gagggcggag	ggagat ggt g	gaggaggacc	t ggat gcagc	cct gcccct g	cct gacgagg	3240
at gaggagga	cct ct ct gag	t at aaat t t g	ccaagt t cgc	ggccacct ac	t t ccaggggga	3300
caaccacgca	ct cct acacc	cggcgggccac	t caaacagcc	act gct ct ac	cat gacgacg	3360
agggt gacca	gct ggcagcc	ct ggcggt ct	ggat caccat	cct ccgct t c	at gggggacc	3420
t ccct gagcc	caagt accac	acagccat ga	gt gat ggcag	t gagaagat c	cct gt gat ga	3480
ccaagat t t a	t gagaccct g	ggcaagaaga	cgt acaagag	ggagct gcag	gccct gcagg	3540
gcgagggcga	ggcccagct c	cccgagggcc	agaagaagag	cagt gt gagg	cacaagct gg	3600
t gcat t t gac	t ct gaaaaag	aagt ccaagc	t cacagagga	ggg gaccaag	aggct gcat g	3660
acggggagtc	cacagt gcag	ggcaacagca	t gct ggagga	ccggcccacc	t ccaacct gg	3720
agaagct gca	ct t cat cat c	ggcaat ggca	t cct gcggcc	agcact ccgg	gacgagat ct	3780
act gccagat	cagcaagcag	ct gaccaca	accct ccaa	gagcagct at	gcccggggct	3840
ggat t ct cgt	gt ct ct ct gc	gt gggct gt t	t cgccccct c	cgagaagt t t	gt caagt acc	3900
t gcggaact t	cat ccacggg	ggcccgcccg	gct acgcccc	gt act gt gag	gagcgcct ga	3960
gaaggacct t	t gt caat ggg	acacggacac	agccgcccag	ct ggct ggag	ct gcaggcca	4020
ccaagt ccaa	gaagccaat c	at gt t gcccg	t gacat t cat	ggat gggacc	accaagaccc	4080
t gct gacgga	ct cggcaacc	acggccaagg	agct ct gcaa	cgcgct ggcc	gacaagat ct	4140
ct ct caagga	ccggt t cggg	t t ct ccct ct	acat t gccct	gt t t gacaag	gt gt cct ccc	4200
t gggcagcgg	cagt gaccac	gt cat ggacg	ccat ct ccca	gt gcgagcag	t acgccaagg	4260
agcagggcgc	ccaggagcgc	aacgccccct	ggaggct ct t	ct t ccgcaaa	gaggt ct t ca	4320
cgccct ggca	cagccccct cc	gaggacaacg	t ggccaccaa	cct cat ct ac	cagcaggt gg	4380
t gcgaggagt	caagt t t ggg	gagt acaggt	gt gagaagga	ggacgacct g	gct gagct gg	4440
cct cccagca	gt act t t gt a	gact at ggct	ct gagat gat	cct ggagcgc	ct cct gaacc	4500
t cgt gcccac	ct acat cccc	gaccgcgaga	t cacgccccct	gaagacgct g	gagaagt ggg	4560
cccagct ggc	cat cgccgcc	cacaagaagg	ggat t t at gc	ccagaggaga	act gat gccc	4620
agaaggt caa	agaggat gt g	gt cagt t at g	cccgct t caa	gt ggccct t g	ct ct t ct cca	4680
ggg t t t at ga	agcct acaaa	t t ct caggcc	ccagt ct ccc	caagaacgac	gt cat cgt gg	4740
ccgt caact g	gacgggt gt g	t act t t gt gg	at gagcagga	gcaggt act t	ct ggagct gt	4800
cct t cccaga	gat cat ggcc	gt gt ccagca	gcagggggagc	gaaaacgacg	gccccagct	4860
t cacgct ggc	cacat caag	ggggacgaat	acacct t cac	ct ccagcaat	gct gaggaca	4920
t t cgt gacct	ggg ggt cacc	t t cct agagg	ggct ccggaa	gagat ct aag	t at gt t gt gg	4980

N3027PCT\_sequ. list . . txt

ccctgcagga	t aaccccaac	cccgcaggcg	aggagt cagg	ct t cct cagc	t t t gccaaagg	5040
gagacct cat	cat cct ggac	cat gacacgg	gcgagcaggt	cat gaact cg	ggct gggcca	5100
acggcat caa	t gagaggacc	aagcagcgt g	gggact t ccc	caccgacagt	gt gt acgt ca	5160
t gcccact gt	cacat gcc	ccgcgggaga	t t gt ggccct	ggc caccat g	act cccgat c	5220
agaggcagga	cgt t gt ccgg	ct ct t gcagc	t gcgaacggc	ggagcccag	gt gcgt gcc	5280
agccct acac	gct ggaggag	t t t t cct at g	act act t cag	gccccaccc	aagcacacgc	5340
t gagccgt gt	cat ggt gt cc	aaggcccgag	gcaaggaccg	gct gt ggagc	cacacgcggg	5400
aaccgct caa	gcaggcgct g	ct caagaagc	t cct gggcag	t gaggagct c	t cgcaggagg	5460
cct gcct ggc	ct t cat t gct	gt gct caagt	acat gggcga	ct acccgt cc	aagaggacac	5520
gct ccgt caa	cgagct cacc	gaccagat ct	t t gagggt cc	cct gaaagcc	gagcccct ga	5580
aggacgaggc	at at gt gcag	at cct gaagc	agct gaccga	caaccacat c	aggt acagcg	5640
aggagcgggg	t t gggagct g	ct ct ggct gt	gcacgggcct	t t t cccaccc	agcaacat cc	5700
t cct gcccc	cgt gcagcgc	t t cct gcagt	ccgaaagca	ct gcccact c	gccat cgact	5760
gcct gcaacg	gct ccagaaa	gccct gagaa	acgggt cccg	gaagt accct	ccgcacct gg	5820
t ggaggt gga	ggccat ccag	cacaagacca	cccagat t t t	ccacaaagt c	t act t ccct g	5880
at gacact ga	cgaggcct t c	gaagt ggagt	ccagcaccaa	ggccaaggac	t t ct gccaga	5940
acat cgccac	caggct gct c	ct caagt cct	cagagggat t	cagcct ct t t	gt caaaat t g	6000
cagacaaggt	cct cagcgt t	cct gagaat g	act t ct t ct t	t gact t t gt t	cgacact t ga	6060
cagact ggat	aaagaaagct	cggcccat ca	aggacggaat	t gt gccct ca	ct cacct acc	6120
aggt gt t ct t	cat gaagaag	ct gt ggacca	ccacggt gcc	agggaaggat	cccat ggccg	6180
at t ccat ct t	ccact at t ac	caggagt t gc	ccaagt at ct	ccgaggct ac	cacaagt gca	6240
cgcgggagga	ggc gct gcag	ct gggggcgc	t gat ct acag	ggc caagt t c	gaggaggaca	6300
agt cct act t	ccccagcat c	cccaagct gc	t gcgggagct	ggc gcccag	gacct t at cc	6360
ggcaggt ct c	acct gat gac	t ggaagcggc	ccat cgt cgc	ct act t caac	aagcacgcag	6420
ggaagt ccaa	ggaggaggcc	aagct ggcct	t cct gaagct	cat ct t caag	t ggcccacct	6480
t t ggct cagc	ct t ct t cgag	caaact acgg	agccaaact t	ccct gagat c	ct cct aat t g	6540
ccat caacaa	gt at ggggt c	agcct cat cg	at cccaaaac	gaaggat at c	ct caccact c	6600
at ccct t cac	caagat ct cc	aact ggagca	gcggcaacac	ct act t ccac	at caccat t g	6660
ggaact t ggt	gcgcgggagc	aaact gct ct	gcgagacgt c	act gggct ac	aagat ggat g	6720
acct cct gac	t t cct acat t	agccagat gc	t cacagccat	gagcaaacag	cggggct cca	6780
ggagcggcaa	gt gaacagt c	acggggaggt	gct ggt t cca	t gcct gct ct	cgaggcagca	6840
gt ggg t cag	gcccacagc	t acccct gca	gct ggggaag	act t at gcc	t cccggcagc	6900
gaggct gggc	t ggccagcca	ccact gact a	t accaact gg	gcct ct gat g	t t ct t ccagt	6960
gaggcat ct c	t ct gggat gc	agaact t ccc	t ccat ccacc	cct ct ggcac	ct ggg t ggt	7020

N3027PCT\_sequ.list.txt

```

ctaatcctag tttgctgtgg ccttcccggg tgtgagagcc tgtgatcctt agatgtgtct 7080
cctgtttcag accagcccca ccatgcaact tcccttgact ttctgtgtac cactgggat a 7140
gaggaatcaa gaggacaatc tagctctcca tactttgaac aaccaaagt gcattgaat a 7200
ctctgaaacc gaagggactg gatctgcagg tgggatgagg gagacagacc acttttctat 7260
attgcagtgt gaatgctggg cccctgctca agtctaccct gatcacctca gggcat aaag 7320
catgtttcat tctctggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 7367

```

<210> 42  
 <211> 2175  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(2175)  
 <223> myosin VIIA MYO7A

<400> 42

Met Val Ile Leu Gln Gln Gly Asp His Val Trp Met Asp Leu Arg Leu  
1 5 10 15

Gly Gln Glu Phe Asp Val Pro Ile Gly Ala Val Val Lys Leu Cys Asp  
20 25 30

Ser Gly Gln Val Gln Val Val Asp Asp Glu Asp Asn Glu His Trp Ile  
35 40 45

Ser Pro Gln Asn Ala Thr His Ile Lys Pro Met His Pro Thr Ser Val  
50 55 60

His Gly Val Glu Asp Met Ile Arg Leu Gly Asp Leu Asn Glu Ala Gly  
65 70 75 80

Ile Leu Arg Asn Leu Leu Ile Arg Tyr Arg Asp His Leu Ile Tyr Thr  
85 90 95

Tyr Thr Gly Ser Ile Leu Val Ala Val Asn Pro Tyr Gln Leu Leu Ser  
100 105 110

Ile Tyr Ser Pro Glu His Ile Arg Gln Tyr Thr Asn Lys Lys Ile Gly  
115 120 125

Glu Met Pro Pro His Ile Phe Ala Ile Ala Asp Asn Cys Tyr Phe Asn  
130 135 140

Met Lys Arg Asn Ser Arg Asp Gln Cys Cys Ile Ile Ser Gly Glu Ser  
145 150 155 160

Gly Ala Gly Lys Thr Glu Ser Thr Lys Leu Ile Leu Gln Phe Leu Ala  
165 170 175

N3027PCT\_sequ.list.txt

Ala Ile Ser Gly Gln His Ser Trp Ile Glu Gln Gln Val Leu Glu Ala  
180 185 190

Thr Pro Ile Leu Glu Ala Phe Gly Asn Ala Lys Thr Ile Arg Asn Asp  
195 200 205

Asn Ser Ser Arg Phe Gly Lys Tyr Ile Asp Ile His Phe Asn Lys Arg  
210 215 220

Gly Ala Ile Glu Gly Ala Lys Ile Glu Gln Tyr Leu Leu Glu Lys Ser  
225 230 235 240

Arg Val Cys Arg Gln Ala Leu Asp Glu Arg Asn Tyr His Val Phe Tyr  
245 250 255

Cys Met Leu Glu Gly Met Ser Glu Asp Gln Lys Lys Lys Leu Gly Leu  
260 265 270

Gly Gln Ala Ser Asp Tyr Asn Tyr Leu Ala Met Gly Asn Cys Ile Thr  
275 280 285

Cys Glu Gly Arg Val Asp Ser Gln Glu Tyr Ala Asn Ile Arg Ser Ala  
290 295 300

Met Lys Val Leu Met Phe Thr Asp Thr Glu Asn Trp Glu Ile Ser Lys  
305 310 315 320

Leu Leu Ala Ala Ile Leu His Leu Gly Asn Leu Gln Tyr Glu Ala Arg  
325 330 335

Thr Phe Glu Asn Leu Asp Ala Cys Glu Val Leu Phe Ser Pro Ser Leu  
340 345 350

Ala Thr Ala Ala Ser Leu Leu Glu Val Asn Pro Pro Asp Leu Met Ser  
355 360 365

Cys Leu Thr Ser Arg Thr Leu Ile Thr Arg Gly Glu Thr Val Ser Thr  
370 375 380

Pro Leu Ser Arg Glu Gln Ala Leu Asp Val Arg Asp Ala Phe Val Lys  
385 390 395 400

Gly Ile Tyr Gly Arg Leu Phe Val Trp Ile Val Asp Lys Ile Asn Ala  
405 410 415

Ala Ile Tyr Lys Pro Pro Ser Gln Asp Val Lys Asn Ser Arg Arg Ser  
420 425 430

Ile Gly Leu Leu Asp Ile Phe Gly Phe Glu Asn Phe Ala Val Asn Ser  
435 440 445

N3027PCT\_sequ.list.txt

Phe Glu Gln Leu Cys Ile Asn Phe Ala Asn Glu His Leu Gln Gln Phe  
450 455 460

Phe Val Arg His Val Phe Lys Leu Glu Gln Glu Glu Tyr Asp Leu Glu  
465 470 475 480

Ser Ile Asp Trp Leu His Ile Glu Phe Thr Asp Asn Gln Asp Ala Leu  
485 490 495

Asp Met Ile Ala Asn Lys Pro Met Asn Ile Ile Ser Leu Ile Asp Glu  
500 505 510

Glu Ser Lys Phe Pro Lys Gly Thr Asp Thr Thr Met Leu His Lys Leu  
515 520 525

Asn Ser Gln His Lys Leu Asn Ala Asn Tyr Ile Pro Pro Lys Asn Asn  
530 535 540

His Glu Thr Gln Phe Gly Ile Asn His Phe Ala Gly Ile Val Tyr Tyr  
545 550 555 560

Glu Thr Gln Gly Phe Leu Glu Lys Asn Arg Asp Thr Leu His Gly Asp  
565 570 575

Ile Ile Gln Leu Val His Ser Ser Arg Asn Lys Phe Ile Lys Gln Ile  
580 585 590

Phe Gln Ala Asp Val Ala Met Gly Ala Glu Thr Arg Lys Arg Ser Pro  
595 600 605

Thr Leu Ser Ser Gln Phe Lys Arg Ser Leu Glu Leu Leu Met Arg Thr  
610 615 620

Leu Gly Ala Cys Gln Pro Phe Phe Val Arg Cys Ile Lys Pro Asn Glu  
625 630 635 640

Phe Lys Lys Pro Met Leu Phe Asp Arg His Leu Cys Val Arg Gln Leu  
645 650 655

Arg Tyr Ser Gly Met Met Glu Thr Ile Arg Ile Arg Arg Ala Gly Tyr  
660 665 670

Pro Ile Arg Tyr Ser Phe Val Glu Phe Val Glu Arg Tyr Arg Val Leu  
675 680 685

Leu Pro Gly Val Lys Pro Ala Tyr Lys Gln Gly Asp Leu Arg Gly Thr  
690 695 700

Cys Gln Arg Met Ala Glu Ala Val Leu Gly Thr His Asp Asp Trp Gln  
705 710 715 720

Ile Gly Lys Thr Lys Ile Phe Leu Lys Asp His His Asp Met Leu Leu  
Page 177

725

730

735

G u Val G u Arg Asp Lys A l a I l e Thr Asp Arg Val I l e Leu Leu G n  
 740 745 750  
 Lys Val I l e Arg G y Phe Lys Asp Arg Ser Asn Phe Leu Lys Leu Lys  
 755 760 765  
 Asn A l a A l a Thr Leu I l e G n Arg H i s Trp Arg G y H i s Asn Cys Arg  
 770 775 780  
 Lys Asn Tyr G y Leu Met Arg Leu G y Phe Leu Arg Leu G n A l a Leu  
 785 790 795 800  
 H i s Arg Ser Arg Lys Leu H i s G n G n Tyr Arg Leu A l a Arg G n Arg  
 805 810 815  
 I l e I l e G n Phe G n A l a Arg Cys Arg A l a Tyr Leu Val Arg Lys A l a  
 820 825 830  
 Phe Arg H i s Arg Leu Trp A l a Val Leu Thr Val G n A l a Tyr A l a Arg  
 835 840 845  
 G y Met I l e A l a Arg Arg Leu H i s G n Arg Leu Arg A l a G u Tyr Leu  
 850 855 860  
 Trp Arg Leu G u A l a G u Lys Met Arg Leu A l a G u G u G u Lys Leu  
 865 870 875 880  
 Arg Lys G u Met Ser A l a Lys Lys A l a Lys G u G u A l a G u Arg Lys  
 885 890 895  
 H i s G n G u Arg Leu A l a G n Leu A l a Arg G u Asp A l a G u Arg G u  
 900 905 910  
 Leu Lys G u Lys G u A l a A l a Arg Arg Lys Lys G u Leu Leu G u G n  
 915 920 925  
 Met G u Arg A l a Arg H i s G u Pro Val Asn H i s Ser Asp Met Val Asp  
 930 935 940  
 Lys Met Phe G y Phe Leu G y Thr Ser G y G y Leu Pro G y G n G u  
 945 950 955 960  
 G y G n A l a Pro Ser G y Phe G u Asp Leu G u Arg G y Arg Arg G u  
 965 970 975  
 Met Val G u G u Asp Leu Asp A l a A l a Leu Pro Leu Pro Asp G u Asp  
 980 985 990  
 G u G u Asp Leu Ser G u Tyr Lys Phe A l a Lys Phe A l a A l a Thr Tyr  
 995 1000 1005

N3027PCT\_sequ.list.txt

Phe	G n	G y	Thr	Thr	Thr	His	Ser	Tyr	Thr	Arg	Arg	Pro	Leu	Lys
1010						1015					1020			
G n	Pro	Leu	Leu	Tyr	His	Asp	Asp	G u	G y	Asp	G n	Leu	Al a	Al a
1025						1030					1035			
Leu	Al a	Val	Trp	I le	Thr	I le	Leu	Arg	Phe	Met	G y	Asp	Leu	Pro
1040						1045					1050			
G u	Pro	Lys	Tyr	His	Thr	Al a	Met	Ser	Asp	G y	Ser	G u	Lys	I le
1055						1060					1065			
Pro	Val	Met	Thr	Lys	I le	Tyr	G u	Thr	Leu	G y	Lys	Lys	Thr	Tyr
1070						1075					1080			
Lys	Arg	G u	Leu	G n	Al a	Leu	G n	G y	G u	G y	G u	Al a	G n	Leu
1085						1090					1095			
Pro	G u	G y	G n	Lys	Lys	Ser	Ser	Val	Arg	His	Lys	Leu	Val	His
1100						1105					1110			
Leu	Thr	Leu	Lys	Lys	Lys	Ser	Lys	Leu	Thr	G u	G u	Val	Thr	Lys
1115						1120					1125			
Arg	Leu	His	Asp	G y	G u	Ser	Thr	Val	G n	G y	Asn	Ser	Met	Leu
1130						1135					1140			
G u	Asp	Arg	Pro	Thr	Ser	Asn	Leu	G u	Lys	Leu	His	Phe	I le	I le
1145						1150					1155			
G y	Asn	G y	I le	Leu	Arg	Pro	Al a	Leu	Arg	Asp	G u	I le	Tyr	Oys
1160						1165					1170			
G n	I le	Ser	Lys	G n	Leu	Thr	His	Asn	Pro	Ser	Lys	Ser	Ser	Tyr
1175						1180					1185			
Al a	Arg	G y	Trp	I le	Leu	Val	Ser	Leu	Oys	Val	G y	Oys	Phe	Al a
1190						1195					1200			
Pro	Ser	G u	Lys	Phe	Val	Lys	Tyr	Leu	Arg	Asn	Phe	I le	His	G y
1205						1210					1215			
G y	Pro	Pro	G y	Tyr	Al a	Pro	Tyr	Oys	G u	G u	Arg	Leu	Arg	Arg
1220						1225					1230			
Thr	Phe	Val	Asn	G y	Thr	Arg	Thr	G n	Pro	Pro	Ser	Trp	Leu	G u
1235						1240					1245			
Leu	G n	Al a	Thr	Lys	Ser	Lys	Lys	Pro	I le	Met	Leu	Pro	Val	Thr
1250						1255					1260			

N3027PCT\_sequ.list.txt

Phe	Met	Asp	Gly	Thr	Thr	Lys	Thr	Leu	Leu	Thr	Asp	Ser	Ala	Thr
	1265					1270					1275			
Thr	Ala	Lys	Glu	Leu	Cys	Asn	Ala	Leu	Ala	Asp	Lys	Ile	Ser	Leu
	1280					1285					1290			
Lys	Asp	Arg	Phe	Gly	Phe	Ser	Leu	Tyr	Ile	Ala	Leu	Phe	Asp	Lys
	1295					1300					1305			
Val	Ser	Ser	Leu	Gly	Ser	Gly	Ser	Asp	His	Val	Met	Asp	Ala	Ile
	1310					1315					1320			
Ser	Gln	Cys	Glu	Gln	Tyr	Ala	Lys	Glu	Gln	Gly	Ala	Gln	Glu	Arg
	1325					1330					1335			
Asn	Ala	Pro	Trp	Arg	Leu	Phe	Phe	Arg	Lys	Glu	Val	Phe	Thr	Pro
	1340					1345					1350			
Trp	His	Ser	Pro	Ser	Glu	Asp	Asn	Val	Ala	Thr	Asn	Leu	Ile	Tyr
	1355					1360					1365			
Gln	Gln	Val	Val	Arg	Gly	Val	Lys	Phe	Gly	Glu	Tyr	Arg	Cys	Glu
	1370					1375					1380			
Lys	Glu	Asp	Asp	Leu	Ala	Glu	Leu	Ala	Ser	Gln	Gln	Tyr	Phe	Val
	1385					1390					1395			
Asp	Tyr	Gly	Ser	Glu	Met	Ile	Leu	Glu	Arg	Leu	Leu	Asn	Leu	Val
	1400					1405					1410			
Pro	Thr	Tyr	Ile	Pro	Asp	Arg	Glu	Ile	Thr	Pro	Leu	Lys	Thr	Leu
	1415					1420					1425			
Glu	Lys	Trp	Ala	Gln	Leu	Ala	Ile	Ala	Ala	His	Lys	Lys	Gly	Ile
	1430					1435					1440			
Tyr	Ala	Gln	Arg	Arg	Thr	Asp	Ala	Gln	Lys	Val	Lys	Glu	Asp	Val
	1445					1450					1455			
Val	Ser	Tyr	Ala	Arg	Phe	Lys	Trp	Pro	Leu	Leu	Phe	Ser	Arg	Phe
	1460					1465					1470			
Tyr	Glu	Ala	Tyr	Lys	Phe	Ser	Gly	Pro	Ser	Leu	Pro	Lys	Asn	Asp
	1475					1480					1485			
Val	Ile	Val	Ala	Val	Asn	Trp	Thr	Gly	Val	Tyr	Phe	Val	Asp	Glu
	1490					1495					1500			
Gln	Glu	Gln	Val	Leu	Leu	Glu	Leu	Ser	Phe	Pro	Glu	Ile	Met	Ala
	1505					1510					1515			

Val	Ser	Ser	Ser	Arg	Gly	Ala	Lys	Thr	Thr	Ala	Pro	Ser	Phe	Thr
1520						1525					1530			
Leu	Ala	Thr	Ile	Lys	Gly	Asp	Glu	Tyr	Thr	Phe	Thr	Ser	Ser	Asn
1535						1540					1545			
Ala	Glu	Asp	Ile	Arg	Asp	Leu	Val	Val	Thr	Phe	Leu	Glu	Gly	Leu
1550						1555					1560			
Arg	Lys	Arg	Ser	Lys	Tyr	Val	Val	Ala	Leu	Gln	Asp	Asn	Pro	Asn
1565						1570					1575			
Pro	Ala	Gly	Glu	Glu	Ser	Gly	Phe	Leu	Ser	Phe	Ala	Lys	Gly	Asp
1580						1585					1590			
Leu	Ile	Ile	Leu	Asp	His	Asp	Thr	Gly	Glu	Gln	Val	Met	Asn	Ser
1595						1600					1605			
Gly	Trp	Ala	Asn	Gly	Ile	Asn	Glu	Arg	Thr	Lys	Gln	Arg	Gly	Asp
1610						1615					1620			
Phe	Pro	Thr	Asp	Ser	Val	Tyr	Val	Met	Pro	Thr	Val	Thr	Met	Pro
1625						1630					1635			
Pro	Arg	Glu	Ile	Val	Ala	Leu	Val	Thr	Met	Thr	Pro	Asp	Gln	Arg
1640						1645					1650			
Gln	Asp	Val	Val	Arg	Leu	Leu	Gln	Leu	Arg	Thr	Ala	Glu	Pro	Glu
1655						1660					1665			
Val	Arg	Ala	Lys	Pro	Tyr	Thr	Leu	Glu	Glu	Phe	Ser	Tyr	Asp	Tyr
1670						1675					1680			
Phe	Arg	Pro	Pro	Pro	Lys	His	Thr	Leu	Ser	Arg	Val	Met	Val	Ser
1685						1690					1695			
Lys	Ala	Arg	Gly	Lys	Asp	Arg	Leu	Trp	Ser	His	Thr	Arg	Glu	Pro
1700						1705					1710			
Leu	Lys	Gln	Ala	Leu	Leu	Lys	Lys	Leu	Leu	Gly	Ser	Glu	Glu	Leu
1715						1720					1725			
Ser	Gln	Glu	Ala	Cys	Leu	Ala	Phe	Ile	Ala	Val	Leu	Lys	Tyr	Met
1730						1735					1740			
Gly	Asp	Tyr	Pro	Ser	Lys	Arg	Thr	Arg	Ser	Val	Asn	Glu	Leu	Thr
1745						1750					1755			
Asp	Gln	Ile	Phe	Glu	Gly	Pro	Leu	Lys	Ala	Glu	Pro	Leu	Lys	Asp
1760						1765					1770			
Glu	Ala	Tyr	Val	Gln	Ile	Leu	Lys	Gln	Leu	Thr	Asp	Asn	His	Ile

1775						1780										1785
Arg	Tyr	Ser	Glu	Glu	Arg	Gly	Trp	Glu	Leu	Leu	Trp	Leu	Cys	Thr		
1790						1795					1800					
Gly	Leu	Phe	Pro	Pro	Ser	Asn	Ile	Leu	Leu	Pro	His	Val	Gln	Arg		
1805						1810					1815					
Phe	Leu	Gln	Ser	Arg	Lys	His	Cys	Pro	Leu	Ala	Ile	Asp	Cys	Leu		
1820						1825					1830					
Gln	Arg	Leu	Gln	Lys	Ala	Leu	Arg	Asn	Gly	Ser	Arg	Lys	Tyr	Pro		
1835						1840					1845					
Pro	His	Leu	Val	Glu	Val	Glu	Ala	Ile	Gln	His	Lys	Thr	Thr	Gln		
1850						1855					1860					
Ile	Phe	His	Lys	Val	Tyr	Phe	Pro	Asp	Asp	Thr	Asp	Glu	Ala	Phe		
1865						1870					1875					
Glu	Val	Glu	Ser	Ser	Thr	Lys	Ala	Lys	Asp	Phe	Cys	Gln	Asn	Ile		
1880						1885					1890					
Ala	Thr	Arg	Leu	Leu	Leu	Lys	Ser	Ser	Glu	Gly	Phe	Ser	Leu	Phe		
1895						1900					1905					
Val	Lys	Ile	Ala	Asp	Lys	Val	Leu	Ser	Val	Pro	Glu	Asn	Asp	Phe		
1910						1915					1920					
Phe	Phe	Asp	Phe	Val	Arg	His	Leu	Thr	Asp	Trp	Ile	Lys	Lys	Ala		
1925						1930					1935					
Arg	Pro	Ile	Lys	Asp	Gly	Ile	Val	Pro	Ser	Leu	Thr	Tyr	Gln	Val		
1940						1945					1950					
Phe	Phe	Met	Lys	Lys	Leu	Trp	Thr	Thr	Thr	Val	Pro	Gly	Lys	Asp		
1955						1960					1965					
Pro	Met	Ala	Asp	Ser	Ile	Phe	His	Tyr	Tyr	Gln	Glu	Leu	Pro	Lys		
1970						1975					1980					
Tyr	Leu	Arg	Gly	Tyr	His	Lys	Cys	Thr	Arg	Glu	Glu	Val	Leu	Gln		
1985						1990					1995					
Leu	Gly	Ala	Leu	Ile	Tyr	Arg	Val	Lys	Phe	Glu	Glu	Asp	Lys	Ser		
2000						2005					2010					
Tyr	Phe	Pro	Ser	Ile	Pro	Lys	Leu	Leu	Arg	Glu	Leu	Val	Pro	Gln		
2015						2020					2025					
Asp	Leu	Ile	Arg	Gln	Val	Ser	Pro	Asp	Asp	Trp	Lys	Arg	Ser	Ile		
2030						2035					2040					

N3027PCT\_sequ.list.txt

Val Ala Tyr Phe Asn Lys His Ala Gly Lys Ser Lys Glu Glu Ala  
2045 2050 2055

Lys Leu Ala Phe Leu Lys Leu Ile Phe Lys Trp Pro Thr Phe Gly  
2060 2065 2070

Ser Ala Phe Phe Glu Gln Thr Thr Glu Pro Asn Phe Pro Glu Ile  
2075 2080 2085

Leu Leu Ile Ala Ile Asn Lys Tyr Gly Val Ser Leu Ile Asp Pro  
2090 2095 2100

Lys Thr Lys Asp Ile Leu Thr Thr His Pro Phe Thr Lys Ile Ser  
2105 2110 2115

Asn Trp Ser Ser Gly Asn Thr Tyr Phe His Ile Thr Ile Gly Asn  
2120 2125 2130

Leu Val Arg Gly Ser Lys Leu Leu Cys Glu Thr Ser Leu Gly Tyr  
2135 2140 2145

Lys Met Asp Asp Leu Leu Thr Ser Tyr Ile Ser Gln Met Leu Thr  
2150 2155 2160

Ala Met Ser Lys Gln Arg Gly Ser Arg Ser Gly Lys  
2165 2170 2175

<210> 43  
<211> 11436  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(11436)  
<223> myosin X MYO10

<400> 43  
gagagctggc t gaggccgcgg cgcggggactg ct cacctcca agcgctcgcg cggggatcgc 60  
ggctcctgct cactttgcgg cccgctgtcc t cctgccgc cccgagggcc cccggccgga 120  
gcgcagaggg agggggccgc gctcgccagc accccgccgc ct tccccgc ctgggggaag 180  
aatgtgccac cagctgttct ccgcttgca gcgctgcgcc cagt agt gag gaacttggag 240  
gaagaagaga caaaggctgc cgtcgggacg ggcgagttag ggacttgggt ttgggcgaac 300  
aaaaggtgag aaggacaaga agggaccggg cgatggcagc aggggagccc cgcgggcgcg 360  
cgtcctcggg agtggcgccg tgacacgcat ggtttccccg gaccgcggc ggcgctgact 420  
tccgcgagtc ggagcggcac tcggcgagtc cgggactgcg ctggaacaat ggataacttc 480  
ttcaccgagg gaacacgggt ctggctgaga gaaaatggcc agcattttcc aagtactgta 540  
aattcctgtg cagaaggcat cgtcgtcttc cggacagact atggtcaggt attcacttac 600

N3027PCT\_sequ. list . . txt

aagcagagca	caattacca	ccagaaggtg	actgctatgc	acccacgaa	cgaggagggc	660	
gtggatgaca	tggcgtcctt	gacagagctc	catggcggct	ccatcatgta	tacttattc	720	
cagcggat	atagagaaat	caaatatacc	tacatcggct	ccatcctggc	ctccgtgaac	780	
ccctaccagc	ccatcgccgg	gctgtacgag	cctgccacca	tggagcagt	acagccggcgc	840	
cacctgggcg	agctgcccc	gcacatcttc	gccatcgcca	acgagtgtc	acgctgcctg	900	
tggaagcgcc	acgacaacca	gtgcatcctc	atcagtggtg	aaagtggggc	aggtaaaacc	960	
gaaagcact	aatlgatcct	caagtttctg	tcagtcata	gtcaacagtc	tttggaattg	1020	
tctttaaagg	agaagacatc	ctgtgttgaa	cgagctattc	ttgaaagcag	ccccatcatg	1080	
gaagctttcg	gcaatgcgaa	gaccgtgtac	aacaacaact	ctagtcgctt	tgggaagttt	1140	
gttcagctga	acatctgtca	gaaaggaaat	attcagggcg	ggagaattgt	agattattta	1200	
ttagaaaaa	accgagtgt	aaggcaaaat	cccggggaaa	ggaattatca	catattttat	1260	
gcactgctgg	cagggctgga	acatgaagaa	agagaagaat	tttatttatc	tacgccagaa	1320	
aactaccact	acttgaatca	gtctggatgt	gtagaagaca	agacaatcag	tgaccaggaa	1380	
tctttaggg	aagttattac	ggcaatggac	gtgatgcagt	tcagcaagga	ggaagttcgg	1440	
gaagtgtcga	ggctgcttgc	tggatactg	catcttggga	acatagaatt	tatcactgct	1500	
gggtggggcac	aggtttcctt	caaaacagct	ttgggcagat	ctgcggagt	tacttgggctg	1560	
gacccaacac	agctcacaga	tgttttgacc	cagagatcaa	tgttctcag	gggagaagag	1620	
atcctcacgc	ctctcaatgt	tcaacaggca	gtagacagca	gggactccct	ggccatggct	1680	
ctgtatcggt	gctgctttga	gtgggtaatc	aagaagatca	acagcaggat	caaaggcaat	1740	
gaggacttca	agtctattgg	catcctcgac	atctttggat	ttgaaaactt	tgaggttaat	1800	
cactttgaac	agttcaatat	aaactatgca	aacgagaaac	ttcaggagt	acttcaacaag	1860	
catatttttt	ctttagaaca	actagaatat	agccgggaag	gattagtgtg	ggaagatat	1920	
gactggatag	acaatggaga	atgcctggac	ttgattgaga	agaaacttgg	cctcctagcc	1980	
cttatcaatg	aagaaagcca	ttttcctcaa	gccacagaca	gcaccttatt	ggagaagcta	2040	
cacagt cagc	atgcgaat	aa	ccacttttat	gtgaagccca	gagttgcagt	taacaatttt	2100
ggagtgaagc	actatgctgg	agaggtgcaa	tatgatgtcc	gaggtatctt	ggagaagaac	2160	
agagat acat	ttcgagatga	ccttctcaat	ttgct aagag	aaagccgat	tgactttatc	2220	
tacgatcttt	ttgaacatgt	ttcaagccgc	aacaaccagg	ataccttgaa	atgtggaagc	2280	
aaacatcggc	ggcctacagt	cagctcacag	ttcaaggact	cactgcattc	cttaatggca	2340	
acgct aagct	cctctaatcc	tttctttgtt	cgctgtatca	agccaaacat	gcagaagatg	2400	
ccagaccagt	ttgaccaggc	ggttgtgctg	aaccagctgc	ggtagtcagg	gatgctggag	2460	
actgtgagaa	tccgcaaagc	tgggtatgcg	gtccgaagac	cctttcagga	ctttt acaaa	2520	
aggtat aaag	tgtgatgag	gaatctggct	ctgcctgagg	acgtccgagg	gaagtgcacg	2580	
agcctgctgc	agctctatga	tgcctccaac	agcgagtggc	agctggggaa	gaccaaggtc	2640	

N3027PCT\_sequ. list .txt

t t t c t t c g a g	a a t c c t t g g a	a c a g a a a c t g	g a g a a g c g g a	g g g a a g a g g a	a g t g a g c c a c	2700
g c g g c c a t g g	t g a t t c g g g c	c c a t g t c t t g	g g c t t c t t a g	c a c g a a a a c a	a t a c a g a a a g	2760
g t c c t t t a t t	g t g t g g t g a t	a a t a c a g a a g	a a t t a c a g a g	c a t t c c t t c t	g a g g a g g a g a	2820
t t t t t g c a c c	t g a a a a a g g c	a g c c a t a g t t	t t c c a g a a g c	a a c t c a g a g g	t c a g a t t g c t	2880
c g g a g a g t t t	a c a g a c a a t t	g c t g g c a g a g	a a a a g g g a g c	a a g a a g a a a a	g a a g a a a c a g	2940
g a a g a g g a a g	a a a a g a a g a a	a c g g g a g g a a	g a a g a a a g a g	a a a g a g a g a g	a g a g c g a a g a	3000
g a a g c c g a g c	t c c g c g c c c a	g c a g g a a g a a	g a a a c g a g g a	a g c a g c a a g a	a c t c g a a g c c	3060
t t g c a g a a g a	g c c a g a a g g a	a g c t g a a c t g	a c c c g t g a a c	t g g a g a a a c a	g a a g g a a a a t	3120
a a g c a g g t g g	a a g a g a t c c t	c c g t c t g g a g	a a a g a a a t c g	a g g a c c t g c a	g c g c a t g a a g	3180
g a g c a g c a g g	a g c t g t c g c t	g a c c g a g g c t	t c c c t g c a g a	a g c t g c a g g a	g c g g c g g g a c	3240
c a g g a g c t c c	g c a g g c t g g a	g g a g g a a g c g	t g c a g g g c g g	c c c a g g a g t t	c c t c g a g t c c	3300
c t c a a t t t c g	a c g a g a t c g a	c g a g t g t g t c	c g g a a t a t c g	a g c g g t c c c t	g t c g g t g g g a	3360
a g c g a a t t t t	c c a g c g a g c t	g g c t g a g a g c	g c a t g c g a g g	a g a a g c c c a a	c t t c a a c t t c	3420
a g c c a g c c c t	a c c c a g a g g a	g g a g g t c g a t	g a g g g c t t c g	a a g c c g a c g a	c g a c g c c t t c	3480
a a g g a c t c c c	c c a a c c c c a g	c g a g c a c g g c	c a c t c a g a c c	a g c g a a c a a g	t g g c a t c c g g	3540
a c c a g c g a t g	a c t c t t c a g a	g g a g g a c c c a	t a c a t g a a c g	a c a c g g t g g t	g c c c a c c a g c	3600
c c c a g t g c g g	a c a g c a c g g t	g c t g c t c g c c	c c a t c a g t g c	a g g a c t c c g g	g a g c c t a c a c	3660
a a c t c c t c c a	g c g g c g a g t c	c a c c t a c t g c	a t g c c c c a g a	a c g c t g g g g a	c t t g c c c t c c	3720
c c a g a c g g c g	a c t a c g a c t a	c g a c c a g g a t	g a c t a t g a g g	a c g g t g c c a t	c a c t t c c g g c	3780
a g c a g c g t g a	c c t t c t c c a a	c t c c t a c g g c	a g c c a g t g g t	c c c c c g a c t a	c c g c t g c t c t	3840
g t g g g g a c c t	a c a a c a g c t c	g g g t g c c t a c	c g g t t c a g c t	c t g a g g g g g c	g c a g t c c t c g	3900
t t t g a a g a t a	g t g a a g a g g a	c t t t g a t t c c	a g g t t t g a t a	c a g a t g a t g a	g c t t t c a t a c	3960
c g g c g t g a c t	c t g t g t a c a g	c t g t g t c a c t	c t g c c g t a t t	t c c a c a g c t t	t c t g t a c a t g	4020
a a a g g t g g c c	t g a t g a a c t c	t t g g a a a c g c	c g c t g g t g c g	t c c t c a a g g a	t g a a a c c t t c	4080
t t g t g g t t c c	g c t c c a a g c a	g g a g g c c c t c	a a g c a a g g c t	g g c t c c a c a a	a a a a g g g g g g	4140
g g c t c c t c c a	c g c t g t c c a g	g a g a a a t t g g	a a g a a g c g c t	g g t t t g t c c t	c c g c c a g t c c	4200
a a g c t g a t g t	a c t t t g a a a a	c g a c a g c g a g	g a g a a g c t c a	a g g g c a c c g t	a g a a g t g c g a	4260
a c g g c a a a a g	a g a t c a t a g a	t a a c a c c a c c	a a g g a g a a t g	g g a t c g a c a t	c a t t a t g g c c	4320
g a t a g g a c t t	t c c a c c t g a t	t g c a g a g t c c	c c a g a a g a t g	c c a g c c a g t g	g t t c a g c g t g	4380
c t g a g t c a g g	t c c a c g c g t c	c a c g g a c c a g	g a g a t c c a g g	a g a t g c a t g a	t g a g c a g g c a	4440
a a c c c a c a g a	a t g c t g t g g g	c a c c t t g g a t	g t g g g g c t g a	t t g a t t c t g t	g t g t g c c t c t	4500
g a c a g c c c t g	a t a g a c c c a a	c t c g t t t g t g	a t c a t c a c g g	c c a a c c g g g t	g c t g c a c t g c	4560
a a c g c c g a c a	c g c c g g a g g a	g a t g c a c c a c	t g g a t a a c c c	t g c t g c a g a g	g t c c a a a g g g	4620
g a c a c c a g a g	t g g a g g g c c a	g g a a t t c a t c	g t g a g a g g a t	g g t t g c a c a a	a g a g g t g a a g	4680
a a c a g t c c a a	a g a t g t c t t c	a c t g a a a c t g	a a g a a a c g g t	g g t t t g t a c t	c a c c c a c a a t	4740

N3027PCT\_sequ. list . . txt

t ccct ggat t	act acaagag	t t cagagaag	aacgcgct ca	aact ggggac	cct ggt cct c	4800
aacagcct ct	gct ct gt cgt	ccccccagat	gagaagat at	t caaagagac	aggct act gg	4860
aacgt caccg	t gt acgggcg	caagcact gt	t accggct ct	acaccaagct	gct caacgag	4920
gccacccggt	ggt ccagt gc	cat t caaaac	gt gact gaca	ccaaggcccc	gat cgacacc	4980
cccacccagc	agct gat t ca	agat at caag	gagaact gcc	t gaact cgga	t gt ggt ggaa	5040
cagat t t aca	agcggaaccc	gat cct t cga	t acacccat c	accct t gca	ct ccccgct c	5100
ct gcccct t c	cgt at gggga	cat aaat ct c	aact t gct ca	aagacaaagg	ct at accacc	5160
ct t caggat g	aggccat caa	gat at t caat	t ccct gcagc	aact ggagt c	cat gt ct gac	5220
ccaat t ccaa	t aat ccaggg	cat cct acag	acagggcat g	acct gcgacc	t ct gcgggac	5280
gagct gt act	gccagct t at	caaacagacc	aacaaagt gc	cccaccccg	cagt gt gggc	5340
aacct gt aca	gct ggagat	cct gacat gc	ct gagct gca	cct t cct gcc	gagt cgaggg	5400
at t ct caagt	at ct caagt t	ccat ct gaaa	aggat acggg	aacagt t t cc	aggaagcgag	5460
at ggaaaaat	acgct ct ct t	cact t acgaa	t ct ct t aaga	aaaccaaat g	ccgagagt t t	5520
gt gcct t ccc	gagat gaaat	agaagct ct g	at ccacaggc	aggaaat gac	at ccacggt c	5580
t at t gccat g	gcggcggt c	ct gcaagat c	accat caact	cccacaccac	cgct ggggag	5640
gt ggt ggaga	agct gat ccg	aggcct ggcc	at ggaggaca	gcaggaacat	gt t t gct t t g	5700
t t t gaat aca	acggccacgt	cgacaaagcc	at t gaaagt c	gaaccgt cgt	agct gat gt c	5760
t t agccaagt	t t gaaaagct	ggct gccaca	t ccgaggt t g	gggacct gcc	at ggaaat t c	5820
t act t caaac	t t t act gct t	cct ggacaca	gacaacgt gc	caaaagacag	t gt ggagt t t	5880
gcat t t at gt	t t gaacaggc	ccacgaagcg	gt t at ccat g	gccaccat cc	agccccggaa	5940
gaaaacct cc	aggt t ct t gc	t gccct gcga	ct ccagt at c	t gcaggggga	t t at act ct g	6000
cacgt gcca	t cccacct ct	cgaagaggt t	t at t ccct gc	agagact caa	ggcccgcct c	6060
agccagt caa	ccaaaacct t	caccct t gt	gaacggct gg	agaagaggcg	gacgagct t c	6120
ct agagggga	ccct gagggcg	gagct t ccgg	acaggat ccg	t ggt ccggca	gaaggt cgag	6180
gaggagcaga	t gct ggacat	gt ggat t aag	gaagaagt ct	cct ct gct cg	agccagt at c	6240
at t gacaagt	ggaggaaat t	t cagggaaat g	aaccaggaac	aggccat ggc	caagt acat g	6300
gcct t gat ca	aggagt ggcc	t ggct at ggc	t cgacgct gt	t t gat gt gga	gt gcaaggaa	6360
ggt ggct t cc	ct caggaact	ct ggt t ggg	gt cagcgcg	acgccgt ct c	cgt ct acaag	6420
cgt ggagagg	gaagaccact	ggaagt ct t c	cagt at gaac	acat cct ct c	t t t t ggggca	6480
cccct ggca	at acgt at aa	gat cgt ggt c	gat gagaggg	agct gct ct t	t gaaaccagt	6540
gaggt ggt gg	at gt ggccaa	gct cat gaaa	gcct acat ca	gcat gat cgt	gaagaagcgc	6600
t acagcacga	cacgt ccgc	cagcagccag	ggcagct cca	ggt gaaggcg	ggacagagcc	6660
cacct gt ct t	t gct acct ga	acgcaccacc	ct ct ggcct a	ggct ggct cc	agt gt gccat	6720
gccagccaa	aacaaacaca	gagct gccca	ggct t t ct gg	aagct t ct gg	t ct gagggag	6780

N3027PCT\_sequ. list.txt

gt gt ct ccga ggat cct t t t gcct gcc gcc t t cat t gat c ct gt at t aag ct gt caact t	6840
t aacagt ct g cacagt t t cc aaagct t t ac t act ct t aga ggacacat gc ct t aaaaaag	6900
gaggggagga accacgct gc caccaaagca gccggaagt g cct t aact t g t ggaaccaac	6960
act aat cgac cgt aact gt g ct act gaagg gaact gcct t t cccct t ct gggggagact	7020
t aacagagcg t ggaaggggg gcatt ct ct g t caat gat gc act aacct cc caacct gat t	7080
t ccccgaa t c t gaggggaagg t gagggagt g ggaaggggga t ggagagct c gaggggacag	7140
t gt gt t t gag ct ggagt gct gcgggcagcc t t t ct cat gg aat gacat ga at caact t t t	7200
t t ct t t gt t t cat ct t t t aa gt gt acgt gc t t gcct gt t c gt gcat gt gt t cat aaact c	7260
aaact t t aa t cat ggt t t c at gagcat t a aaaagcaaag ggaaaaagga t gt gt aat gg	7320
t gt acacagt ct gt at at t t t aat aat gca gagct at agt ct caat t gt t act t t at aag	7380
gt ggt t t t at t aacaaaccc aaat cct gga t t t t cct gt c t t t gct gt at t t t gaaaaac	7440
acgt gt t gac t ccat t gt t t t acat gt agc aaagt ct gcc at ct gt gt ct gct gt at t at	7500
aaacagat aa gcagcct aca agat aact gt at t t at aaac cact ct t caa cagct ggct c	7560
cagt gct ggt t t t agaacaa gaat gaagt c at t t t ggagt ct t t cat gt c t aaaagat t t	7620
aagt t aaaaa caaagt gt t a ct t ggaaggt t agct t ct at cat t ct ggat agat t acaga	7680
t at aat aacc at gt t gact a t gggggagag acgct gcat t ccagaaacgt ct t aacact t	7740
gagt gaat ct t caaaggacc ct gacat t aa at gct gaggc t t t aat acac acat at t t t a	7800
t cccaagt t t at aat ggt gg t ct gaacaag gcacct gt aa at aaat cagc at t t at gacc	7860
agaagaaaaa t aat ct ggt c t t ggact t t t t at t t t at a t ggaaaagt t t t aaggact t	7920
gggccaact a agt ct accca cacgaaaaaa gaaat t t gcc t t gt ccct t t gt gt acaacc	7980
at gcaaaact gt t t gt t ggc t cacagaagt t ct gacaat a aaagat act a gct aacacgc	8040
t gt gt gt t t c ct t t at caga ggaggct ct a aaaacat gg aggggaggct t at t t t t gt t	8100
t t ggct t t t t ggt ggt t t t t t t t t t t c t t t agagaca gagt ct cact ct gt t accca	8160
ggct ggagt a cagt ggcgt g at ct cggct c act gcagcct ct gcct cct g ggt t ct agcg	8220
at t ct cct gc ct cagcct cc caaggagt t g ggagt acagg cat gcat cac cacgcct ggc	8280
t aggt t t t gt at t t t t agt a gagat ggggt t t caccat gt t ggccaggct ggt ct cgat c	8340
cacct gcct c agcct ccaa agt gct ggga t t acagggt gt gagct accgc acccggccgg	8400
ct t t t t ggt g t t aat gct at ggt t t cagt g t ct gggct t t gt gt t t gt t t cat ggact t g	8460
ct cat caggt ct aaacacag at ct gcagct gt ct ccact g ct ct t gt aga cact gagt gt	8520
gact t caaga aagcaaaaga agggact ggt aaat gaagt c acacacagct gaggact t ga	8580
aat gt gt t t a t gt cagacag t cccct at gt cagccccaaa gt gt gcct ga t ct t gcaacc	8640
ct ggat cct a gaacct gcct gcacct ccct gt ggaccaga acacacaggt aggcagt t t g	8700
gt t gccaat g t acccaaac accaggccag gcgt ct agca t gagcaagcg ccact t ct ct	8760
t gcagaccac t gact cccac cct ct gct ca t gct cacgga t ggct t ct t c ccat t ct gca	8820
gggat t ggga t ggaacct ga agccagggt gc t gcct gaagc ct gt ggcccc gccaggcacc	8880

N3027PCT\_sequ.list.txt

caaggaaagc	cggcaaagac	ttggatgtgt	gttgtctttg	tttttat	aggctcagaa	8940
agaatttgac	agaagcttc	tttctactgc	tcacctctca	ggattccctc	tgtgacttaa	9000
tttactctgg	aaggctgtcg	cccgccctca	attatagatg	gggaaatagg	caaggaaagg	9060
catgactcag	attggggggg	ttagagcagc	accatagtta	gaacatagat	ttacatgtga	9120
gcctttacat	ggcatagtig	tggttttgtt	ttagcctttt	atttagaaat	aattacagac	9180
tcagagaaaag	ttgcaacaga	acgtacaggg	aggcctgcgt	gcccttcagt	ttccccagt g	9240
gtagcatccc	ccatcactgt	agagcagcat	cacagctgac	aaagtaccgt	tgagcttccc	9300
ctagccacag	aacctattcc	aattttactg	cttttacctg	cactcattgg	tgtgtgtgat	9360
gtcagttgct	ttcaacaagg	tcagtgaagt	gcagtcgtcc	cttggatcc	aaggggagatt	9420
ggttccagga	ccccctcccc	ccaccctga	ggatacaaaa	ttcacagatg	ctcaagtccc	9480
tgtatacag	tggatataa	tttgcataga	acctgcacac	atctttcctt	accctttaaa	9540
tcactctccag	gttacagata	cctagcacia	cataaatgct	gcataaatag	ctgttatacc	9600
gtgtgtgtct	gtgttttaa	cattgtttat	ttgagacagg	gtctcactct	gtcaccaggc	9660
tacagtgcag	aggcacagtc	acagctcatt	gcagcctcaa	cctcctgggc	tcaagcagtc	9720
ctccacctca	gcctccaaa	gtgctaggat	gacaggtgtg	agccactgtg	ccccacaaa	9780
aaaagttttt	tcaaatattt	tctatctgtg	gttggattca	gaccacatga	acactgaggg	9840
ctgactgtag	ttttgaatgt	ctgttactga	ggaggcacca	gcataaagta	ttttatcact	9900
tcagacgctg	acaatctagt	atttttaatt	tttaaatctt	ttgaaagcta	atacatatag	9960
gtgat ttgt a	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	actagaagta	10020
aaatgttact	tttttccagc	tgtagcccta	attacccatt	ttcctttccc	agaaacagct	10080
atttttactg	ttttattgaa	tattctctca	aaaataattt	aagctgtcca	atcatttact	10140
catacataca	tatatatccc	catcctcatt	tttaaatagat	ggaaacaaac	tgttgtagct	10200
tacttttttc	tcagcatagt	attttagctc	tatacctaca	tttaaatacct	atagaattgcc	10260
ttattctttt	tgatgattat	atagtacctc	agatagctct	gtggaaaaac	aggatagggc	10320
catctgtatt	agtcatttct	cacactgcta	gaaggacatg	cctgagactg	ggtaatttat	10380
aaagaaaaag	aagttgaatg	gactcagctc	cacatgcctg	gggaggcctc	acaatcatgg	10440
tggacagcaa	aggaggagaa	aaggcacatc	ttatatggca	gcaggcaaga	gagcttgcac	10500
aggggaactc	ccttttataa	aacctatagc	tcttccgaga	catactcact	atggacaaga	10560
acagcatggg	aaaaccacc	cccatgattc	aattacctcc	catcaggtcc	ctcccgtgac	10620
agggtgggat	tatgggagct	ataattcaag	atgagatttg	gggtggggaca	gagccaaacc	10680
atatcaccac	ctaagtctc	tgtaaaaata	gtttcagcca	ggcatgctgg	ctcacgcctg	10740
ttaatcccagc	atgttggaag	gccgaggcaa	gaggatcgct	tgagctccgg	agttcaagac	10800
cagctctgggc	aacatgacaa	gaccctgtct	ccacagaaaa	ttaacattag	ccaggtgtgg	10860
tgggtgcgcat	ctgtagtccc	agctactggg	gaggctgaga	tgagaaaatc	gtttgaaccc	10920

N3027PCT\_sequ.list.txt

```
aggaggt caa agctgcaggg agccatgat g gtgccactgc attctgggtgt ggggtgacaga 10980
gcaagactct gtctccaaaa aaaaaaaaaa aaaaaaaaaa tagttcagaa atctaagaca 11040
gcactttttt tagttactaa gcctttttat cagatagcac actaaattgg ggtcaaaaat 11100
ctgctatagt aaagtctgt atttgtgtgt attgggtata aaaataagcg ctttaattaa 11160
tttgaaaatc cctattcacc aaaagtttat actgtaatag gggacaaaac aagtgcataa 11220
agctaaattt agccagtaca ttataactg ttcatctcag ttgatcagag aagcatcacg 11280
attgctggaa aatatcggac ctggattcaa ggtttggcat tgctgttttc aaagtatgta 11340
atcttttaga tcaggggtca gtgaactaca gtacagagac caaatctacc ctgccacctg 11400
tttttgtgaa taaagtttta ttgaaacaga aaaaaa 11436
```

<210> 44  
 <211> 2058  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(2058)  
 <223> myosin X MYO10

<400> 44

```
Met Asp Asn Phe Phe Thr Glu Gly Thr Arg Val Trp Leu Arg Glu Asn
1      5      10      15

Gly Gln His Phe Pro Ser Thr Val Asn Ser Cys Ala Glu Gly Ile Val
20      25      30

Val Phe Arg Thr Asp Tyr Gly Gln Val Phe Thr Tyr Lys Gln Ser Thr
35      40      45

Ile Thr His Gln Lys Val Thr Ala Met His Pro Thr Asn Glu Glu Gly
50      55      60

Val Asp Asp Met Ala Ser Leu Thr Glu Leu His Gly Gly Ser Ile Met
65      70      75      80

Tyr Asn Leu Phe Gln Arg Tyr Lys Arg Asn Gln Ile Tyr Thr Tyr Ile
85      90      95

Gly Ser Ile Leu Ala Ser Val Asn Pro Tyr Gln Pro Ile Ala Gly Leu
100     105     110

Tyr Glu Pro Ala Thr Met Glu Gln Tyr Ser Arg Arg His Leu Gly Glu
115     120     125

Leu Pro Pro His Ile Phe Ala Ile Ala Asn Glu Cys Tyr Arg Cys Leu
130     135     140

Trp Lys Arg His Asp Asn Gln Cys Ile Leu Ile Ser Gly Glu Ser Gly
```

145		150		155		160									
Ala	Gly	Lys	Thr	Glu 165	Ser	Thr	Lys	Leu	Ile 170	Leu	Lys	Phe	Leu	Ser 175	Val
Ile	Ser	Gln 180	Gln	Ser	Leu	Glu	Leu	Ser 185	Leu	Lys	Glu	Lys	Thr 190	Ser	Oys
Val	Glu	Arg 195	Ala	Ile	Leu	Glu	Ser 200	Ser	Pro	Ile	Met	Glu 205	Ala	Phe	Gly
Asn 210	Ala	Lys	Thr	Val	Tyr	Asn 215	Asn	Asn	Ser	Ser	Arg 220	Phe	Gly	Lys	Phe
Val 225	Gln	Leu	Asn	Ile	Oys 230	Gln	Lys	Gly	Asn	Ile 235	Gln	Gly	Gly	Arg	Ile 240
Val	Asp	Tyr	Leu	Leu 245	Glu	Lys	Asn	Arg	Val 250	Val	Arg	Gln	Asn	Pro 255	Gly
Glu	Arg	Asn	Tyr 260	His	Ile	Phe	Tyr	Ala 265	Leu	Leu	Ala	Gly	Leu 270	Glu	His
Glu	Glu	Arg 275	Glu	Glu	Phe	Tyr	Leu 280	Ser	Thr	Pro	Glu	Asn 285	Tyr	His	Tyr
Leu	Asn 290	Gln	Ser	Gly	Oys 295	Val	Glu	Asp	Lys	Thr	Ile 300	Ser	Asp	Gln	Glu
Ser 305	Phe	Arg	Glu	Val	Ile 310	Thr	Ala	Met	Asp	Val 315	Met	Gln	Phe	Ser	Lys 320
Glu	Glu	Val	Arg	Glu 325	Val	Ser	Arg	Leu	Leu 330	Ala	Gly	Ile	Leu	His 335	Leu
Gly	Asn	Ile	Glu 340	Phe	Ile	Thr	Ala	Gly 345	Gly	Ala	Gln	Val	Ser 350	Phe	Lys
Thr	Ala	Leu 355	Gly	Arg	Ser	Ala	Glu 360	Leu	Leu	Gly	Leu	Asp 365	Pro	Thr	Gln
Leu	Thr 370	Asp	Ala	Leu	Thr	Gln 375	Arg	Ser	Met	Phe	Leu 380	Arg	Gly	Glu	Glu
Ile 385	Leu	Thr	Pro	Leu	Asn 390	Val	Gln	Gln	Ala	Val 395	Asp	Ser	Arg	Asp	Ser 400
Leu	Ala	Met	Ala	Leu 405	Tyr	Ala	Oys	Oys	Phe 410	Glu	Trp	Val	Ile	Lys 415	Lys
Ile	Asn	Ser	Arg 420	Ile	Lys	Gly	Asn 425	Glu	Asp	Phe	Lys	Ser	Ile 430	Gly	Ile

N3027PCT\_sequ.list.txt

Leu Asp Ile Phe Gly Phe Glu Asn Phe Glu Val Asn His Phe Glu Gln  
 435 440 445  
 Phe Asn Ile Asn Tyr Ala Asn Glu Lys Leu Gln Glu Tyr Phe Asn Lys  
 450 455 460  
 His Ile Phe Ser Leu Glu Gln Leu Glu Tyr Ser Arg Glu Gly Leu Val  
 465 470 475 480  
 Trp Glu Asp Ile Asp Trp Ile Asp Asn Gly Glu Cys Leu Asp Leu Ile  
 485 490 495  
 Glu Lys Lys Leu Gly Leu Leu Ala Leu Ile Asn Glu Glu Ser His Phe  
 500 505 510  
 Pro Gln Ala Thr Asp Ser Thr Leu Leu Glu Lys Leu His Ser Gln His  
 515 520 525  
 Ala Asn Asn His Phe Tyr Val Lys Pro Arg Val Ala Val Asn Asn Phe  
 530 535 540  
 Gly Val Lys His Tyr Ala Gly Glu Val Gln Tyr Asp Val Arg Gly Ile  
 545 550 555 560  
 Leu Glu Lys Asn Arg Asp Thr Phe Arg Asp Asp Leu Leu Asn Leu Leu  
 565 570 575  
 Arg Glu Ser Arg Phe Asp Phe Ile Tyr Asp Leu Phe Glu His Val Ser  
 580 585 590  
 Ser Arg Asn Asn Gln Asp Thr Leu Lys Cys Gly Ser Lys His Arg Arg  
 595 600 605  
 Pro Thr Val Ser Ser Gln Phe Lys Asp Ser Leu His Ser Leu Met Ala  
 610 615 620  
 Thr Leu Ser Ser Ser Asn Pro Phe Phe Val Arg Cys Ile Lys Pro Asn  
 625 630 635 640  
 Met Gln Lys Met Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln  
 645 650 655  
 Leu Arg Tyr Ser Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly  
 660 665 670  
 Tyr Ala Val Arg Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val  
 675 680 685  
 Leu Met Arg Asn Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr  
 690 695 700

N3027PCT\_sequ.list.txt

Ser Leu Leu Gln Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly  
 705 710 715 720  
 Lys Thr Lys Val Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys  
 725 730 735  
 Arg Arg Glu Glu Glu Val Ser His Ala Ala Met Val Ile Arg Ala His  
 740 745 750  
 Val Leu Gly Phe Leu Ala Arg Lys Gln Tyr Arg Lys Val Leu Tyr Cys  
 755 760 765  
 Val Val Ile Ile Gln Lys Asn Tyr Arg Ala Phe Leu Leu Arg Arg Arg  
 770 775 780  
 Phe Leu His Leu Lys Lys Ala Ala Ile Val Phe Gln Lys Gln Leu Arg  
 785 790 795 800  
 Gly Gln Ile Ala Arg Arg Val Tyr Arg Gln Leu Leu Ala Glu Lys Arg  
 805 810 815  
 Glu Gln Glu Glu Lys Lys Lys Gln Glu Glu Glu Glu Lys Lys Lys Arg  
 820 825 830  
 Glu Glu Glu Glu Arg Glu Arg Glu Arg Glu Arg Arg Glu Ala Glu Leu  
 835 840 845  
 Arg Ala Gln Gln Glu Glu Glu Thr Arg Lys Gln Gln Glu Leu Glu Ala  
 850 855 860  
 Leu Gln Lys Ser Gln Lys Glu Ala Glu Leu Thr Arg Glu Leu Glu Lys  
 865 870 875 880  
 Gln Lys Glu Asn Lys Gln Val Glu Glu Ile Leu Arg Leu Glu Lys Glu  
 885 890 895  
 Ile Glu Asp Leu Gln Arg Met Lys Glu Gln Gln Glu Leu Ser Leu Thr  
 900 905 910  
 Glu Ala Ser Leu Gln Lys Leu Gln Glu Arg Arg Asp Gln Glu Leu Arg  
 915 920 925  
 Arg Leu Glu Glu Glu Ala Cys Arg Ala Ala Gln Glu Phe Leu Glu Ser  
 930 935 940  
 Leu Asn Phe Asp Glu Ile Asp Glu Cys Val Arg Asn Ile Glu Arg Ser  
 945 950 955 960  
 Leu Ser Val Gly Ser Glu Phe Ser Ser Glu Leu Ala Glu Ser Ala Cys  
 965 970 975

N3027PCT\_sequ.list.txt

G u G u Lys P r o A s n P h e A s n P h e S e r G n P r o T y r P r o G u G u G u  
 980 985 990  
  
 V a l A s p G u G y P h e G u A l a A s p A s p A s p A l a P h e L y s A s p S e r P r o  
 995 1000 1005  
  
 A s n P r o S e r G u H i s G y H i s S e r A s p G n A r g T h r S e r G y I l e  
 1010 1015  
  
 A r g T h r S e r A s p A s p S e r S e r G u G u A s p P r o T y r M e t A s n A s p  
 1025 1030 1035  
  
 T h r V a l V a l P r o T h r S e r P r o S e r A l a A s p S e r T h r V a l L e u L e u  
 1040 1045 1050  
  
 A l a P r o S e r V a l G n A s p S e r G y S e r L e u H i s A s n S e r S e r S e r  
 1055 1060 1065  
  
 G y G u S e r T h r T y r O y s M e t P r o G n A s n A l a G y A s p L e u P r o  
 1070 1075 1080  
  
 S e r P r o A s p G y A s p T y r A s p T y r A s p G n A s p A s p T y r G u A s p  
 1085 1090 1095  
  
 G y A l a I l e T h r S e r G y S e r S e r V a l T h r P h e S e r A s n S e r T y r  
 1100 1105 1110  
  
 G y S e r G n T r p S e r P r o A s p T y r A r g O y s S e r V a l G y T h r T y r  
 1115 1120 1125  
  
 A s n S e r S e r G y A l a T y r A r g P h e S e r S e r G u G y A l a G n S e r  
 1130 1135 1140  
  
 S e r P h e G u A s p S e r G u G u A s p P h e A s p S e r A r g P h e A s p T h r  
 1145 1150 1155  
  
 A s p A s p G u L e u S e r T y r A r g A r g A s p S e r V a l T y r S e r O y s V a l  
 1160 1165 1170  
  
 T h r L e u P r o T y r P h e H i s S e r P h e L e u T y r M e t L y s G y G y L e u  
 1175 1180 1185  
  
 M e t A s n S e r T r p L y s A r g A r g T r p O y s V a l L e u L y s A s p G u T h r  
 1190 1195 1200  
  
 P h e L e u T r p P h e A r g S e r L y s G n G u A l a L e u L y s G n G y T r p  
 1205 1210 1215  
  
 L e u H i s L y s L y s G y G y G y S e r S e r T h r L e u S e r A r g A r g A s n  
 1220 1225 1230  
  
 T r p L y s L y s A r g T r p P h e V a l L e u A r g G n S e r L y s L e u M e t T y r  
 Page 193

Phe	Glu 1250	Asn	Asp	Ser	Glu	Glu 1255	Lys	Leu	Lys	Gly	Thr 1260	Val	Glu	Val
Arg	Thr 1265	Ala	Lys	Glu	Ile	Ile 1270	Asp	Asn	Thr	Thr	Lys 1275	Glu	Asn	Gly
Ile	Asp 1280	Ile	Ile	Met	Ala	Asp 1285	Arg	Thr	Phe	His	Leu 1290	Ile	Ala	Glu
Ser	Pro 1295	Glu	Asp	Ala	Ser	Gln 1300	Trp	Phe	Ser	Val	Leu 1305	Ser	Gln	Val
His	Ala 1310	Ser	Thr	Asp	Gln	Glu 1315	Ile	Gln	Glu	Met	His 1320	Asp	Glu	Gln
Ala	Asn 1325	Pro	Gln	Asn	Ala	Val 1330	Gly	Thr	Leu	Asp	Val 1335	Gly	Leu	Ile
Asp	Ser 1340	Val	Cys	Ala	Ser	Asp 1345	Ser	Pro	Asp	Arg	Pro 1350	Asn	Ser	Phe
Val	Ile 1355	Ile	Thr	Ala	Asn	Arg 1360	Val	Leu	His	Cys	Asn 1365	Ala	Asp	Thr
Pro	Glu 1370	Glu	Met	His	His	Trp 1375	Ile	Thr	Leu	Leu	Gln 1380	Arg	Ser	Lys
Gly	Asp 1385	Thr	Arg	Val	Glu	Gly 1390	Gln	Glu	Phe	Ile	Val 1395	Arg	Gly	Trp
Leu	His 1400	Lys	Glu	Val	Lys	Asn 1405	Ser	Pro	Lys	Met	Ser 1410	Ser	Leu	Lys
Leu	Lys 1415	Lys	Arg	Trp	Phe	Val 1420	Leu	Thr	His	Asn	Ser 1425	Leu	Asp	Tyr
Tyr	Lys 1430	Ser	Ser	Glu	Lys	Asn 1435	Ala	Leu	Lys	Leu	Gly 1440	Thr	Leu	Val
Leu	Asn 1445	Ser	Leu	Cys	Ser	Val 1450	Val	Pro	Pro	Asp	Glu 1455	Lys	Ile	Phe
Lys	Glu 1460	Thr	Gly	Tyr	Trp	Asn 1465	Val	Thr	Val	Tyr	Gly 1470	Arg	Lys	His
Cys	Tyr 1475	Arg	Leu	Tyr	Thr	Lys 1480	Leu	Leu	Asn	Glu	Ala 1485	Thr	Arg	Trp
Ser	Ser 1490	Ala	Ile	Gln	Asn	Val 1495	Thr	Asp	Thr	Lys	Ala 1500	Pro	Ile	Asp

N3027PCT\_sequ.list.txt

Thr	Pro	Thr	Gln	Gln	Leu	Ile	Gln	Asp	Ile	Lys	Glu	Asn	Cys	Leu
	1505					1510					1515			
Asn	Ser	Asp	Val	Val	Glu	Gln	Ile	Tyr	Lys	Arg	Asn	Pro	Ile	Leu
	1520					1525					1530			
Arg	Tyr	Thr	His	His	Pro	Leu	His	Ser	Pro	Leu	Leu	Pro	Leu	Pro
	1535					1540					1545			
Tyr	Gly	Asp	Ile	Asn	Leu	Asn	Leu	Leu	Lys	Asp	Lys	Gly	Tyr	Thr
	1550					1555					1560			
Thr	Leu	Gln	Asp	Glu	Ala	Ile	Lys	Ile	Phe	Asn	Ser	Leu	Gln	Gln
	1565					1570					1575			
Leu	Glu	Ser	Met	Ser	Asp	Pro	Ile	Pro	Ile	Ile	Gln	Gly	Ile	Leu
	1580					1585					1590			
Gln	Thr	Gly	His	Asp	Leu	Arg	Pro	Leu	Arg	Asp	Glu	Leu	Tyr	Cys
	1595					1600					1605			
Gln	Leu	Ile	Lys	Gln	Thr	Asn	Lys	Val	Pro	His	Pro	Gly	Ser	Val
	1610					1615					1620			
Gly	Asn	Leu	Tyr	Ser	Trp	Gln	Ile	Leu	Thr	Cys	Leu	Ser	Cys	Thr
	1625					1630					1635			
Phe	Leu	Pro	Ser	Arg	Gly	Ile	Leu	Lys	Tyr	Leu	Lys	Phe	His	Leu
	1640					1645					1650			
Lys	Arg	Ile	Arg	Glu	Gln	Phe	Pro	Gly	Ser	Glu	Met	Glu	Lys	Tyr
	1655					1660					1665			
Ala	Leu	Phe	Thr	Tyr	Glu	Ser	Leu	Lys	Lys	Thr	Lys	Cys	Arg	Glu
	1670					1675					1680			
Phe	Val	Pro	Ser	Arg	Asp	Glu	Ile	Glu	Ala	Leu	Ile	His	Arg	Gln
	1685					1690					1695			
Glu	Met	Thr	Ser	Thr	Val	Tyr	Cys	His	Gly	Gly	Gly	Ser	Cys	Lys
	1700					1705					1710			
Ile	Thr	Ile	Asn	Ser	His	Thr	Thr	Ala	Gly	Glu	Val	Val	Glu	Lys
	1715					1720					1725			
Leu	Ile	Arg	Gly	Leu	Ala	Met	Glu	Asp	Ser	Arg	Asn	Met	Phe	Ala
	1730					1735					1740			
Leu	Phe	Glu	Tyr	Asn	Gly	His	Val	Asp	Lys	Ala	Ile	Glu	Ser	Arg
	1745					1750					1755			

## N3027PCT\_sequ.list.txt

Thr	Val	Val	Ala	Asp	Val	Leu	Ala	Lys	Phe	Glu	Lys	Leu	Ala	Ala
	1760					1765					1770			
Thr	Ser	Glu	Val	Gly	Asp	Leu	Pro	Trp	Lys	Phe	Tyr	Phe	Lys	Leu
	1775					1780					1785			
Tyr	Cys	Phe	Leu	Asp	Thr	Asp	Asn	Val	Pro	Lys	Asp	Ser	Val	Glu
	1790					1795					1800			
Phe	Ala	Phe	Met	Phe	Glu	Gln	Ala	His	Glu	Ala	Val	Ile	His	Gly
	1805					1810					1815			
His	His	Pro	Ala	Pro	Glu	Glu	Asn	Leu	Gln	Val	Leu	Ala	Ala	Leu
	1820					1825					1830			
Arg	Leu	Gln	Tyr	Leu	Gln	Gly	Asp	Tyr	Thr	Leu	His	Ala	Ala	Ile
	1835					1840					1845			
Pro	Pro	Leu	Glu	Glu	Val	Tyr	Ser	Leu	Gln	Arg	Leu	Lys	Ala	Arg
	1850					1855					1860			
Ile	Ser	Gln	Ser	Thr	Lys	Thr	Phe	Thr	Pro	Cys	Glu	Arg	Leu	Glu
	1865					1870					1875			
Lys	Arg	Arg	Thr	Ser	Phe	Leu	Glu	Gly	Thr	Leu	Arg	Arg	Ser	Phe
	1880					1885					1890			
Arg	Thr	Gly	Ser	Val	Val	Arg	Gln	Lys	Val	Glu	Glu	Glu	Gln	Met
	1895					1900					1905			
Leu	Asp	Met	Trp	Ile	Lys	Glu	Glu	Val	Ser	Ser	Ala	Arg	Ala	Ser
	1910					1915					1920			
Ile	Ile	Asp	Lys	Trp	Arg	Lys	Phe	Gln	Gly	Met	Asn	Gln	Glu	Gln
	1925					1930					1935			
Ala	Met	Ala	Lys	Tyr	Met	Ala	Leu	Ile	Lys	Glu	Trp	Pro	Gly	Tyr
	1940					1945					1950			
Gly	Ser	Thr	Leu	Phe	Asp	Val	Glu	Cys	Lys	Glu	Gly	Gly	Phe	Pro
	1955					1960					1965			
Gln	Glu	Leu	Trp	Leu	Gly	Val	Ser	Ala	Asp	Ala	Val	Ser	Val	Tyr
	1970					1975					1980			
Lys	Arg	Gly	Glu	Gly	Arg	Pro	Leu	Glu	Val	Phe	Gln	Tyr	Glu	His
	1985					1990					1995			
Ile	Leu	Ser	Phe	Gly	Ala	Pro	Leu	Ala	Asn	Thr	Tyr	Lys	Ile	Val
	2000					2005					2010			

N3027PCT\_sequ.list.txt

Val Asp Glu Arg Glu Leu Leu Phe Glu Thr Ser Glu Val Val Asp  
2015 2020 2025

Val Ala Lys Leu Met Lys Ala Tyr Ile Ser Met Ile Val Lys Lys  
2030 2035 2040

Arg Tyr Ser Thr Thr Arg Ser Ala Ser Ser Gln Gly Ser Ser Arg  
2045 2050 2055

<210> 45  
<211> 3209  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(3209)  
<223> myosin XIX

<400> 45  
gttcttcccgcgcctgacctggccccgccctttccagttctggccgggcgggggcctg 60  
aagcacggcggtcggggccgtgggacctgtttcacacctttccagaaattcttggctgg 120  
taaccgcgaaccgactgga gcaggagctgggagaactgg agaaaactgc tctaatctca 180  
cttgactcca gctaggagct gatgctgcat cgtaat aaca ttgtgcagagc gctttcacag 240  
gcgctggagt gacttgtctg agattcctcc agaactgagc cctttgttgg aacctacctc 300  
cagcccatgg tcccatgact aggtggatag tactccttgt acctcctgca acccagaacc 360  
ctggctgacc actttgaagg aggatgctcc agcagggtcaa tggccacaat ccgggggtctg 420  
atggccaagc cagggagtac ctcagagaag acctgcagga gttcctgggt ggggaggtcc 480  
tgctgtacaa actggatgac ctaccagggtgaatcctgt gacactagag acagtcctga 540  
gggtgcctgca ggccccgtac atggcagaca catctctacac caatgctggc tgcacctgg 600  
tagccttgaa ccccttcaag cctgttctc agctctactc gcccgagcta atgagagagt 660  
acctgctgc gcctcagccc cagaaactga agcccatgt gttcactgtg ggtgaacaga 720  
cctacaggaa tgtcaagagc ctgattgaac cagtcaacca gtctattgtt gtcagtgag 780  
agagtggtgc tggaaagaca tggacgtctc gctgcctaat gaagtctat gctgtggtgg 840  
ccacctcacc tgcatttgg gagagccaca agattgcaga gaggatagaa cagaggatcc 900  
tgaactcaa cctgtcatg gaagcttttg ggaatgcgtg taaactgagg aataacaaca 960  
gcagtcgctt tgggaagtac atccagctcc agctgaacag ggctcagcaa atgactggag 1020  
ccgcagttca gacctacctc ctagagaaaa ctgagtggtc ctgccaggct tccagtgaga 1080  
ggaaacttcca catcttctat cagatttgca aaggagccag tgaggacgag aggctccagt 1140  
ggcaccttcc tgaggggagct gccttctcct ggctgcccaa cccagagagg agcttgaag 1200  
aggattgttt tgaggtgacc agagaggcca tgcctcat ttgggcat tgcacccctacct 1260  
agaacaacat ctttaaggctc ctagctggac tgcctgcacct tggcaatata cagtttgcctg 1320  
cctccgagga tgaagcccag cctgccagc cgatggatga tgccaagtac tctgtcagga 1380

N3027PCT\_sequ. list . . txt

cggcagcct c	gct gct gggg	ct cccagagg	acgt gct gct	ggagat ggt g	cagat t agaa	1440
ccat cagggc	aggcagacag	cagcaggt gt	t ccggaagcc	ct gcgcccga	gccgagt gt g	1500
acacccgt ag	agact gcct g	gccaaact ga	t ct at gcgcg	gt t gt t t gac	t ggct ggt at	1560
cagt gat caa	cagcagcat c	t gt gcagaca	ccgact cgt g	gaccact t t c	at aggct gc	1620
t ggat gt gt a	t ggat t t gaa	t cat t t cct g	acaacagt ct	ggaacagt t g	t gcat caact	1680
acgccaat ga	gaagct gcag	ct ggaggcct	gt ggcct cgt	ggagaccat c	cat at cagt g	1740
ct gct ggct t	ccccat ccgg	gt ct ct cacc	gaaact t t gt	agaacgat ac	aagt t act aa	1800
gaaggct t ca	t cct t gcaca	t cct ct ggcc	ccgacagccc	at at cct gcc	aaagggct cc	1860
ct gaat ggt g	t ccacacagc	gaggaagcca	cgct t gaacc	t ct cat ccag	gacat t ct cc	1920
acact ct gcc	ggt cct aact	caggcagcag	ccat aact gg	t gact cggct	gaggccat gc	1980
cagcccccat	gcact gt ggc	aggaccaagg	t gt t cat gac	t gact ct at g	ct ggagct t c	2040
t ggaat gt gg	gcgt gcccg	gt gct ggagc	agt gt gcccg	ct gcat ccag	ggt ggct gga	2100
ggcgacaccg	gcaccgagag	caggagcggc	agt ggcgggc	cgt cat gct c	at ccaggcag	2160
ccat t cgt t c	ct ggt t aact	cggaaacaca	t ccagaggct	gcat gcagct	gccacagt ca	2220
t caagcgt gc	at ggagaag	t ggagaat ca	gaat ggcct g	cct t gct gct	aaagagct gg	2280
at ggt gt gga	agaaaaacac	t t ct ct caag	ct ccct gt t c	cct gagcacc	t cgccgct gc	2340
agaccaggct	cct ggaggca	at aat ccgcc	t ct ggccccct	gggact ggt c	ct ggccaat a	2400
cggct at ggg	t gt aggcagc	t t t cagagga	aat t agt ggt	ct gggct t gc	ct ccagct cc	2460
ccaggggcag	ccccagt agc	t acact gt cc	agacagcaca	agaccaggct	ggt gt cacgt	2520
ccat ccgagc	gct gcct cag	ggat cgat aa	agt t t cact g	cagaaagt ct	ccact gcggt	2580
at gct gacat	ct gccct gaa	cct t caccct	acagcat t ac	aggct t t aat	cagat t ct gc	2640
t ggaaagaca	caggct gat c	cacgt gacct	ct t ct gcct t	cact gggct g	gggt gat cct	2700
t ggt gcct t t	gt t t ccacaa	ggcct t t t cc	t gccccct gc	ct t gccaaag	acat t t aat c	2760
agcacacagc	t gccagact a	t t cccacagt	gct ccaaat g	cacat gaaca	acagt gacgg	2820
ct ccagcct t	cgaccagag	ccccgt gcc	agt gcgt cag	t gggcct ggg	gt t ccaggct	2880
acat caagca	ct gat ggt gt	cagggt ggt	agt t accaaa	t cagggt t aa	gaaacat cag	2940
ggccacat t t	cact acct t c	acagat caaa	ct cagcagca	gt cat gact g	t ct gt cact a	3000
cact ggggat	cccaat t cca	cat aagcact	t t t ggaagaa	aacagccaaa	gt t ggcct aa	3060
aat t ggcgct	ggaat t t ggg	ct gggaaaaa	t ct t gt ggt t	at t t cct t t a	aaaaggaaca	3120
aaact t t agt	at t t aat t ag	t t gat t t at t	t aat gt aat t	t caaacaat t	aaat t at gaa	3180
t aat gcaat g	t aaaaaaaaaa	aaaaaaaaaa				3209

<210> 46  
 <211> 770  
 <212> PRT  
 <213> Homo sapi ens

N3027PCT\_sequ.list.txt

<220>

<221> M SC\_FEATURE

<222> (1)..(770)

<223> myosin XIX

<400> 46

Met Leu Gln Gln Val Asn Gly His Asn Pro Gly Ser Asp Gly Gln Ala  
1 5 10 15

Arg Glu Tyr Leu Arg Glu Asp Leu Gln Glu Phe Leu Gly Gly Glu Val  
20 25 30

Leu Leu Tyr Lys Leu Asp Asp Leu Thr Arg Val Asn Pro Val Thr Leu  
35 40 45

Glu Thr Val Leu Arg Cys Leu Gln Ala Arg Tyr Met Ala Asp Thr Phe  
50 55 60

Tyr Thr Asn Ala Gly Cys Thr Leu Val Ala Leu Asn Pro Phe Lys Pro  
65 70 75 80

Val Pro Gln Leu Tyr Ser Pro Glu Leu Met Arg Glu Tyr His Ala Ala  
85 90 95

Pro Gln Pro Gln Lys Leu Lys Pro His Val Phe Thr Val Gly Glu Gln  
100 105 110

Thr Tyr Arg Asn Val Lys Ser Leu Ile Glu Pro Val Asn Gln Ser Ile  
115 120 125

Val Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Trp Thr Ser Arg Cys  
130 135 140

Leu Met Lys Phe Tyr Ala Val Val Ala Thr Ser Pro Ala Ser Trp Glu  
145 150 155 160

Ser His Lys Ile Ala Glu Arg Ile Glu Gln Arg Ile Leu Asn Ser Asn  
165 170 175

Pro Val Met Glu Ala Phe Gly Asn Ala Cys Thr Leu Arg Asn Asn Asn  
180 185 190

Ser Ser Arg Phe Gly Lys Phe Ile Gln Leu Gln Leu Asn Arg Ala Gln  
195 200 205

Gln Met Thr Gly Ala Ala Val Gln Thr Tyr Leu Leu Glu Lys Thr Arg  
210 215 220

Val Ala Cys Gln Ala Ser Ser Glu Arg Asn Phe His Ile Phe Tyr Gln  
225 230 235 240

Ile Cys Lys Gly Ala Ser Glu Asp Glu Arg Leu Gln Trp His Leu Pro  
Page 199



N3027PCT\_sequ.list.txt

Ala Glu Ala Met Pro Ala Pro Met His Cys Gly Arg Thr Lys Val Phe  
530 535 540

Met Thr Asp Ser Met Leu Glu Leu Leu Glu Cys Gly Arg Ala Arg Val  
545 550 555 560

Leu Glu Gln Cys Ala Arg Cys Ile Gln Gly Gly Trp Arg Arg His Arg  
565 570 575

His Arg Glu Gln Glu Arg Gln Trp Arg Ala Val Met Leu Ile Gln Ala  
580 585 590

Ala Ile Arg Ser Trp Leu Thr Arg Lys His Ile Gln Arg Leu His Ala  
595 600 605

Ala Ala Thr Val Ile Lys Arg Ala Trp Gln Lys Trp Arg Ile Arg Met  
610 615 620

Ala Cys Leu Ala Ala Lys Glu Leu Asp Gly Val Glu Glu Lys His Phe  
625 630 635 640

Ser Gln Ala Pro Cys Ser Leu Ser Thr Ser Pro Leu Gln Thr Arg Leu  
645 650 655

Leu Glu Ala Ile Ile Arg Leu Trp Pro Leu Gly Leu Val Leu Ala Asn  
660 665 670

Thr Ala Met Gly Val Gly Ser Phe Gln Arg Lys Leu Val Val Trp Ala  
675 680 685

Cys Leu Gln Leu Pro Arg Gly Ser Pro Ser Ser Tyr Thr Val Gln Thr  
690 695 700

Ala Gln Asp Gln Ala Gly Val Thr Ser Ile Arg Ala Leu Pro Gln Gly  
705 710 715 720

Ser Ile Lys Phe His Cys Arg Lys Ser Pro Leu Arg Tyr Ala Asp Ile  
725 730 735

Cys Pro Glu Pro Ser Pro Tyr Ser Ile Thr Gly Phe Asn Gln Ile Leu  
740 745 750

Leu Glu Arg His Arg Leu Ile His Val Thr Ser Ser Ala Phe Thr Gly  
755 760 765

Leu Gly  
770

<210> 47  
<211> 7591  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(7591)

&lt;223&gt; myosin XVIII A MYO18A transcript variant 1

&lt;400&gt; 47

t ccat ccct g accggggccga ggct gct gga t gccgcgt ct ccgct t ct gc t gcct gccgg	60
gcgggct ccg gt ggccgcag caaagt gggg caccaaggcc ct gt gct aag cact cat aat	120
cct ct ggggg t gct acccct acaaacagca cccccacat gt t t aacct a at gaagaaag	180
acaaggacaa agat ggccgg cggaaggaga agaaggagaa aaaggagaaa aaggagcgga	240
t gt cagcggc agagct t cgg agcct ggagg agat gagcct gcgacgt ggc t t ct t caacc	300
t gaaccgct c ct ccaagcgt gaat ccaaga cgcgcct gga aat ct ccaac cccat cccca	360
t caagggt ggc cagcggct ct gacct gcacc t gact gacat t gact ccgat agt aaccggg	420
gcagcgt cat cct ggact cg ggccacct aa gt acagccag ct ccagcgat gacct caagg	480
gt gaggagg t agct t ccgt ggct cgggt gc t gcagcgggc agccaagt t c ggct cact gg	540
ccaagcagaa ct cacagat g at t gt caagc gct t t t cct t ct cccagcgt agccgggat g	600
agagcgcct c agaaacct cg acgccct cag agcact ct gc cgccccct cg ccacaggt gg	660
aggt gaggac t ct agaggga cagct ggt gc agcat cct gg cccaggcat c cct cgaccag	720
ggcaccgat c ccgagcccc t gagct agt ga ct aaaaagt t cccagt cgac ct gcgcct gc	780
ccccct ggt gccct gcc ccacct accc t ccgggagct ggagct gcaa cgacggccca	840
ct ggagact t t ggct t ct cc ct gcggcgca caacct gct ggat cggggc cccgagggcc	900
aggcct gt cg gcgt gt ggt c cact t t gct g agcct ggt gc aggcaccaag gacct ggccc	960
t ggggct ggt gccaggagat cgact ggt gg agat t aat gg gcacaat gt g gagagcaagt	1020
ccagggat ga gat t gt ggag at gat ccggc agt cagggga cagcgt gcgg ct caagggt gc	1080
agcccat t cc agagct cagc gagct cagca ggagct ggct gcggagcggc gagggacct c	1140
gcagggagcc at ccgat gcg aaaacagaag aacagat t gc agcagaagag gcct ggaat g	1200
agacggagaa ggt gt ggct g gt ccat aggg acggct t ct c act ggccagt caact caaat	1260
ct gaggagct caact t gcct gaggggaagg t gcgt gt gaa gct ggaccac gat ggggcca	1320
t cct ggat gt ggat gaggat gacgt t gaga aggct aat gc t ccct cct gc gaccgt ct gg	1380
aggat ct ggc ct cact ggt g t acct caat g agt ccagcgt cct gcacacc t t gcgccagc	1440
gct at ggcg t agcct gct g cacacgt at g ct ggccccag cct gct ggt t ct t ggcccc	1500
gt ggggcccc t gct gt gt ac t ct gagaagg t gat gcacat gt t caagggt t gt cggcggg	1560
aggacat ggc accccacat c t at gcagt gg cccagaccgc at acagggcg at gct gat ga	1620
gccgt cagga t cagt caat c at cct cct gg gcagt agt gg cagt ggcaag accaccagct	1680
gccagcat ct ggt gcagt ac ct ggccacca t cgcgggcat cagcgggaac aagggt gt t t t	1740
ct gt ggagaa gt ggcaggct ct gt acacc t cct ggaagc ct t t gggaac agccccacca	1800

N3027PCT\_sequ. list .txt

t cat t aat gg caat gccacc cgct t ct ccc agat cct ct c cct ggact t t gaccaagct g	1860
gccaggt ggc ct cagcct cc at t cagacaa t gct t ct gga gaagct gcgt gt ggct cggc	1920
gcccagccag t gaagccaca t t caacgt ct t ct act acct gct ggcct gt ggggat ggca	1980
ccct caggac agagct ccac ct caaccact t ggcagagaa caat gt gt t t gggat t gt gc	2040
cact ggccaa gcct gaggaa aagcagaagg cagct cagca gt t t agt aag ct gcaggcgg	2100
ccat gaaggt gct gggcat c t ccccgat g aacagaaggc ct gct ggt t c at t ct ggct g	2160
ccat ct acca cct gggggct gcgggagcca ccaaagaagc t gct gaagct gggcgcaagc	2220
agt t t gcccg ccat gagt gg gcccagaagg ct gcgt acct act gggct gc agcct ggagg	2280
agct gt cct c agccat ct t c aagcaccagc acaagggt gg caccct gcag cgct ccacct	2340
cct t ccgcca gggccccgag gagagt ggcc t gggagat gg gacaggcccc aaact gagt g	2400
cact ggagt g cct t gagggc at ggcggccg gcct ct acag cgagct ct t c accct t ct cg	2460
t ct ccct ggt gaat agggct ct caagt cca gccagcact c act ct gct cc at gat gat t g	2520
t cgacacccc gggct t ccag aaccct gagg aggggt ggggt c agcccgcgga gcct cct t t g	2580
aggagct gt g ccacaact ac acccaagacc ggct gcagag gct ct t ccac gagcgcacct	2640
t cgt gcagga gt t ggaaaga t acaaggagg agaacat cga gct ggcgt t t gacgact t gg	2700
aacccccgac ggat gact ct gt ggct gct g t ggaccaggc ct cccat cag t ccct ggt cc	2760
gct cgct ggc ccgcacagac gaggcgaggg gcct gct ct g gct at t ggaa gaggaggct c	2820
t ggt gccagg ggccagt gag gacacct cc t ggagcgct t t t ct cct at t at gggcccc	2880
aggaagggt ga caaaaaaggc caaagcccc t t ct gcacag cagcaaacca caccact t t c	2940
t cct gggcca cagccat ggc accaact ggg t agagt acaa t gt gact ggc t ggct gaact	3000
acaccaagca gaaccagcc acccagaat g cccccggct cct gcaggac t cccagaaaa	3060
aaat cat cag caacct gt t t ct gggccgcg caggcagt gc cacggt gct c t ct ggct cca	3120
t cgcgggcct ggagggcggc t cgagct gg cact gcgccg ggccaccagc at gcggaaaa	3180
cct t t accac aggcat ggcg gct gt caaaa agaagt cact gt gcat ccag at gaagct ac	3240
agggt ggacgc cct cat cgac accat caaga agt caaagct gcat t t t gt g cact gct t cc	3300
t gcct gt agc t gagggt gg gct ggggagc cccgt t ccgc ct cct cccgc cgagt cagca	3360
gcagcagt ga gct ggacct g ccct cgggag accact gcga ggct gggct c ct gcagct cg	3420
acgt gcccct gct ccgcacc cagct ccgcg gct cccgcct gct cgat gcc at gcgcat gt	3480
accgccaagg t t accct gac cacat ggt gt t t t ccgagt t ccgccgccgc t t t gat gt cc	3540
t ggccccgca cct gaccaag aaacacgggc gt aact acat cgt ggt ggat gaaaggcggg	3600
cagt ggagga gct gct ggag t gct t ggat c t ggagaagag cagct gct gc at gggcct ga	3660
gccgggt gt t ct t ccgggcg ggcacct t gg cacggct gga ggagcagcg gat gaacaaa	3720
ccagcaggaa cct aacct g t t ccaagcag cct gcagggg ct acct ggcc cgccagcact	3780
t caagaagag aaagat ccag gacct ggcca t t cgct gt gt acagaagaac at caagaaga	3840
acaaaggggt gaaggact gg ccct ggt gga agct t t t t ac cacagt gagg cccct cat cg	3900

N3027PCT\_sequ. list . . txt

aagt acagct	gt cagaggag	cagat ccgga	acaaagacga	ggagat ccag	cagct gcgga	3960
gcaagct cga	gaaggcggag	aaggagagga	acgagct gcg	gct caacagt	gaccggct gg	4020
agagccggat	ct cagagct g	acat cggagc	t gacagat ga	gcgt aacaca	ggagagt ccg	4080
cct cccagct	gct ggacgcg	gagacagcag	agaggct ccg	ggct gagaag	gagat gaagg	4140
aact gcagac	ccagt acgat	gcact gaaga	agcagat gga	ggt t at ggaa	at ggaggt ga	4200
t ggaggccccg	t ct cat ccgg	gcagcggaga	t caacgggga	agt ggat gat	gat gat gcag	4260
gt ggcgagt g	gcggct gaag	t at gagcggg	ct gt gcggga	ggt ggact t c	accaagaaac	4320
ggct ccagca	ggagt t t gag	gacaagct gg	aggt ggagca	gcagaacaag	aggcagct gg	4380
aacggcggct	cggggacct g	caggcagat a	gt gaggagag	t cagcgggct	ct gcagcagc	4440
t caagaagaa	gt gccagcga	ct gacggct g	agct gcaaga	caccaagct g	cacct ggagg	4500
gccagcaggt	ccgcaaccac	gaact ggaga	agaagcagag	gaggt t t gac	agt gagct ct	4560
cgcaggcgca	t gaggaggcc	cagcgggaga	agct gcagcg	ggagaagct g	cagcgggaga	4620
aggacat gct	cct cgct gag	gct t t cagcc	t gaagcagca	act agaggaa	aaagacat gg	4680
acat t gcagg	gt t caccag	aaggt t gt gt	ct ct agaggc	agagct ccag	gacat t t ct t	4740
cccaagagt c	caaggat gag	gct t ct ct gg	ccaaggt caa	gaaacagct c	cgggacct gg	4800
aggccaaagt	caaggat cag	gaagaagagc	t ggat gagca	ggcagggacc	at ccagat gc	4860
t ggaacaggc	caagct gcgt	ct ggagat gg	agat ggagcg	gat gagacag	acccat t ct a	4920
aggagat gga	gagt cgggat	gaggaggt gg	aggaggccccg	gcagt cgt gt	cagaagaagt	4980
t aaaacagat	ggaggt gcag	ct agaggaag	agt at gagga	caagcagaag	gt t ct gcgag	5040
agaagcggga	gct ggagggc	aagct cgcca	ccct cagcga	ccaggt gaac	cggcgggact	5100
t t gagt caga	gaagcggct g	cggaaggacc	t gaagcgcac	caaggccct g	ct ggcagat g	5160
cccagct cat	gct ggaccac	ct gaagaaca	gt gct cccag	caagcgagag	at t gcccagc	5220
t caagaacca	gct ggaggag	t cagagt t ca	cct gt gcggc	agccgt gaaa	gcacggaaag	5280
caat ggaggt	ggagat cgaa	gacct gcacc	t gcagat t ga	t gacat cgcc	aaagccaaga	5340
cagcgct gga	ggagcagct g	agccgcct t c	agcgt gagaa	gaat gagat c	cagaaccggc	5400
t ggaggaaga	t caggaagac	at gaacgaat	t gat gaagaa	gcacaaggct	gccgt ggct c	5460
aggct t cccg	ggacct ggct	cagat aaat g	at ct ccaagc	t cagct agaa	gaagccaaca	5520
aagagaagca	ggagct gcag	gagaagct ac	aagccct cca	gagccaggt g	gagt t cct gg	5580
agcagt ccat	ggt ggacaag	t ccct ggt ga	gcaggcagga	agct aagat a	cgggagct gg	5640
agacacgcct	ggagt t t gaa	aggacgcaag	t gaaacggct	ggagagcct g	gct agccgt c	5700
t caaggaaaa	cat ggagaag	ct gact gagg	agcgggat ca	gcgcat t gca	gccgagaacc	5760
gggagaagga	acagaacaag	cggct acaga	ggcagct ccg	ggacaccaag	gaggagat gg	5820
gcgagct t gc	caggaaggag	gccgaggcga	gccgcaagaa	gcacgaact g	gagat ggat c	5880
t agaaagcct	ggaggct gct	aaccagagcc	t gcaggct ga	cct aaagt t g	gcat t caagc	5940

N3027PCT\_sequ. list . . txt

gcat cgggga cct gcaggct gccat t gagg at gagat gga gagt gat gag aat gaggacc	6000
t cat caacag t t t gcaggac at ggt gacaa agt at cagaa aagaaagaat aaact t gagg	6060
gagact ct ga t gt ggact cg gagct ggagg accgt gt t ga cggggt caag t cct ggt t gt	6120
caaaaaacaa gggacct t cc aaggcagct t ct gat gat gg cagct t aaag agt t ccagcc	6180
ccaccagct a ct ggaagt cc ct t gcccct g at cggt caga t gat gagcac gaccct ct cg	6240
acaacacct c cagaccgca t act cccaca gt t at ct gag t gacagcgac acagaggcca	6300
agct gacgga gact aacgca t agcccaggg gagt ggt t gg cagccct ct c accccagggc	6360
ct gt ggct gc ct gggcacct ct cccaggaa gt ggt ggggc accggt ct cc cccacccgac	6420
t gct gat ct g cat gggaaac accct gacct t ct t ct gt ca ggggcact t t ccaggct at g	6480
gggt gt ct gat gt ct ccacgt ggaagaggt g ggggaaagag gagt t t ct ga agagaact t t	6540
t t gct cct ct gt ct caaaat gccagact ct t ggct t ct ac cct gt gt cac cgt gggcagt	6600
ggcaggt ggc ct ggcact gc at ggagccag cacgt t gacc t ccct ct cag ct ccct gct c	6660
agggacgggt g gacaggt t gc ct act gggac act ct aggt t gct ggggt cca t ggggaggat	6720
t gggggagga gaagcagt gc ct t ccct ct c gt gt ggggt g ggggct ct ct ct t ct t ggt g	6780
cct gct gt ct t t ct act t t t t aat t t aaat acccaacct c t ccat cacag ct gcat ccct	6840
gagagt ggga gggggct gt a gt ggt agct g gggct ccaa gaacgact cg ggaat gt cat	6900
ct ccat ct t c accct t caga gagcagt cct t t ct ct gt gc agct ggagac gct ggt gagg	6960
agagccgggt ccaggt t ct t aagaat gagg t gcggagggg ct ct ccggt g ct gct gggct	7020
gggt t gagca agcct acgca gacaagt gt g t gt gt ggacc at ccgcacct ccagccccc	7080
ccccaccct c t t t gt ct cag cgt gt t at gt gcaat gacct at t t aaggt a aacccat t cc	7140
aact acagca gt t cagggct gat ccaagca ct gcct ccct cct gct ct gt ccaggt ggt c	7200
t ggaccat aa act caact t g agaggaagg ct t ggggt t g aggact t gt g at cagaaaaa	7260
ct gaagat gg aagt t t t ggc cgggt gct cat t agacat gag t cct cact ct gt gt cct gag	7320
cccgt gt cat t ct t ccaacc t ccct gcccc cacacact t a t ccagacac aacacat gt	7380
gggt ct ggagg t ccagcccc caccct aaaa aggt t at ccc t gagaact cc accagact t g	7440
ggagcccaag t gcagt gcct ggt gct gct c ccat ct gccg cccccct t ct ct cct gcaat	7500
t ggt t t gt ac t cact gggct gt gct ct ccc ct gt t t accc gat gt at gga aat aaaggcc	7560
ct t t t cct cc t ggct gcgcc agt aaaaaa a	7591

<210> 48  
 <211> 2054  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1) . . (2054)  
 <223> myosin XVIII A MYO18A transcript variant 1

<400> 48

N3027PCT\_sequ.list.txt

```

Met Phe Asn Leu Met Lys Lys Asp Lys Asp Lys Asp Gly Gly Arg Lys
1      5      10      15

Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Arg Met Ser Ala Ala Glu
20      25      30

Leu Arg Ser Leu Glu Glu Met Ser Leu Arg Arg Gly Phe Phe Asn Leu
35      40      45

Asn Arg Ser Ser Lys Arg Glu Ser Lys Thr Arg Leu Glu Ile Ser Asn
50      55      60

Pro Ile Pro Ile Lys Val Ala Ser Gly Ser Asp Leu His Leu Thr Asp
65      70      75      80

Ile Asp Ser Asp Ser Asn Arg Gly Ser Val Ile Leu Asp Ser Gly His
85      90      95

Leu Ser Thr Ala Ser Ser Ser Asp Asp Leu Lys Gly Glu Glu Gly Ser
100      105      110

Phe Arg Gly Ser Val Leu Gn Arg Ala Ala Lys Phe Gly Ser Leu Ala
115      120      125

Lys Gn Asn Ser Gn Met Ile Val Lys Arg Phe Ser Phe Ser Gn Arg
130      135      140

Ser Arg Asp Glu Ser Ala Ser Glu Thr Ser Thr Pro Ser Glu His Ser
145      150      155      160

Ala Ala Pro Ser Pro Gn Val Glu Val Arg Thr Leu Glu Gly Gn Leu
165      170      175

Val Gn His Pro Gly Pro Gly Ile Pro Arg Pro Gly His Arg Ser Arg
180      185      190

Ala Pro Glu Leu Val Thr Lys Lys Phe Pro Val Asp Leu Arg Leu Pro
195      200      205

Pro Val Val Pro Leu Pro Pro Pro Thr Leu Arg Glu Leu Glu Leu Gn
210      215      220

Arg Arg Pro Thr Gly Asp Phe Gly Phe Ser Leu Arg Arg Thr Thr Met
225      230      235      240

Leu Asp Arg Gly Pro Glu Gly Gn Ala Cys Arg Arg Val Val His Phe
245      250      255

Ala Glu Pro Gly Ala Gly Thr Lys Asp Leu Ala Leu Gly Leu Val Pro
260      265      270

```

G y A s p A r g L e u V a l G u I l e A s n G y H i s A s n V a l G u S e r L y s S e r  
 275 280 285  
 A r g A s p G u I l e V a l G u M e t I l e A r g G n S e r G y A s p S e r V a l A r g  
 290 295 300  
 L e u L y s V a l G n P r o I l e P r o G u L e u S e r G u L e u S e r A r g S e r T r p  
 305 310 315 320  
 L e u A r g S e r G y G u G y P r o A r g A r g G u P r o S e r A s p A l a L y s T h r  
 325 330 335  
 G u G u G n I l e A l a A l a G u G u A l a T r p A s n G u T h r G u L y s V a l  
 340 345 350  
 T r p L e u V a l H i s A r g A s p G y P h e S e r L e u A l a S e r G n L e u L y s S e r  
 355 360 365  
 G u G u L e u A s n L e u P r o G u G y L y s V a l A r g V a l L y s L e u A s p H i s  
 370 375 380  
 A s p G y A l a I l e L e u A s p V a l A s p G u A s p A s p V a l G u L y s A l a A s n  
 385 390 395 400  
 A l a P r o S e r C y s A s p A r g L e u G u A s p L e u A l a S e r L e u V a l T y r L e u  
 405 410 415  
 A s n G u S e r S e r V a l L e u H i s T h r L e u A r g G n A r g T y r G y A l a S e r  
 420 425 430  
 L e u L e u H i s T h r T y r A l a G y P r o S e r L e u L e u V a l L e u G y P r o A r g  
 435 440 445  
 G y A l a P r o A l a V a l T y r S e r G u L y s V a l M e t H i s M e t P h e L y s G y  
 450 455 460  
 C y s A r g A r g G u A s p M e t A l a P r o H i s I l e T y r A l a V a l A l a G n T h r  
 465 470 475 480  
 A l a T y r A r g A l a M e t L e u M e t S e r A r g G n A s p G n S e r I l e I l e L e u  
 485 490 495  
 L e u G y S e r S e r G y S e r G y L y s T h r T h r S e r C y s G n H i s L e u V a l  
 500 505 510  
 G n T y r L e u A l a T h r I l e A l a G y I l e S e r G y A s n L y s V a l P h e S e r  
 515 520 525  
 V a l G u L y s T r p G n A l a L e u T y r T h r L e u L e u G u A l a P h e G y A s n  
 530 535 540  
 S e r P r o T h r I l e I l e A s n G y A s n A l a T h r A r g P h e S e r G n I l e L e u  
 Page 207

545                      550                      555                      560  
 Ser Leu Asp Phe Asp 565 Gln Ala Gly Gln Val 570 Ala Ser Ala Ser Ile Gln 575  
 Thr Met Leu Leu 580 Glu Lys Leu Arg Val 585 Ala Arg Arg Pro Ala Ser Glu 590  
 Ala Thr Phe 595 Asn Val Phe Tyr Tyr 600 Leu Leu Ala Cys Gly 605 Asp Gly Thr  
 Leu Arg 610 Thr Glu Leu His Leu 615 Asn His Leu Ala Glu 620 Asn Asn Val Phe  
 Gly Ile Val Pro Leu Ala 630 Lys Pro Glu Glu Lys 635 Gln Lys Ala Ala Gln 640  
 Gln Phe Ser Lys Leu 645 Gln Ala Ala Met Lys 650 Val Leu Gly Ile Ser Pro 655  
 Asp Glu Gln Lys 660 Ala Cys Trp Phe Ile 665 Leu Ala Ala Ile Tyr 670 His Leu  
 Gly Ala Ala 675 Gly Ala Thr Lys Glu 680 Ala Ala Glu Ala Gly 685 Arg Lys Gln  
 Phe Ala 690 Arg His Glu Trp Ala 695 Gln Lys Ala Ala Tyr 700 Leu Leu Gly Cys  
 Ser 705 Leu Glu Glu Leu Ser 710 Ser Ala Ile Phe Lys 715 His Gln His Lys Gly 720  
 Gly Thr Leu Gln Arg 725 Ser Thr Ser Phe Arg 730 Gln Gly Pro Glu Glu Ser 735  
 Gly Leu Gly Asp 740 Gly Thr Gly Pro Lys 745 Leu Ser Ala Leu Glu Cys Leu 750  
 Glu Gly Met 755 Ala Ala Gly Leu Tyr 760 Ser Glu Leu Phe Thr 765 Leu Leu Val  
 Ser Leu 770 Val Asn Arg Ala Leu 775 Lys Ser Ser Gln His 780 Ser Leu Cys Ser  
 Met Met Ile Val Asp Thr 790 Pro Gly Phe Gln Asn 795 Pro Glu Gln Gly Gly 800  
 Ser Ala Arg Gly Ala 805 Ser Phe Glu Glu Leu Cys His Asn Tyr Thr Gln 815  
 Asp Arg Leu Gln 820 Arg Leu Phe His Glu 825 Arg Thr Phe Val Gln 830 Glu Leu

N3027PCT\_sequ.list.txt

Glu Arg Tyr Lys Glu Glu Asn Ile Glu Leu Ala Phe Asp Asp Leu Glu  
 835 840 845  
 Pro Pro Thr Asp Asp Ser Val Ala Ala Val Asp Gln Ala Ser His Gln  
 850 855 860  
 Ser Leu Val Arg Ser Leu Ala Arg Thr Asp Glu Ala Arg Gly Leu Leu  
 865 870 875 880  
 Trp Leu Leu Glu Glu Glu Ala Leu Val Pro Gly Ala Ser Glu Asp Thr  
 885 890 895  
 Leu Leu Glu Arg Leu Phe Ser Tyr Tyr Gly Pro Gln Glu Gly Asp Lys  
 900 905 910  
 Lys Gly Gln Ser Pro Leu Leu His Ser Ser Lys Pro His His Phe Leu  
 915 920 925  
 Leu Gly His Ser His Gly Thr Asn Trp Val Glu Tyr Asn Val Thr Gly  
 930 935 940  
 Trp Leu Asn Tyr Thr Lys Gln Asn Pro Ala Thr Gln Asn Ala Pro Arg  
 945 950 955 960  
 Leu Leu Gln Asp Ser Gln Lys Lys Ile Ile Ser Asn Leu Phe Leu Gly  
 965 970 975  
 Arg Ala Gly Ser Ala Thr Val Leu Ser Gly Ser Ile Ala Gly Leu Glu  
 980 985 990  
 Gly Gly Ser Gln Leu Ala Leu Arg Arg Ala Thr Ser Met Arg Lys Thr  
 995 1000 1005  
 Phe Thr Thr Gly Met Ala Ala Val Lys Lys Lys Ser Leu Cys Ile  
 1010 1015 1020  
 Gln Met Lys Leu Gln Val Asp Ala Leu Ile Asp Thr Ile Lys Lys  
 1025 1030 1035  
 Ser Lys Leu His Phe Val His Cys Phe Leu Pro Val Ala Glu Gly  
 1040 1045 1050  
 Trp Ala Gly Glu Pro Arg Ser Ala Ser Ser Arg Arg Val Ser Ser  
 1055 1060 1065  
 Ser Ser Glu Leu Asp Leu Pro Ser Gly Asp His Cys Glu Ala Gly  
 1070 1075 1080  
 Leu Leu Gln Leu Asp Val Pro Leu Leu Arg Thr Gln Leu Arg Gly  
 1085 1090 1095

N3027PCT\_sequ.list.txt

Ser	Arg	Leu	Leu	Asp	Ala	Met	Arg	Met	Tyr	Arg	Gln	Gly	Tyr	Pro
	1100					1105					1110			
Asp	His	Met	Val	Phe	Ser	Glu	Phe	Arg	Arg	Arg	Phe	Asp	Val	Leu
	1115					1120					1125			
Ala	Pro	His	Leu	Thr	Lys	Lys	His	Gly	Arg	Asn	Tyr	Ile	Val	Val
	1130					1135					1140			
Asp	Glu	Arg	Arg	Ala	Val	Glu	Glu	Leu	Leu	Glu	Cys	Leu	Asp	Leu
	1145					1150					1155			
Glu	Lys	Ser	Ser	Cys	Cys	Met	Gly	Leu	Ser	Arg	Val	Phe	Phe	Arg
	1160					1165					1170			
Ala	Gly	Thr	Leu	Ala	Arg	Leu	Glu	Glu	Gln	Arg	Asp	Glu	Gln	Thr
	1175					1180					1185			
Ser	Arg	Asn	Leu	Thr	Leu	Phe	Gln	Ala	Ala	Cys	Arg	Gly	Tyr	Leu
	1190					1195					1200			
Ala	Arg	Gln	His	Phe	Lys	Lys	Arg	Lys	Ile	Gln	Asp	Leu	Ala	Ile
	1205					1210					1215			
Arg	Cys	Val	Gln	Lys	Asn	Ile	Lys	Lys	Asn	Lys	Gly	Val	Lys	Asp
	1220					1225					1230			
Trp	Pro	Trp	Trp	Lys	Leu	Phe	Thr	Thr	Val	Arg	Pro	Leu	Ile	Glu
	1235					1240					1245			
Val	Gln	Leu	Ser	Glu	Glu	Gln	Ile	Arg	Asn	Lys	Asp	Glu	Glu	Ile
	1250					1255					1260			
Gln	Gln	Leu	Arg	Ser	Lys	Leu	Glu	Lys	Ala	Glu	Lys	Glu	Arg	Asn
	1265					1270					1275			
Glu	Leu	Arg	Leu	Asn	Ser	Asp	Arg	Leu	Glu	Ser	Arg	Ile	Ser	Glu
	1280					1285					1290			
Leu	Thr	Ser	Glu	Leu	Thr	Asp	Glu	Arg	Asn	Thr	Gly	Glu	Ser	Ala
	1295					1300					1305			
Ser	Gln	Leu	Leu	Asp	Ala	Glu	Thr	Ala	Glu	Arg	Leu	Arg	Ala	Glu
	1310					1315					1320			
Lys	Glu	Met	Lys	Glu	Leu	Gln	Thr	Gln	Tyr	Asp	Ala	Leu	Lys	Lys
	1325					1330					1335			
Gln	Met	Glu	Val	Met	Glu	Met	Glu	Val	Met	Glu	Ala	Arg	Leu	Ile
	1340					1345					1350			

Arg Ala Ala Glu Ile Asn Gly 1355 1360 1365  
 Glu Val Asp Asp Asp Asp Ala Gly  
 Gly Glu Trp Arg Leu Lys Tyr 1370 1375 1380  
 Glu Val Asp  
 Phe Thr Lys Lys Arg Leu Gln 1385 1390 1395  
 Glu Phe Glu Asp Lys Leu Glu  
 Val Glu Gln Gln Asn Lys Arg 1400 1405 1410  
 Glu Leu Glu Arg Arg Leu Gly Asp  
 Leu Gln Ala Asp Ser Glu Glu 1415 1420 1425  
 Ser Gln Arg Ala Leu Gln Gln Leu  
 Lys Lys Lys Cys Gln Arg Leu 1430 1435 1440  
 Thr Ala Glu Leu Gln Asp Thr Lys  
 Leu His Leu Glu Gly Gln Gln 1445 1450 1455  
 Val Arg Asn His Glu Leu Glu Lys  
 Lys Gln Arg Arg Phe Asp Ser 1460 1465 1470  
 Glu Leu Ser Gln Ala His Glu Glu  
 Ala Gln Arg Glu Lys Leu Gln 1475 1480 1485  
 Arg Glu Lys Leu Gln Arg Glu Lys  
 Asp Met Leu Leu Ala Glu Ala 1490 1495 1500  
 Phe Ser Leu Lys Gln Gln Leu Glu  
 Glu Lys Asp Met Asp Ile Ala 1505 1510 1515  
 Gly Phe Thr Gln Lys Val Val Ser  
 Leu Glu Ala Glu Leu Gln Asp 1520 1525 1530  
 Ile Ser Ser Gln Glu Ser Lys Asp  
 Glu Ala Ser Leu Ala Lys Val 1535 1540 1545  
 Lys Lys Gln Leu Arg Asp Leu Glu  
 Ala Lys Val Lys Asp Gln Glu 1550 1555 1560  
 Glu Glu Leu Asp Glu Gln Ala Gly  
 Thr Ile Gln Met Leu Glu Gln 1565 1570 1575  
 Ala Lys Leu Arg Leu Glu Met Glu  
 Met Glu Arg Met Arg Gln Thr 1580 1585 1590  
 His Ser Lys Glu Met Glu Ser Arg  
 Asp Glu Glu Val Glu Glu Ala 1595 1600 1605  
 Arg Gln Ser Cys Gln Lys Lys Leu  
 Lys Gln Met Glu Val Gln Leu Glu Glu Glu Tyr Glu Asp Lys Gln

1610						1615						1620			
Lys	Val	Leu	Arg	Glu	Lys	Arg	Glu	Leu	Glu	Gly	Lys	Leu	Ala	Thr	
	1625					1630					1635				
Leu	Ser	Asp	Gln	Val	Asn	Arg	Arg	Asp	Phe	Glu	Ser	Glu	Lys	Arg	
	1640					1645					1650				
Leu	Arg	Lys	Asp	Leu	Lys	Arg	Thr	Lys	Ala	Leu	Leu	Ala	Asp	Ala	
	1655					1660					1665				
Gln	Leu	Met	Leu	Asp	His	Leu	Lys	Asn	Ser	Ala	Pro	Ser	Lys	Arg	
	1670					1675					1680				
Glu	Ile	Ala	Gln	Leu	Lys	Asn	Gln	Leu	Glu	Glu	Ser	Glu	Phe	Thr	
	1685					1690					1695				
Cys	Ala	Ala	Ala	Val	Lys	Ala	Arg	Lys	Ala	Met	Glu	Val	Glu	Ile	
	1700					1705					1710				
Glu	Asp	Leu	His	Leu	Gln	Ile	Asp	Asp	Ile	Ala	Lys	Ala	Lys	Thr	
	1715					1720					1725				
Ala	Leu	Glu	Glu	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Glu	Lys	Asn	Glu	
	1730					1735					1740				
Ile	Gln	Asn	Arg	Leu	Glu	Glu	Asp	Gln	Glu	Asp	Met	Asn	Glu	Leu	
	1745					1750					1755				
Met	Lys	Lys	His	Lys	Ala	Ala	Val	Ala	Gln	Ala	Ser	Arg	Asp	Leu	
	1760					1765					1770				
Ala	Gln	Ile	Asn	Asp	Leu	Gln	Ala	Gln	Leu	Glu	Glu	Ala	Asn	Lys	
	1775					1780					1785				
Glu	Lys	Gln	Glu	Leu	Gln	Glu	Lys	Leu	Gln	Ala	Leu	Gln	Ser	Gln	
	1790					1795					1800				
Val	Glu	Phe	Leu	Glu	Gln	Ser	Met	Val	Asp	Lys	Ser	Leu	Val	Ser	
	1805					1810					1815				
Arg	Gln	Glu	Ala	Lys	Ile	Arg	Glu	Leu	Glu	Thr	Arg	Leu	Glu	Phe	
	1820					1825					1830				
Glu	Arg	Thr	Gln	Val	Lys	Arg	Leu	Glu	Ser	Leu	Ala	Ser	Arg	Leu	
	1835					1840					1845				
Lys	Glu	Asn	Met	Glu	Lys	Leu	Thr	Glu	Glu	Arg	Asp	Gln	Arg	Ile	
	1850					1855					1860				
Ala	Ala	Glu	Asn	Arg	Glu	Lys	Glu	Gln	Asn	Lys	Arg	Leu	Gln	Arg	
	1865					1870					1875				

N3027PCT\_sequ.list.txt

Gln Leu Arg Asp Thr Lys Glu Glu Met Gly Glu Leu Ala Arg Lys  
1880 1885 1890

Glu Ala Glu Ala Ser Arg Lys Lys His Glu Leu Glu Met Asp Leu  
1895 1900 1905

Glu Ser Leu Glu Ala Ala Asn Gln Ser Leu Gln Ala Asp Leu Lys  
1910 1915 1920

Leu Ala Phe Lys Arg Ile Gly Asp Leu Gln Ala Ala Ile Glu Asp  
1925 1930 1935

Glu Met Glu Ser Asp Glu Asn Glu Asp Leu Ile Asn Ser Leu Gln  
1940 1945 1950

Asp Met Val Thr Lys Tyr Gln Lys Arg Lys Asn Lys Leu Glu Gly  
1955 1960 1965

Asp Ser Asp Val Asp Ser Glu Leu Glu Asp Arg Val Asp Gly Val  
1970 1975 1980

Lys Ser Trp Leu Ser Lys Asn Lys Gly Pro Ser Lys Ala Ala Ser  
1985 1990 1995

Asp Asp Gly Ser Leu Lys Ser Ser Ser Pro Thr Ser Tyr Trp Lys  
2000 2005 2010

Ser Leu Ala Pro Asp Arg Ser Asp Asp Glu His Asp Pro Leu Asp  
2015 2020 2025

Asn Thr Ser Arg Pro Arg Tyr Ser His Ser Tyr Leu Ser Asp Ser  
2030 2035 2040

Asp Thr Glu Ala Lys Leu Thr Glu Thr Asn Ala  
2045 2050

<210> 49  
<211> 7546  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(7546)  
<223> myosin XVIII A MYO18A transcript variant 2

<400> 49  
tccatccctg accgggccga ggctgctgga tggcgcgtct ccgcttctgc tgcctgccgg 60  
gcgggctccg gtggccgcag caaagtgggg caccaaggcc ctgtgct aag cactcat aat 120  
cctctggggg tgcctaccct acaaacagca cccccacat gtttaacct a atgaagaaag 180  
acaaggacaa agatggcggg cggaaggaga agaaggagaa aaaggagaaa aaggagcgga 240

N3027PCT\_sequ. list . . txt

t gt cagcggc	agagct t cgg	agcct ggagg	agat gacgct	gcgacgt ggc	t t ct t caacc	300
t gaaccgct c	ct ccaagcgt	gaat ccaaga	cgcgccct gga	aat ct ccaac	cccat cccca	360
t caaggt ggc	cagcggct ct	gacct gcacc	t gact gacat	t gact ccgat	agt aaccggg	420
gcagcgt cat	cct ggact cg	ggccacct aa	gt acagccag	ct ccagcgat	gacct caagg	480
gt gaggaggg	t agct t ccgt	ggct cgggt gc	t gcagcgggc	agccaagt t c	ggct cact gg	540
ccaagcagaa	ct cacagat g	at t gt caagc	gct t t t cct t	ct cccagcgt	agccgggat g	600
agagcgcct c	agaaacct cg	acgccct cag	agcact ct gc	cgccccct cg	ccacaggt gg	660
aggt gaggac	t ct agaggga	cagct ggt gc	agcat cct gg	cccaggcat c	cct cgaccag	720
ggcaccgat c	ccgagccccct	gagct agt ga	ct aaaaagt t	cccagt cgac	ct gcgcct gc	780
cccccggt ggt	gccccct gccc	ccacct accc	t ccgggagct	ggagct gcaa	cgacggccca	840
ct ggagact t	t ggct t ct cc	ct gcggcgca	caacct gct	ggat cggggc	cccgagggcc	900
aggcct gt cg	gcgt gt ggt c	cact t t gct g	agcct ggt gc	aggcaccaag	gacct ggccc	960
t ggggct ggt	gccaggagat	cgact ggt gg	agat t aat gg	gcacaat gt g	gagagcaagt	1020
ccagggat ga	gat t gt ggag	at gat ccggc	agt cagggga	cagcgt gcgg	ct caaggt gc	1080
agcccat t cc	agagct cagc	gagct cagca	ggagct ggct	gcggagcggc	gagggacct c	1140
gcagggagcc	at ccgat gcg	aaaacagaag	aacagat t gc	agcagaagag	gcct ggaat g	1200
agacggagaa	ggt gt ggct g	gt ccat aggg	acggct t ct c	act ggccagt	caact caaat	1260
ct gaggagct	caact t gcct	gaggggaagg	t gcgt gt gaa	gct ggaccac	gat ggggcca	1320
t cct ggat gt	ggat gaggat	gacgt t gaga	aggct aat gc	t ccct cct gc	gaccgt ct gg	1380
aggat ct ggc	ct cact ggt g	t acct caat g	agt ccagcgt	cct gcacacc	t t gcgccagc	1440
gct at ggcg	t agcct gct g	cacacgt at g	ct ggccccag	cct gct ggt t	ct t ggcccc	1500
gt ggggcccc	t gct gt gt ac	t ct gagaagg	t gat gcacat	gt t caagggt	t gt cggcggg	1560
aggacat ggc	accccat c	t at gcagt gg	cccagaccgc	at acagggcg	at gct gat ga	1620
gccgt cagga	t cagt caat c	at cct cct gg	gcagt agt gg	cagt ggcaag	accaccagct	1680
gccagcat ct	ggt gcagt ac	ct ggccacca	t cgcgggcat	cagcgggaac	aaggt gt t t t	1740
ct gt ggagaa	gt ggcaggct	ct gt acacc	t cct ggaagc	ct t t gggaac	agccccacca	1800
t cat t aat gg	caat gccacc	cgct t ct ccc	agat cct ct c	cct ggact t t	gaccaagct g	1860
gccaggt ggc	ct cagcct cc	at t cagacaa	t gct t ct gga	gaagct gcgt	gt ggct cggc	1920
gcccagccag	t gaagccaca	t t caacgt ct	t ct act acct	gct ggcct gt	ggggat ggca	1980
ccct caggac	agagct ccac	ct caaccact	t ggcagagaa	caat gt gt t t	gggat t gt gc	2040
cact ggccaa	gcct gaggaa	aagcagaagg	cagct cagca	gt t t agt aag	ct gcaggcgg	2100
ccat gaaggt	gct gggcat c	t cccccgat g	aacagaaggc	ct gct ggt t c	at t ct ggct g	2160
ccat ct acca	cct gggggct	gcgggagcca	caaagaagc	t gct gaagct	gggcgcaagc	2220
agt t t gccc	ccat gagt gg	gcccagaagg	ct gcgt acct	act gggct gc	agcct ggagg	2280

N3027PCT\_sequ. list.txt

agct gt cct c	agccat ct t c	aagcaccagc	acaagggg gg	caccct gcag	cgct ccacct	2340
cct t ccgcca	gggccccgag	gagagt ggcc	t gggagat gg	gacaggcccg	aaact gagt g	2400
cact ggagt g	cct t gagggc	at ggcgggcg	gcct ct acag	cgagct ct t c	accct t ct cg	2460
t ct ccct ggt	gaat agggct	ct caagt cca	gccagcact c	act ct gct cc	at gat gat t g	2520
t cgacacccc	gggct t ccag	aaccct gagc	agggt gggg c	agcccgcgga	gcct cct t t g	2580
aggagct gt g	ccacaact ac	acccaagacc	ggct gcagag	gct ct t ccac	gagcgcacct	2640
t cgt gcagga	gt t ggaaaga	t acaaggagg	agaacat cga	gct ggcgt t t	gacgact t gg	2700
aacccccgac	ggat gact ct	gt ggct gct g	t ggaccaggc	ct cccat cag	t ccct ggt cc	2760
gct cgct ggc	ccgcacagac	gaggcgaggg	gcct gct ct g	gct at t ggaa	gaggaggct c	2820
t ggt gccagg	ggccagt gag	gacaccct cc	t ggagcgcct	t t t ct cct at	t at ggcccc	2880
aggaaggt ga	caaaaaaggc	caaagccccc	t t ct gcacag	cagcaaacca	caccact t t c	2940
t cct gggcca	cagccat ggc	accaact ggg	t agagt acaa	t gt gact ggc	t ggct gaact	3000
acaccaagca	gaaccagacc	accagaat g	ccccccggct	cct gcaggac	t cccagaaaa	3060
aaat cat cag	caacct gt t t	ct gggcccg	caggcagt gc	cacggg gct c	t ct ggct cca	3120
t cgcgggcct	ggagggcggc	t cgagct gg	cact gcgccg	ggccaccagc	at gcggaaaa	3180
cct t t accac	aggcat ggcg	gct gt caaaa	agaagt cact	gt gcat ccag	at gaagct ac	3240
agggt ggacgc	cct cat cgac	accat caaga	agt caaagct	gcat t t t gt g	cact gct t cc	3300
t gcct gt agc	t gagggct gg	gct ggggagc	cccgt t ccgc	ct cct cccgc	cgagt cagca	3360
gcagcagt ga	gct ggacct g	ccct cgggag	accact gcga	ggct gggct c	ct gcagct cg	3420
acgt gcccct	gct ccgcacc	cagct ccgcg	gct cccgcct	gct cgat gcc	at gcgcat gt	3480
accgccaagg	t t accct gac	cacat ggt gt	t t t ccgagt t	ccgccgccgc	t t t gat gt cc	3540
t ggccccgca	cct gaccaag	aaacacgggc	gt aact acat	cgt ggt ggat	gaaaggcggg	3600
cagt ggagga	gct gct ggag	t gct t ggat c	t ggagaagag	cagct gct gc	at gggcct ga	3660
gccgggt gt t	ct t ccggg	ggcacct t gg	cacggct gga	ggagcagcgg	gat gaacaaa	3720
ccagcaggaa	cct aacct g	t t ccaagcag	cct gcagggg	ct acct ggcc	cgccagcact	3780
t caagaagag	aaagat ccag	gacct ggcca	t t cgct gt gt	acagaagaac	at caagaaga	3840
acaaaggggt	gaaggact gg	ccct ggt gga	agct t t t t ac	cacagt gagg	cccct cat cg	3900
aagt acagct	gt cagaggag	cagat ccgga	acaaagacga	ggagat ccag	cagct gcgga	3960
gcaagct cga	gaaggcgag	aaggagagga	acgagct gcg	gct caacagt	gaccggct gg	4020
agagccggat	ct cagagct g	acat cggagc	t gacagat ga	gcgt aacaca	ggagagt ccg	4080
cct cccagct	gct ggacgcg	gagacagcag	agaggct ccg	ggct gagaag	gagat gaagg	4140
aact gcagac	ccagt acgat	gcact gaaga	agcagat gga	ggg t at ggaa	at ggaggt ga	4200
t ggaggcccg	t ct cat ccgg	gcagcggaga	t caacgggga	agt ggat gat	gat gat gcag	4260
gt ggcgagt g	gcggct gaag	t at gagcggg	ct gt gcggga	ggg ggact t c	accaagaaac	4320
ggct ccagca	ggagt t t gag	gacaagct gg	aggt ggagca	gcagaacaag	aggcagct gg	4380

N3027PCT\_sequ. list . . txt

aacggcggct	cggggacct g	caggcagat a	gt gaggagag	t cagcgggct	ct gcagcagc	4440
t caagaagaa	gt gccagcga	ct gacggct g	agct gcaaga	caccaagct g	cacct ggagg	4500
gccagcaggt	ccgcaaccac	gaact ggaga	agaagcagag	gaggt t t gac	agt gagct ct	4560
cgcaggcgca	t gaggaggcc	cagcgggaga	agct gcagcg	ggagaagct g	cagcgggaga	4620
aggacat gct	cct cgct gag	gct t t cagcc	t gaagcagca	act agaggaa	aaagacat gg	4680
acat t gcagg	gt t caccag	aaggt t gt gt	ct ct agaggc	agagct ccag	gacat t t ct t	4740
cccaagagt c	caaggat gag	gct t ct ct gg	ccaaggt caa	gaaacagct c	cgggacct gg	4800
aggccaaagt	caaggat cag	gaagaagagc	t ggat gagca	ggcaggggacc	at ccagat gc	4860
t ggaacaggc	caagct gcgt	ct ggagat gg	agat ggagcg	gat gagacag	acccat t ct a	4920
aggagat gga	gagt cgggat	gaggaggt gg	aggaggcccg	gcagt cgt gt	cagaagaagt	4980
t aaaacagat	ggaggt gcag	ct agaggaag	agt at gagga	caagcagaag	gt t ct gcgag	5040
agaagcggga	gct ggagggc	aagct cgcca	ccct cagcga	ccaggt gaac	cggcgggact	5100
t t gagt caga	gaagcggct g	cggaaggacc	t gaagcgcac	caaggccct g	ct ggcagat g	5160
cccagct cat	gct ggaccac	ct gaagaaca	gt gct cccag	caagcgagag	at t gcccagc	5220
t caagaacca	gct ggaggag	t cagagt t ca	cct gt gcggc	agccgt gaaa	gcacggaaag	5280
caat ggaggt	ggagat cgaa	gacct gcacc	t gcagat t ga	t gacat cgcc	aaagccaaga	5340
cagcgct gga	ggagcagct g	agccgcct t c	agcgt gagaa	gaat gagat c	cagaaccggc	5400
t ggaggaaga	t caggaagac	at gaacgaat	t gat gaagaa	gcacaaggct	gccgt ggct c	5460
aggct t cccg	ggacct ggct	cagat aaat g	at ct ccaagc	t cagct agaa	gaagccaaca	5520
aagagaagca	ggagct gcag	gagaagct ac	aagccct cca	gagccaggt g	gagt t cct gg	5580
agcagt ccat	ggt ggacaag	t ccct ggt ga	gcaggcagga	agct aagat a	cgggagct gg	5640
agacacgcct	ggagt t t gaa	aggacgcaag	t gaaacggct	ggagagcct g	gct agccgt c	5700
t caaggaaaa	cat ggagaag	ct gact gagg	agcgggat ca	gcgcat t gca	gccgagaacc	5760
gggagaagga	acagaacaag	cggct acaga	ggcagct ccg	ggacaccaag	gaggagat gg	5820
gcgagct t gc	caggaaggag	gccgaggcga	gccgcaagaa	gcacgaact g	gagat ggat c	5880
t agaaagcct	ggaggct gct	aaccagagcc	t gcaggct ga	cct aaagt t g	gcat t caagc	5940
gcat cgggga	cct gcaggct	gccat t gagg	at gagat gga	gagt gat gag	aat gaggacc	6000
t cat caacag	t gaggggagac	t ct gat gt gg	act cggagct	ggaggaccgt	gt t gacgggg	6060
t caagt cct g	gt t gt caaaa	aacaaggac	ct t ccaaggc	agct t ct gat	gat ggcagct	6120
t aaagagt t c	cagccccacc	agct act gga	agt ccct t gc	ccct gat cgg	t cagat gat g	6180
agcacgaccc	t ct cgacaac	acct ccagac	cgcgat act c	ccacagt t at	ct gagt gaca	6240
gcgacacaga	ggccaagct g	acggagact a	acgcat agcc	caggggaggt g	gt t ggcagcc	6300
ct ct caccac	agggcct gt g	gct gcct ggg	cacct ct ccc	aggaagt ggt	ggggcaccgg	6360
t ct ccccccac	ccgact gct g	at ct gcat gg	gaaacaccct	gacct t ct t c	t gt caggggc	6420

N3027PCT\_sequ.list.txt

```

act t t ccagg ct at gggg gt ct gat gt ct c cacgt ggaag aggt ggggga aagaggagt t 6480
t ct gaagaga act t t t t gct cct ct gt ct c aaaat gccag act ct t ggct t ct accct gt 6540
gt caccgt gg gcagt ggcag gt ggcct ggc act gcat gga gccagcacgt t gacct ccct 6600
ct cagct ccc t gct cagggg cggt ggacag gt t gcct act gggacact ct aggt t gct gg 6660
gt ccat gggg aggat t gggg gaggagaagc agt gcct t cc ct ct cgt gt g gggg gggggc 6720
t ct ct ct t ct t ggt gcct gc t gt ct t t ct a ct t t t aat t t aaat accca acct ct ccat 6780
cacagct gca t ccct gagag t gggaggggg ct gt agt ggt agct ggggct cccaagaacg 6840
act cggaat gt cat ct cca t ct t caccct t cagagagca gt cct t t ct c t gt gcagct g 6900
gagacgt gg t gaggagagc cgggt ccagg t t ct t aagaa t gaggt gcgg aggggct ct c 6960
cggt gct gct gggct ggggt t gagcaagcct acgcagacaa gt gt gt gt gt ggacat ccg 7020
cacct ccagc ccccccacca cct ct t t gt ct cagcgt gt t at gt gcaat gacct at t t a 7080
aggt aaaccc at t ccaact a cagcagt t ca gggct gat cc aagcact gcc t ccct cct gc 7140
t ct gt ccagg t ggt ct ggac cat aaact ca act t gagagg gaaggct t gg ggt t gaggac 7200
t t gt gat cag aaaaact gaa gat ggaagt t t t ggccgggt g ct cat t agac at gagt cct c 7260
act ct gt gt c ct gagcccggt gt cat t ct t c caacct ccct gccccacac act t at ccca 7320
gacacaacac cat gt ggt ct ggaggt ccca gccccaccc t aaaaagggt t at ccct gaga 7380
act ccaccag act t gggagc ccaagt gcag t gcct ggt gc t gct cccat c t gccgcccc 7440
ct t ct ct cct gcaat t ggt t t gt act cact gggct gt gct ct cccct gt t t acccgat gt 7500
at ggaaat aa aggccct t t t cct cct ggct gcgccagt aa aaaaaa 7546

```

<210> 50  
 <211> 2039  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> M SC\_FEATURE  
 <222> (1)..(2039)  
 <223> myosin XVIII A MYO18A transcript variant 2

<400> 50

Met Phe Asn Leu Met Lys Lys Asp Lys Asp Lys Asp Gly Gly Arg Lys  
 1 5 10 15

Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Arg Met Ser Ala Ala Glu  
 20 25 30

Leu Arg Ser Leu Glu Glu Met Ser Leu Arg Arg Gly Phe Phe Asn Leu  
 35 40 45

Asn Arg Ser Ser Lys Arg Glu Ser Lys Thr Arg Leu Glu Ile Ser Asn  
 50 55 60

Pro Ile Pro Ile Lys Val Ala Ser Gly Ser Asp Leu His Leu Thr Asp  
 Page 217

```

65              70              75              80
I l e A s p S e r A s p S e r 85 A s n A r g G l y S e r V a l 90 I l e L e u A s p S e r G l y 95 H i s
L e u S e r T h r A l a 100 S e r S e r S e r A s p 105 L e u L y s G l y G l u G l u G l y S e r
P h e A r g G l y 115 S e r V a l L e u G l n A r g 120 A l a A l a L y s P h e G l y 125 S e r L e u A l a
L y s G l n 130 A s n S e r G l n M e t I l e 135 V a l L y s A r g P h e S e r 140 P h e S e r G l n A r g
S e r 145 A r g A s p G l u S e r A l a 150 S e r G l u T h r S e r T h r 155 P r o S e r G l u H i s S e r 160
A l a A l a P r o S e r P r o 165 G l n V a l G l u V a l A r g 170 T h r L e u G l u G l y G l n 175 L e u
V a l G l n H i s P r o 180 G l y P r o G l y I l e P r o 185 A r g P r o G l y H i s A r g 190 S e r A r g
A l a P r o G l u 195 L e u V a l T h r L y s L y s 200 P h e P r o V a l A s p L e u 205 A r g L e u P r o
P r o V a l 210 V a l P r o L e u P r o P r o 215 P r o T h r L e u A r g G l u 220 L e u G l u L e u G l n
A r g 225 A r g P r o T h r G l y A s p 230 P h e G l y P h e S e r L e u 235 A r g A r g T h r T h r M e t 240
L e u A s p A r g G l y P r o 245 G l u G l y G l n A l a C y s 250 A r g A r g V a l V a l H i s 255 P h e
A l a G l u P r o G l y 260 A l a G l y T h r L y s A s p 265 L e u A l a L e u G l y L e u 270 V a l P r o
G l y A s p A r g 275 L e u V a l G l u I l e A s n 280 G l y H i s A s n V a l G l u 285 S e r L y s S e r
A r g A s p 290 G l u I l e V a l G l u M e t 295 I l e A r g G l n S e r G l y 300 A s p S e r V a l A r g
L e u L y s V a l G l n P r o I l e 310 P r o G l u L e u S e r G l u 315 L e u S e r A r g S e r T r p 320
L e u A r g S e r G l y G l u 325 G l y P r o A r g A r g G l u 330 P r o S e r A s p A l a L y s 335 T h r
G l u G l u G l n I l e 340 A l a A l a G l u G l u A l a 345 T r p A s n G l u T h r G l u 350 L y s V a l

```

N3027PCT\_sequ.list.txt

Trp Leu Val His Arg Asp Gly Phe Ser Leu Ala Ser Gln Leu Lys Ser  
355 360 365

Glu Glu Leu Asn Leu Pro Glu Gly Lys Val Arg Val Lys Leu Asp His  
370 375 380

Asp Gly Ala Ile Leu Asp Val Asp Glu Asp Asp Val Glu Lys Ala Asn  
385 390 395 400

Ala Pro Ser Cys Asp Arg Leu Glu Asp Leu Ala Ser Leu Val Tyr Leu  
405 410 415

Asn Glu Ser Ser Val Leu His Thr Leu Arg Gln Arg Tyr Gly Ala Ser  
420 425 430

Leu Leu His Thr Tyr Ala Gly Pro Ser Leu Leu Val Leu Gly Pro Arg  
435 440 445

Gly Ala Pro Ala Val Tyr Ser Glu Lys Val Met His Met Phe Lys Gly  
450 455 460

Cys Arg Arg Glu Asp Met Ala Pro His Ile Tyr Ala Val Ala Gln Thr  
465 470 475 480

Ala Tyr Arg Ala Met Leu Met Ser Arg Gln Asp Gln Ser Ile Ile Leu  
485 490 495

Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Ser Cys Gln His Leu Val  
500 505 510

Gln Tyr Leu Ala Thr Ile Ala Gly Ile Ser Gly Asn Lys Val Phe Ser  
515 520 525

Val Glu Lys Trp Gln Ala Leu Tyr Thr Leu Leu Glu Ala Phe Gly Asn  
530 535 540

Ser Pro Thr Ile Ile Asn Gly Asn Ala Thr Arg Phe Ser Gln Ile Leu  
545 550 555 560

Ser Leu Asp Phe Asp Gln Ala Gly Gln Val Ala Ser Ala Ser Ile Gln  
565 570 575

Thr Met Leu Leu Glu Lys Leu Arg Val Ala Arg Arg Pro Ala Ser Glu  
580 585 590

Ala Thr Phe Asn Val Phe Tyr Tyr Leu Leu Ala Cys Gly Asp Gly Thr  
595 600 605

Leu Arg Thr Glu Leu His Leu Asn His Leu Ala Glu Asn Asn Val Phe  
610 615 620

N3027PCT\_sequ.list.txt

Gly Ile Val Pro Leu Ala Lys Pro Gu Gu Lys Gln Lys Ala Ala Gln  
 625 630 635 640  
 Gln Phe Ser Lys Leu Gln Ala Ala Met Lys Val Leu Gly Ile Ser Pro  
 645 650 655  
 Asp Gu Gln Lys Ala Cys Trp Phe Ile Leu Ala Ala Ile Tyr His Leu  
 660 665 670  
 Gly Ala Ala Gly Ala Thr Lys Gu Ala Ala Gu Ala Gly Arg Lys Gln  
 675 680 685  
 Phe Ala Arg His Gu Trp Ala Gln Lys Ala Ala Tyr Leu Leu Gly Cys  
 690 695 700  
 Ser Leu Gu Gu Leu Ser Ser Ala Ile Phe Lys His Gln His Lys Gly  
 705 710 715 720  
 Gly Thr Leu Gln Arg Ser Thr Ser Phe Arg Gln Gly Pro Gu Gu Ser  
 725 730 735  
 Gly Leu Gly Asp Gly Thr Gly Pro Lys Leu Ser Ala Leu Gu Cys Leu  
 740 745 750  
 Gu Gly Met Ala Ala Gly Leu Tyr Ser Gu Leu Phe Thr Leu Leu Val  
 755 760 765  
 Ser Leu Val Asn Arg Ala Leu Lys Ser Ser Gln His Ser Leu Cys Ser  
 770 775 780  
 Met Met Ile Val Asp Thr Pro Gly Phe Gln Asn Pro Gu Gln Gly Gly  
 785 790 795 800  
 Ser Ala Arg Gly Ala Ser Phe Gu Gu Leu Cys His Asn Tyr Thr Gln  
 805 810 815  
 Asp Arg Leu Gln Arg Leu Phe His Gu Arg Thr Phe Val Gln Gu Leu  
 820 825 830  
 Gu Arg Tyr Lys Gu Gu Asn Ile Gu Leu Ala Phe Asp Asp Leu Gu  
 835 840 845  
 Pro Pro Thr Asp Asp Ser Val Ala Ala Val Asp Gln Ala Ser His Gln  
 850 855 860  
 Ser Leu Val Arg Ser Leu Ala Arg Thr Asp Gu Ala Arg Gly Leu Leu  
 865 870 875 880  
 Trp Leu Leu Gu Gu Gu Ala Leu Val Pro Gly Ala Ser Gu Asp Thr  
 885 890 895

N3027PCT\_sequ.list.txt

Leu Leu G u Arg Leu Phe Ser Tyr Tyr G y Pro G n G u G y Asp Lys  
900 905 910

Lys G y G n Ser Pro Leu Leu H i s Ser Ser Lys Pro H i s H i s Phe Leu  
915 920 925

Leu G y H i s Ser H i s G y Thr Asn Trp Val G u Tyr Asn Val Thr G y  
930 935 940

Trp Leu Asn Tyr Thr Lys G n Asn Pro Al a Thr G n Asn Al a Pro Arg  
945 950 955 960

Leu Leu G n Asp Ser G n Lys Lys I l e I l e Ser Asn Leu Phe Leu G y  
965 970 975

Arg Al a G y Ser Al a Thr Val Leu Ser G y Ser I l e Al a G y Leu G u  
980 985 990

G y G y Ser G n Leu Al a Leu Arg Arg Al a Thr Ser Met Arg Lys Thr  
995 1000 1005

Phe Thr Thr G y Met Al a Al a Val Lys Lys Lys Ser Leu Oys I l e  
1010 1015 1020

G n Met Lys Leu G n Val Asp Al a Leu I l e Asp Thr I l e Lys Lys  
1025 1030 1035

Ser Lys Leu H i s Phe Val H i s Oys Phe Leu Pro Val Al a G u G y  
1040 1045 1050

Trp Al a G y G u Pro Arg Ser Al a Ser Ser Arg Arg Val Ser Ser  
1055 1060 1065

Ser Ser G u Leu Asp Leu Pro Ser G y Asp H i s Oys G u Al a G y  
1070 1075 1080

Leu Leu G n Leu Asp Val Pro Leu Leu Arg Thr G n Leu Arg G y  
1085 1090 1095

Ser Arg Leu Leu Asp Al a Met Arg Met Tyr Arg G n G y Tyr Pro  
1100 1105 1110

Asp H i s Met Val Phe Ser G u Phe Arg Arg Arg Phe Asp Val Leu  
1115 1120 1125

Al a Pro H i s Leu Thr Lys Lys H i s G y Arg Asn Tyr I l e Val Val  
1130 1135 1140

Asp G u Arg Arg Al a Val G u G u Leu Leu G u Oys Leu Asp Leu  
1145 1150 1155

G u Lys Ser Ser Oys Oys Met G y Leu Ser Arg Val Phe Phe Arg  
Page 221

Ala	Gly 1175	Thr	Leu	Ala	Arg	Leu 1180	Glu	Glu	Gln	Arg	Asp 1185	Glu	Gln	Thr
Ser	Arg 1190	Asn	Leu	Thr	Leu	Phe 1195	Gln	Ala	Ala	Cys	Arg 1200	Gly	Tyr	Leu
Ala	Arg 1205	Gln	His	Phe	Lys	Lys 1210	Arg	Lys	Ile	Gln	Asp 1215	Leu	Ala	Ile
Arg	Cys 1220	Val	Gln	Lys	Asn	Ile 1225	Lys	Lys	Asn	Lys	Gly 1230	Val	Lys	Asp
Trp	Pro 1235	Trp	Trp	Lys	Leu	Phe 1240	Thr	Thr	Val	Arg	Pro 1245	Leu	Ile	Glu
Val	Gln 1250	Leu	Ser	Glu	Glu	Gln 1255	Ile	Arg	Asn	Lys	Asp 1260	Glu	Glu	Ile
Gln	Gln 1265	Leu	Arg	Ser	Lys	Leu 1270	Glu	Lys	Ala	Glu	Lys 1275	Glu	Arg	Asn
Glu	Leu 1280	Arg	Leu	Asn	Ser	Asp 1285	Arg	Leu	Glu	Ser	Arg 1290	Ile	Ser	Glu
Leu	Thr 1295	Ser	Glu	Leu	Thr	Asp 1300	Glu	Arg	Asn	Thr	Gly 1305	Glu	Ser	Ala
Ser	Gln 1310	Leu	Leu	Asp	Ala	Glu 1315	Thr	Ala	Glu	Arg	Leu 1320	Arg	Ala	Glu
Lys	Glu 1325	Met	Lys	Glu	Leu	Gln 1330	Thr	Gln	Tyr	Asp	Ala 1335	Leu	Lys	Lys
Gln	Met 1340	Glu	Val	Met	Glu	Met 1345	Glu	Val	Met	Glu	Ala 1350	Arg	Leu	Ile
Arg	Ala 1355	Ala	Glu	Ile	Asn	Gly 1360	Glu	Val	Asp	Asp	Asp 1365	Asp	Ala	Gly
Gly	Glu 1370	Trp	Arg	Leu	Lys	Tyr 1375	Glu	Arg	Ala	Val	Arg 1380	Glu	Val	Asp
Phe	Thr 1385	Lys	Lys	Arg	Leu	Gln 1390	Gln	Glu	Phe	Glu	Asp 1395	Lys	Leu	Glu
Val	Glu 1400	Gln	Gln	Asn	Lys	Arg 1405	Gln	Leu	Glu	Arg	Arg 1410	Leu	Gly	Asp
Leu	Gln 1415	Ala	Asp	Ser	Glu	Glu 1420	Ser	Gln	Arg	Ala	Leu 1425	Gln	Gln	Leu

N3027PCT\_sequ.list.txt

Lys	Lys	Lys	Cys	Gln	Arg	Leu	Thr	Ala	Glu	Leu	Gln	Asp	Thr	Lys
	1430					1435					1440			
Leu	His	Leu	Glu	Gly	Gln	Gln	Val	Arg	Asn	His	Glu	Leu	Glu	Lys
	1445					1450					1455			
Lys	Gln	Arg	Arg	Phe	Asp	Ser	Glu	Leu	Ser	Gln	Ala	His	Glu	Glu
	1460					1465					1470			
Ala	Gln	Arg	Glu	Lys	Leu	Gln	Arg	Glu	Lys	Leu	Gln	Arg	Glu	Lys
	1475					1480					1485			
Asp	Met	Leu	Leu	Ala	Glu	Ala	Phe	Ser	Leu	Lys	Gln	Gln	Leu	Glu
	1490					1495					1500			
Glu	Lys	Asp	Met	Asp	Ile	Ala	Gly	Phe	Thr	Gln	Lys	Val	Val	Ser
	1505					1510					1515			
Leu	Glu	Ala	Glu	Leu	Gln	Asp	Ile	Ser	Ser	Gln	Glu	Ser	Lys	Asp
	1520					1525					1530			
Glu	Ala	Ser	Leu	Ala	Lys	Val	Lys	Lys	Gln	Leu	Arg	Asp	Leu	Glu
	1535					1540					1545			
Ala	Lys	Val	Lys	Asp	Gln	Glu	Glu	Glu	Leu	Asp	Glu	Gln	Ala	Gly
	1550					1555					1560			
Thr	Ile	Gln	Met	Leu	Glu	Gln	Ala	Lys	Leu	Arg	Leu	Glu	Met	Glu
	1565					1570					1575			
Met	Glu	Arg	Met	Arg	Gln	Thr	His	Ser	Lys	Glu	Met	Glu	Ser	Arg
	1580					1585					1590			
Asp	Glu	Glu	Val	Glu	Glu	Ala	Arg	Gln	Ser	Cys	Gln	Lys	Lys	Leu
	1595					1600					1605			
Lys	Gln	Met	Glu	Val	Gln	Leu	Glu	Glu	Glu	Tyr	Glu	Asp	Lys	Gln
	1610					1615					1620			
Lys	Val	Leu	Arg	Glu	Lys	Arg	Glu	Leu	Glu	Gly	Lys	Leu	Ala	Thr
	1625					1630					1635			
Leu	Ser	Asp	Gln	Val	Asn	Arg	Arg	Asp	Phe	Glu	Ser	Glu	Lys	Arg
	1640					1645					1650			
Leu	Arg	Lys	Asp	Leu	Lys	Arg	Thr	Lys	Ala	Leu	Leu	Ala	Asp	Ala
	1655					1660					1665			
Gln	Leu	Met	Leu	Asp	His	Leu	Lys	Asn	Ser	Ala	Pro	Ser	Lys	Arg
	1670					1675					1680			

N3027PCT\_sequ.list.txt

G u	I l e	A l a	G n	L e u	L y s	A s n	G n	L e u	G u	G u	S e r	G u	P h e	T h r
1685						1690					1695			
C y s	A l a	A l a	A l a	V a l	L y s	A l a	A r g	L y s	A l a	M e t	G u	V a l	G u	I l e
1700						1705					1710			
G u	A s p	L e u	H i s	L e u	G n	I l e	A s p	A s p	I l e	A l a	L y s	A l a	L y s	T h r
1715						1720					1725			
A l a	L e u	G u	G u	G n	L e u	S e r	A r g	L e u	G n	A r g	G u	L y s	A s n	G u
1730						1735					1740			
I l e	G n	A s n	A r g	L e u	G u	G u	A s p	G n	G u	A s p	M e t	A s n	G u	L e u
1745						1750					1755			
M e t	L y s	L y s	H i s	L y s	A l a	A l a	V a l	A l a	G n	A l a	S e r	A r g	A s p	L e u
1760						1765					1770			
A l a	G n	I l e	A s n	A s p	L e u	G n	A l a	G n	L e u	G u	G u	A l a	A s n	L y s
1775						1780					1785			
G u	L y s	G n	G u	L e u	G n	G u	L y s	L e u	G n	A l a	L e u	G n	S e r	G n
1790						1795					1800			
V a l	G u	P h e	L e u	G u	G n	S e r	M e t	V a l	A s p	L y s	S e r	L e u	V a l	S e r
1805						1810					1815			
A r g	G n	G u	A l a	L y s	I l e	A r g	G u	L e u	G u	T h r	A r g	L e u	G u	P h e
1820						1825					1830			
G u	A r g	T h r	G n	V a l	L y s	A r g	L e u	G u	S e r	L e u	A l a	S e r	A r g	L e u
1835						1840					1845			
L y s	G u	A s n	M e t	G u	L y s	L e u	T h r	G u	G u	A r g	A s p	G n	A r g	I l e
1850						1855					1860			
A l a	A l a	G u	A s n	A r g	G u	L y s	G u	G n	A s n	L y s	A r g	L e u	G n	A r g
1865						1870					1875			
G n	L e u	A r g	A s p	T h r	L y s	G u	G u	M e t	G y	G u	L e u	A l a	A r g	L y s
1880						1885					1890			
G u	A l a	G u	A l a	S e r	A r g	L y s	L y s	H i s	G u	L e u	G u	M e t	A s p	L e u
1895						1900					1905			
G u	S e r	L e u	G u	A l a	A l a	A s n	G n	S e r	L e u	G n	A l a	A s p	L e u	L y s
1910						1915					1920			
L e u	A l a	P h e	L y s	A r g	I l e	G y	A s p	L e u	G n	A l a	A l a	I l e	G u	A s p
1925						1930					1935			

N3027PCT\_sequ.list.txt

G u Met 1940 G u Ser Asp G u Asn 1945 G u Asp Leu Ile Asn 1950 Ser G u G y

Asp Ser 1955 Asp Val Asp Ser G u 1960 Leu G u Asp Arg Val 1965 Asp G y Val

Lys Ser 1970 Trp Leu Ser Lys Asn 1975 Lys G y Pro Ser Lys 1980 Ala Ala Ser

Asp Asp 1985 G y Ser Leu Lys Ser 1990 Ser Ser Pro Thr Ser 1995 Tyr Trp Lys

Ser Leu 2000 Ala Pro Asp Arg Ser 2005 Asp Asp G u His Asp 2010 Pro Leu Asp

Asn Thr 2015 Ser Arg Pro Arg Tyr 2020 Ser His Ser Tyr Leu 2025 Ser Asp Ser

Asp Thr 2030 G u Ala Lys Leu Thr 2035 G u Thr Asn Ala

<210> 51  
<211> 8565  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_feat ure  
<222> (1)..(8565)  
<223> myosi n XVI I I B MYO18B

<400> 51  
gggaagggat gtgtgtcggt gtgtgtggag aggggtgctcc ttcgctcctg ctttcccggc 60  
tcggtggggt cccttcgcgg ccacccgggg agacgtctta gacagt cgtg gttcctgtga 120  
tctgtgtcct ctttgcagaa gttctgtgtc catctcatgt gctgcgtgtg tctgtaaagc 180  
ctcat tccgt gctgtctggc aggaagctcc atctcatctc atcatctcac ggccctggca 240  
ctgcctcagc atggccatct catcacgcct cgccctgtgg gagcagaaga ttcggggaaga 300  
ggacaagagc cctccacat cctcgcccc tctcttttc tctgtcatcc cagggggctt 360  
cat taaagcaa ctggtccggg ggactgaaaa agaggccaag gaagcgagac agaggaagca 420  
gttagctgtc gcctctccag aacgagagat cccagaaat tccatcagcc aaccaacag 480  
caagtccagc agtggacca gatctggaag ccagcagatc tctcaggacg accagtcaag 540  
ctctcctggg agctcagaca ttctgggcaa ggagagcgag ggggtccgca gccccgacct 600  
tgagcagatg acaagcatca atggtgagaa ggcccaggag ctgggctcca gtgcgacacc 660  
aacaaaaag actgtcccct tcaagagggg cgtgaggagg ggtgatgtgt tgttgatggt 720  
ggccaagctg gacccggact cagccaagcc agagaagact catccccatg acgccccccc 780  
ttgcaagacc tctcccccg ccacagat ac tggaaaggaa aagaaagggg agacctctag 840  
gactccttgt ggctcccagg ccagcaccga gatcttggcc ccgaaagctg agaagacctg 900

N3027PCT\_sequ. list . . txt

gact gggggt	ct t ggggacc	caggccaagg	aact gt ggca	ct gaaaaaag	gcgaggaggg	960
t caaagcat a	gt ggggaagg	ggct t gggac	ccccagacc	acagagct ga	aagaggct ga	1020
gccccagggc	aaagacaggc	aggggaccag	gccccagcc	caagggcccg	gcgagggggt	1080
gcgaccaggg	aaagcagaga	aggaggggagc	agagcccaca	aacacggt gg	aaaaggggaa	1140
t gt ct ct aag	gacgt aggga	gt gaaggga	gcacgt aagg	ccccaaat cc	ct gggagaaa	1200
gt ggggaggt	t t cct gggaa	gaaggagt aa	gt gggacggt	ccccagaat a	agaaggacaa	1260
agaaggggt g	ct ct t aagt a	aggcagagaa	gacaggt gag	cct cagaccc	agat ggagaa	1320
gacaagccaa	gt gcaggggc	agt t ggggga	cgat ct gaga	at gggggaga	aagcaggt ga	1380
gct t cggagc	acgact ggga	aggcaggt ga	gt cct gggat	aagaaggaaa	agat ggggca	1440
accccaggggt	aagt ccggga	acgcaggt ga	agct cggagt	cagacagaga	agggt gt ga	1500
agccccaaag	gaggt gagca	caat ggt gga	gt cgccagca	gct cct ggga	agggaggct g	1560
gccaggaagc	cgt gggcagg	aagcagagga	gccct gct ca	agagcaggt g	at ggggct gg	1620
t gccct ggag	acagagct gg	aaggaccag	ccagcct gct	ct ggagaagg	at gcagaaag	1680
gcct cggat a	cggaaggaga	accaagacgg	gccagccccg	caggaggagg	gcaaaggagg	1740
ccagagcaga	gact cagacc	aggct cct ga	ggacagat gg	t at gaggcag	agaaagt ct g	1800
gct ggct cag	aaggat ggat	t t act ct t gc	t acggt gct a	aagccagat g	agggaacagc	1860
agacct gcca	gcaggaagg	t gagact t t g	gat t gat gct	gacaaaacca	t cact gaggt	1920
ggat gaggag	cat gt ccat c	gggccaacc	t cct gagct g	gaccaggt cg	aggacct ggc	1980
ct ct ct cat c	agt gt caacg	aat ccagt gt	cct gaacacg	ct t ct gcagc	gct acaaagc	2040
t cagct gct g	cacacct gca	cagggcct ga	t ct gat t gt c	ct ccagcccc	gggggccct c	2100
gggt gcct t ct	gcagggaagg	t gccaagg	ccgccgggat	ggcct gcct g	cccacat t gg	2160
ct ccat ggca	cagcgggcat	act gggcgct	gct gaaccag	cggagagacc	agagcat t gt	2220
ggccct gggc	t ggagt ggcg	ct gggaagac	cacct gct gt	gagcaggt cc	t ggaacacct	2280
gggt ggggat g	gcaggcagt g	t ggat ggcag	gggt ct cagt g	gagaagat cc	gagccacct t	2340
cact gt cct c	cgggcct t cg	gct ct gt gt c	cat ggcccac	agccgcagt g	ccacccggt t	2400
ct ccat ggt g	at gt cgct gg	act t caacgc	t acaggccgc	at cacagct g	ct cagct cca	2460
gacaat gct t	t t ggagaaga	gccgcgt ggc	acggcagccg	gaaggggaaa	gt aact t cct	2520
gggt t t t ct cc	cagat gct gg	ct ggat t gga	ct t ggat ct c	aggacggagc	t gaacct gca	2580
ccagat ggca	gat agcagct	cct t t ggcat	gggcgt gt gg	t ccaagcct g	aagat aaaca	2640
gaaggcggca	gct gcct t t g	cccagct cca	gggt gccat g	gagat gct cg	gcat ct caga	2700
gagcgagcag	cgggct gt t t	ggcgggt cct	ggcagccat c	t accacct gg	gt gcggcggg	2760
ggcct gcaaa	gt ggggt cgga	agcagt t cat	gaggt t t gag	t gggcaaact	acgcagct ga	2820
ggccct gggc	t gcgagt at g	aggagct gaa	cacggccacc	t t caagcacc	acct t cgaca	2880
gat cat ccag	caaat gacgt	t t gggccaag	ccgat ggggc	ct cgaggat g	aggaaaccag	2940

N3027PCT\_sequ. list.txt

ct cagggct c	aagat gacag	gagt ggact g	t gt ggagggg	at ggcct cgg	gcct gt acca	3000
ggaact ct t t	gcggct gt gg	t ct cact cat	caacagat cc	t t t t cct ccc	accat ct ct c	3060
cat ggcct cc	at cat ggt gg	t ggact ct cc	aggct t ccag	aacccccggc	accagggcaa	3120
ggaccgggcg	gccacct t t g	aggagct gt g	ccacaact ac	gccccat gage	gcct gcagct	3180
gct gt t ct ac	cagcggacct	t t gt ct ccac	gct acagcga	t at caagagg	aaggt gt t cc	3240
t gt gcagt t t	gacct cccgg	accct cccc	agggaccacc	gt ggct gt t g	t ggat caaaa	3300
t cct ct cag	gt ccgct t ac	cagct ggagg	aggt gcccag	gat gccagag	gcct t t t ct g	3360
ggc t t agat	gaggaagt cc	at gt agaggg	ct ccagt gac	agt gt ggt gc	t cgagcgt ct	3420
gt gt gct gct	t t cgagaaga	aaggagct gg	gact gaaggg	t cct ct gccc	t gcggacct g	3480
t gagcagccc	ct ccagt gt g	agat t t t cca	ccagt t ggga	t gggaccct g	t gcgggt acga	3540
cct cacgggc	t ggct ccaca	gagccaagcc	caacct ct cg	gccct ggat g	caccccaggt	3600
cct gcaccag	t caaaaagag	aggagct gcg	gagt ct at t c	caggccccggg	ccaagct gcc	3660
t cct gt gt gc	cgggct gt gg	caggcct gga	gggcacct cc	cagcaggccc	t gcagaggag	3720
ccgcat ggt g	aggaggacct	t t gccagcag	cct t gccgcg	gt gaggagga	aagccccgt g	3780
ct cccagat c	aagct gcaga	t ggat gcgct	gaccagcat g	at caaaaggt	cccggt gca	3840
ct t t at ccac	t gcct ggt ac	caaaccct gt	ggg gaaagc	aggagt gggc	aggaat ct cc	3900
accaccaccg	cagcct ggt a	gagacaagcc	t ggggcaggt	ggacct ct gg	ccct ggat at	3960
cccagcact g	agggt ccagc	t t gct ggg t	ccacat cct g	gaggct ct gc	gt ct gcat ag	4020
gacaggct at	gct gaccaca	t ggggct cac	t cgct t ccgc	cggcaat t cc	aggt gct gga	4080
cgct cact c	ct gaagaagc	t cat gt cgac	ct ccgagggg	at agat gaaa	ggaaggccgt	4140
ggaggagct c	ct ggagaccc	t ggat ct gga	aaagaaggcg	gt ggct gt gg	ggcacagcca	4200
agt t t t t ct c	aaggcaggt g	t gat ct ccag	gct t gagaag	cagcgagaga	agct ggt at c	4260
t cagagcat c	gt t ct ct t cc	aggcggct t g	caagggct t t	ct gt ct cgcc	aggaat t caa	4320
gaagct gaag	at t cgccgac	t ggct gcaca	gt gcat ccag	aagaat gt gg	ct gt gt t cct	4380
cgcagt caag	gact ggccat	ggg ggcagct	gct t ggt t cc	ct ccagcct c	t act t agt gc	4440
caccat t gga	act gagcagc	t ccgagccaa	ggaggaggag	ct t acaacgc	t aagacggaa	4500
gct agaaaaa	t cagagaagt	t gcggaat ga	act ccggcag	aacacagat c	t gct agaaag	4560
caagat t gct	gact t gacct	ct gacct t gc	cgat gagcgc	t t caaaggt g	at gt ggcct g	4620
ccaggt gct g	gagagt gagc	gggcagagcg	gct acaggcc	t t ccgggagg	t ccaggagct	4680
caagagcaag	cat gaacaag	t ccagaaaaa	act gggagat	gt gaat aaac	agt t ggaaga	4740
agcccagcag	aaaat t cagt	t gaat gact t	ggaaaggaat	cccact ggag	gagcagacga	4800
gt ggcagat g	cgct t cgact	gt gct cagat	ggagaacgag	t t cct cagaa	agcgt ct gca	4860
gcaat gcgag	gagaggct gg	act cggagct	gacagccagg	aaagagct gg	agcaaaagct	4920
t ggggagt t g	caaagt gct t	at gacggggc	caagaagat g	gct caccaac	t gaagaggaa	4980
gt gccaccat	ct t acct gt g	acct t gagga	t acct gcgt c	ct gct agaga	accaacaaag	5040

N3027PCT\_sequ. list . . txt

t cgaacccat	gagct ggaga	agaagcagaa	gaagt t t gac	ct gcagct gg	cccaggccct	5100
aggt gagt ca	gt gt t t gaga	aggggt ct ccg	t gagaaagt g	acccaggaga	acaccagt gt	5160
ccggt gggag	ct aggccagc	t t cagcagca	gct gaagcaa	aaggagcagg	aagcct caca	5220
gct gaagcag	caggt ggaga	t gct acagga	ccat aaacgg	gagct gct gg	ggg caccct c	5280
t ct gggggaa	aat t gcgt t g	ct ggct t gaa	ggagaggct c	t ggaagt t gg	aat ccagcgc	5340
cct t gagcaa	cagaaaat cc	agagccagca	ggaaaacacc	at caagcagc	t ggagcagct	5400
ccgccagcgg	t t t gagct gg	agat cgagcg	gat gaagcag	at gcaccaga	aggaccgt ga	5460
ggaccaggag	gaggaact gg	aggat gt ccg	t cagt cct gc	cagaagcggc	t t cat cagct	5520
ggaaat gcag	ct ggagcaag	agt at gaaga	gaagcagat g	gt cct ccat g	agaagcaaga	5580
t t t ggaaggc	t t gat cggaa	ccct ct gt ga	ccagat t ggc	cat cgggact	t t gat gt gga	5640
gaagcgcact t	cggagagacc	t caggaggac	acat gcact g	t t gt cagacg	t gcagct cct	5700
t ct gggcacc	at ggaggat g	gcaagacat c	agt cagcaag	gaggagct gg	agaaagt gca	5760
cagccagct g	gagcagagt g	aagccaagt g	t gaggaggcc	t t gaagacgc	agaaggt gct	5820
cacagcggac	ct ggagagca	t gcacagcga	gct ggagaac	at gacgcgga	acaagagcct	5880
ggg ggat gag	cagct gt aca	ggct gcagt t	t gagaaggcg	gacct cct ga	agcgcat cga	5940
t gaggaccag	gat gacct ga	at gagct gat	gcagaagcac	aaggacct ca	t t gct cagt c	6000
t gct gct gac	at t gggcaga	t ccaagaact	gcagct gcag	ct ggaggaag	ccaagaagga	6060
gaagcacaag	ct acaagaac	aact gcaggt	ggct cagat g	cgcat cgagt	acct ggaaca	6120
gt ccaccgt g	gat cgagcca	t cgt cagcag	gcaggaggcg	gt cat ct gt g	acct agagaa	6180
caagacagag	t t ccagaagg	t gcagat t aa	gagat t t gag	gt cct ggt ga	t ccggct t cg	6240
ggacagcct g	at caagat gg	gggaggagct	t t cacaggcg	gccacct ccg	agt cccagca	6300
gcgggagagc	agccagt act	accagcggcg	cct ggaagag	ct gaaggccg	acat ggaaga	6360
gct ggt gcag	cgggaggcag	aggccagccg	gcggt gcat g	gagct ggaga	agt acgt gga	6420
ggaact t gca	gcagt gaggc	aaacct cca	gacagacct g	gagacat cca	t t cggcggat	6480
t gccgacct g	caggct gcct	t ggaagaagt	ggcat ccagt	gacagt gat a	ct gagagt gt	6540
ccagacggca	gt ggat t gt g	gcagcagcgg	ccgaaaagag	at ggat aacg	t ct ccat cct	6600
cagct cccag	ccagagggca	gcct gcagt c	ct ggt t gage	t gt act ct gt	ccct ggccac	6660
agat act at g	aggact cct t	ct cgacagt c	agccaccagc	agccgcat cc	t cagccccag	6720
gat aaacgaa	gaggct gggg	acact gagag	gacctagt cg	gcat t ggcac	t gagcagagc	6780
ccggt ccacc	aat gt ccaca	gcaagacct c	aggagacaag	cct gt t t ct c	cccact t t gt	6840
ccgccggcaa	aagt act gt c	at t t t gggga	cggcgaagt g	ct t gccgt cc	agagaaagt c	6900
cacagagaga	t t agaacct g	ct t cct ct cc	cct ggct t ct	cggagt acaa	at acat cccc	6960
gct gt cgagg	gaaaagct gc	ccagt cct t c	agcggccct c	t cggagt t cg	t ggaagggct	7020
ccggaggaag	agagcccaga	gaggccaggg	gt ccacgct g	ggcct agagg	act ggcccac	7080

N3027PCT\_sequ.list.txt

tctccccattt taccagacga ctggggcctc cacactaagg aggggcaggg ctggcagtga 7140  
cgagggaaac ctctcgctga ggggtggggc aaagt cacco ctggaaatcg aaggggccgc 7200  
tgggtggtctc ttgaggtcca ccagcctcaa atgcatctct tcagacggtg ttgggggcac 7260  
aaccctactc cccgaaaagt cgaaaacca attcagttcc tgcgagtccc tcttagaatc 7320  
cagaccgagc atggggagaa aactgagctc tccgaccaca cccagggaca tgcgtgtgtc 7380  
gcccacactg cgtcctcgga ggcggtgtct ggagtcctct gtggacgatg cgggctgtcc 7440  
agaccttggg aaggagccgc ttgttttcca gaaccgccag tttgccacc tgatggagga 7500  
acctctaggc agtgacccat tcagctggaa actccaagc ctcgactacg aacgcaagac 7560  
caaagtggac ttcgatgact tcctcccagc tatccggaag cccagacac ctacctcctt 7620  
ggctggatca gccaaagggtg ggcaagacgg ttcacagcgt tcaagcatcc actttgaaac 7680  
ggaagaggct aaccgttcct ttctctcggg gatcaagacc attttgaaga agagcccgga 7740  
gccaaggag gatcccgctc acctgtctga ctcgtcctca tcctccggct ccatcgtgtc 7800  
cttcaaaagt gctgacagca tcaaaagtcg accaggaatc ccacgacttg cgggtgacgg 7860  
tggcgagcga acgtccccg agcggagaga gccagggacg gggaggaaaag acgacgatgt 7920  
tgcgagcat a atgaagaaat acctccagaa gtaggaaacca gttcagcctc cttgaagctg 7980  
cccttgaaga cttcccgact ctacaataac ttggagacag agagactggc caggcctccc 8040  
cgggtggccag agccagccag catggccacc ctcaagaggc gagatgagcc cacagaggca 8100  
tatcctgcgg ggatgctggg ctcccagtgt ggttggcctg aacaaaat aa agtgttgact 8160  
cctgggcatc tgtgccttct ctatggcctt gctacctggg attcagaga gttgatgggg 8220  
tgcagatagg ggtaggactg ttagaataga accaaccxaa actgtgtgt a gtttggggtg 8280  
tatacttcta tttctcttcc tacatgtcta catgcatga ccttcctcct cctcttcaact 8340  
tggccagttt cagctcactt cctccaggaa gtctttcctg atatatcaaa ctgaaacaaa 8400  
tgcctcctcct ccatgctccc ttaatccca tgcctgtcga ttatatcct ttgccaattc 8460  
atftctctat cctgtgtatg tataagtgtg tacaagcat t caagaaactg atgaatgatg 8520  
aatgaatgaa tgagccaaag aacaaataaa tgagcccaca cacco 8565

<210> 52  
<211> 2567  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(2567)  
<223> myosin XVIIIB MYO18B

<400> 52

Met Ala Ile Ser Ser Arg Leu Ala Leu Trp Glu Gln Lys Ile Arg Glu  
1 5 10 15

Glu Asp Lys Ser Pro Pro Pro Ser Ser Pro Pro Pro Leu Phe Ser Val  
Page 229

Ile Pro Gly Gly Phe Ile Lys Gln Leu Val Arg Gly Thr Glu Lys Glu  
 35 40 45  
 Ala Lys Glu Ala Arg Gln Arg Lys Gln Leu Ala Val Ala Ser Pro Glu  
 50 55 60  
 Arg Glu Ile Pro Glu Ile Ser Ile Ser Gln Pro Asn Ser Lys Ser Ser  
 65 70 75 80  
 Ser Gly Thr Arg Ser Gly Ser Gln Gln Ile Ser Gln Asp Asp Gln Ser  
 85 90 95  
 Ser Ser Pro Gly Ser Ser Asp Ile Leu Gly Lys Glu Ser Glu Gly Ser  
 100 105 110  
 Arg Ser Pro Asp Pro Glu Gln Met Thr Ser Ile Asn Gly Glu Lys Ala  
 115 120 125  
 Gln Glu Leu Gly Ser Ser Ala Thr Pro Thr Lys Lys Thr Val Pro Phe  
 130 135 140  
 Lys Arg Gly Val Arg Arg Gly Asp Val Leu Leu Met Val Ala Lys Leu  
 145 150 155 160  
 Asp Pro Asp Ser Ala Lys Pro Glu Lys Thr His Pro His Asp Ala Pro  
 165 170 175  
 Pro Cys Lys Thr Ser Pro Pro Ala Thr Asp Thr Gly Lys Glu Lys Lys  
 180 185 190  
 Gly Glu Thr Ser Arg Thr Pro Cys Gly Ser Gln Ala Ser Thr Glu Ile  
 195 200 205  
 Leu Ala Pro Lys Ala Glu Lys Thr Arg Thr Gly Gly Leu Gly Asp Pro  
 210 215 220  
 Gly Gln Gly Thr Val Ala Leu Lys Lys Gly Glu Glu Gly Gln Ser Ile  
 225 230 235 240  
 Val Gly Lys Gly Leu Gly Thr Pro Lys Thr Thr Glu Leu Lys Glu Ala  
 245 250 255  
 Glu Pro Gln Gly Lys Asp Arg Gln Gly Thr Arg Pro Gln Ala Gln Gly  
 260 265 270  
 Pro Gly Glu Gly Val Arg Pro Gly Lys Ala Glu Lys Glu Gly Ala Glu  
 275 280 285  
 Pro Thr Asn Thr Val Glu Lys Gly Asn Val Ser Lys Asp Val Gly Ser  
 290 295 300

N3027PCT\_sequ.list.txt

G u G y L y s H i s V a l A r g P r o G n I l e P r o G y A r g L y s T r p G y G y  
 305 310 315 320  
 P h e L e u G y A r g A r g S e r L y s T r p A s p G y P r o G n A s n L y s L y s A s p  
 325 330 335  
 L y s G u G y V a l L e u L e u S e r L y s A l a G u L y s T h r G y G u P r o G n  
 340 345 350  
 T h r G n M e t G u L y s T h r S e r G n V a l G n G y G u L e u G y A s p A s p  
 355 360 365  
 L e u A r g M e t G y G u L y s A l a G y G u L e u A r g S e r T h r T h r G y L y s  
 370 375 380  
 A l a G y G u S e r T r p A s p L y s L y s G u L y s M e t G y G n P r o G n G y  
 385 390 395 400  
 L y s S e r G y A s n A l a G y G u A l a A r g S e r G n T h r G u L y s G y C y s  
 405 410 415  
 G u A l a P r o L y s G u V a l S e r T h r M e t V a l G u S e r P r o A l a A l a P r o  
 420 425 430  
 G y L y s G y G y T r p P r o G y S e r A r g G y G n G u A l a G u G u P r o  
 435 440 445  
 C y s S e r A r g A l a G y A s p G y A l a G y A l a L e u G u T h r G u L e u G u  
 450 455 460  
 G y P r o S e r G n P r o A l a L e u G u L y s A s p A l a G u A r g P r o A r g I l e  
 465 470 475 480  
 A r g L y s G u A s n G n A s p G y P r o A l a P r o G n G u G u G y L y s G y  
 485 490 495  
 G y G n S e r A r g A s p S e r A s p G n A l a P r o G u A s p A r g T r p T y r G u  
 500 505 510  
 A l a G u L y s V a l T r p L e u A l a G n L y s A s p G y P h e T h r L e u A l a T h r  
 515 520 525  
 V a l L e u L y s P r o A s p G u G y T h r A l a A s p L e u P r o A l a G y A r g V a l  
 530 535 540  
 A r g L e u T r p I l e A s p A l a A s p L y s T h r I l e T h r G u V a l A s p G u G u  
 545 550 555 560  
 H i s V a l H i s A r g A l a A s n P r o P r o G u L e u A s p G n V a l G u A s p L e u  
 565 570 575

N3027PCT\_sequ.list.txt

Ala Ser Leu Ile Ser Val Asn Gu Ser Ser Val Leu Asn Thr Leu Leu  
580 585 590

Gln Arg Tyr Lys Ala Gln Leu Leu His Thr Cys Thr Gly Pro Asp Leu  
595 600 605

Ile Val Leu Gln Pro Arg Gly Pro Ser Val Pro Ser Ala Gly Lys Val  
610 615 620

Pro Lys Gly Arg Arg Asp Gly Leu Pro Ala His Ile Gly Ser Met Ala  
625 630 635 640

Gln Arg Ala Tyr Trp Ala Leu Leu Asn Gln Arg Arg Asp Gln Ser Ile  
645 650 655

Val Ala Leu Gly Trp Ser Gly Ala Gly Lys Thr Thr Cys Cys Glu Gln  
660 665 670

Val Leu Glu His Leu Val Gly Met Ala Gly Ser Val Asp Gly Arg Val  
675 680 685

Ser Val Glu Lys Ile Arg Ala Thr Phe Thr Val Leu Arg Ala Phe Gly  
690 695 700

Ser Val Ser Met Ala His Ser Arg Ser Ala Thr Arg Phe Ser Met Val  
705 710 715 720

Met Ser Leu Asp Phe Asn Ala Thr Gly Arg Ile Thr Ala Ala Gln Leu  
725 730 735

Gln Thr Met Leu Leu Glu Lys Ser Arg Val Ala Arg Gln Pro Glu Gly  
740 745 750

Glu Ser Asn Phe Leu Val Phe Ser Gln Met Leu Ala Gly Leu Asp Leu  
755 760 765

Asp Leu Arg Thr Glu Leu Asn Leu His Gln Met Ala Asp Ser Ser Ser  
770 775 780

Phe Gly Met Gly Val Trp Ser Lys Pro Glu Asp Lys Gln Lys Ala Ala  
785 790 795 800

Ala Ala Phe Ala Gln Leu Gln Gly Ala Met Glu Met Leu Gly Ile Ser  
805 810 815

Glu Ser Glu Gln Arg Ala Val Trp Arg Val Leu Ala Ala Ile Tyr His  
820 825 830

Leu Gly Ala Ala Gly Ala Cys Lys Val Gly Arg Lys Gln Phe Met Arg  
835 840 845

N3027PCT\_sequ.list.txt

Phe Glu Trp Ala Asn Tyr Ala Ala Glu Ala Leu Gly Cys Glu Tyr Glu  
 850 855 860  
 Glu Leu Asn Thr Ala Thr Phe Lys His His Leu Arg Gln Ile Ile Gln  
 865 870 875 880  
 Gln Met Thr Phe Gly Pro Ser Arg Trp Gly Leu Glu Asp Glu Glu Thr  
 885 890 895  
 Ser Ser Gly Leu Lys Met Thr Gly Val Asp Cys Val Glu Gly Met Ala  
 900 905 910  
 Ser Gly Leu Tyr Gln Glu Leu Phe Ala Ala Val Val Ser Leu Ile Asn  
 915 920 925  
 Arg Ser Phe Ser Ser His His Leu Ser Met Ala Ser Ile Met Val Val  
 930 935 940  
 Asp Ser Pro Gly Phe Gln Asn Pro Arg His Gln Gly Lys Asp Arg Ala  
 945 950 955 960  
 Ala Thr Phe Glu Glu Leu Cys His Asn Tyr Ala His Glu Arg Leu Gln  
 965 970 975  
 Leu Leu Phe Tyr Gln Arg Thr Phe Val Ser Thr Leu Gln Arg Tyr Gln  
 980 985 990  
 Glu Glu Gly Val Pro Val Gln Phe Asp Leu Pro Asp Pro Ser Pro Gly  
 995 1000 1005  
 Thr Thr Val Ala Val Val Asp Gln Asn Pro Ser Gln Val Arg Leu  
 1010 1015 1020  
 Pro Ala Gly Gly Gly Ala Gln Asp Ala Arg Gly Leu Phe Trp Val  
 1025 1030 1035  
 Leu Asp Glu Glu Val His Val Glu Gly Ser Ser Asp Ser Val Val  
 1040 1045 1050  
 Leu Glu Arg Leu Cys Ala Ala Phe Glu Lys Lys Gly Ala Gly Thr  
 1055 1060 1065  
 Glu Gly Ser Ser Ala Leu Arg Thr Cys Glu Gln Pro Leu Gln Cys  
 1070 1075 1080  
 Glu Ile Phe His Gln Leu Gly Trp Asp Pro Val Arg Tyr Asp Leu  
 1085 1090 1095  
 Thr Gly Trp Leu His Arg Ala Lys Pro Asn Leu Ser Ala Leu Asp  
 1100 1105 1110  
 Ala Pro Gln Val Leu His Gln Ser Lys Arg Glu Glu Leu Arg Ser

1115						1120						1125			
Leu	Phe	G n	Al a	Arg	Al a	Lys	Leu	Pro	Pro	Val	Cys	Arg	Al a	Val	
1130						1135					1140				
Al a	G y	Leu	G u	G y	Thr	Ser	G n	G n	Al a	Leu	G n	Arg	Ser	Arg	
1145						1150					1155				
Met	Val	Arg	Arg	Thr	Phe	Al a	Ser	Ser	Leu	Al a	Al a	Val	Arg	Arg	
1160						1165					1170				
Lys	Al a	Pro	Cys	Ser	G n	I le	Lys	Leu	G n	Met	Asp	Al a	Leu	Thr	
1175						1180					1185				
Ser	Met	I le	Lys	Arg	Ser	Arg	Leu	Hi s	Phe	I le	Hi s	Cys	Leu	Val	
1190						1195					1200				
Pro	Asn	Pro	Val	Val	G u	Ser	Arg	Ser	G y	G n	G u	Ser	Pro	Pro	
1205						1210					1215				
Pro	Pro	G n	Pro	G y	Arg	Asp	Lys	Pro	G y	Al a	G y	G y	Pro	Leu	
1220						1225					1230				
Al a	Leu	Asp	I le	Pro	Al a	Leu	Arg	Val	G n	Leu	Al a	G y	Phe	Hi s	
1235						1240					1245				
I le	Leu	G u	Al a	Leu	Arg	Leu	Hi s	Arg	Thr	G y	Tyr	Al a	Asp	Hi s	
1250						1255					1260				
Met	G y	Leu	Thr	Arg	Phe	Arg	Arg	G n	Phe	G n	Val	Leu	Asp	Al a	
1265						1270					1275				
Pro	Leu	Leu	Lys	Lys	Leu	Met	Ser	Thr	Ser	G u	G y	I le	Asp	G u	
1280						1285					1290				
Arg	Lys	Al a	Val	G u	G u	Leu	Leu	G u	Thr	Leu	Asp	Leu	G u	Lys	
1295						1300					1305				
Lys	Al a	Val	Al a	Val	G y	Hi s	Ser	G n	Val	Phe	Leu	Lys	Al a	G y	
1310						1315					1320				
Val	I le	Ser	Arg	Leu	G u	Lys	G n	Arg	G u	Lys	Leu	Val	Ser	G n	
1325						1330					1335				
Ser	I le	Val	Leu	Phe	G n	Al a	Al a	Cys	Lys	G y	Phe	Leu	Ser	Arg	
1340						1345					1350				
G n	G u	Phe	Lys	Lys	Leu	Lys	I le	Arg	Arg	Leu	Al a	Al a	G n	Cys	
1355						1360					1365				
I le	G n	Lys	Asn	Val	Al a	Val	Phe	Leu	Al a	Val	Lys	Asp	Trp	Pro	
1370						1375					1380				

N3027PCT\_sequ.list.txt

Trp	Trp	Gln	Leu	Leu	Gly	Ser	Leu	Gln	Pro	Leu	Leu	Ser	Ala	Thr
	1385					1390					1395			
Ile	Gly	Thr	Glu	Gln	Leu	Arg	Ala	Lys	Glu	Glu	Glu	Leu	Thr	Thr
	1400					1405					1410			
Leu	Arg	Arg	Lys	Leu	Glu	Lys	Ser	Glu	Lys	Leu	Arg	Asn	Glu	Leu
	1415					1420					1425			
Arg	Gln	Asn	Thr	Asp	Leu	Leu	Glu	Ser	Lys	Ile	Ala	Asp	Leu	Thr
	1430					1435					1440			
Ser	Asp	Leu	Ala	Asp	Glu	Arg	Phe	Lys	Gly	Asp	Val	Ala	Cys	Gln
	1445					1450					1455			
Val	Leu	Glu	Ser	Glu	Arg	Ala	Glu	Arg	Leu	Gln	Ala	Phe	Arg	Glu
	1460					1465					1470			
Val	Gln	Glu	Leu	Lys	Ser	Lys	His	Glu	Gln	Val	Gln	Lys	Lys	Leu
	1475					1480					1485			
Gly	Asp	Val	Asn	Lys	Gln	Leu	Glu	Glu	Ala	Gln	Gln	Lys	Ile	Gln
	1490					1495					1500			
Leu	Asn	Asp	Leu	Glu	Arg	Asn	Pro	Thr	Gly	Gly	Ala	Asp	Glu	Trp
	1505					1510					1515			
Gln	Met	Arg	Phe	Asp	Cys	Ala	Gln	Met	Glu	Asn	Glu	Phe	Leu	Arg
	1520					1525					1530			
Lys	Arg	Leu	Gln	Gln	Cys	Glu	Glu	Arg	Leu	Asp	Ser	Glu	Leu	Thr
	1535					1540					1545			
Ala	Arg	Lys	Glu	Leu	Glu	Gln	Lys	Leu	Gly	Glu	Leu	Gln	Ser	Ala
	1550					1555					1560			
Tyr	Asp	Gly	Ala	Lys	Lys	Met	Ala	His	Gln	Leu	Lys	Arg	Lys	Cys
	1565					1570					1575			
His	His	Leu	Thr	Cys	Asp	Leu	Glu	Asp	Thr	Cys	Val	Leu	Leu	Glu
	1580					1585					1590			
Asn	Gln	Gln	Ser	Arg	Asn	His	Glu	Leu	Glu	Lys	Lys	Gln	Lys	Lys
	1595					1600					1605			
Phe	Asp	Leu	Gln	Leu	Ala	Gln	Ala	Leu	Gly	Glu	Ser	Val	Phe	Glu
	1610					1615					1620			
Lys	Gly	Leu	Arg	Glu	Lys	Val	Thr	Gln	Glu	Asn	Thr	Ser	Val	Arg
	1625					1630					1635			

N3027PCT\_sequ.list.txt

Trp	Glu	Leu	Gly	Gln	Leu	Gln	Gln	Gln	Leu	Lys	Gln	Lys	Glu	Gln
	1640					1645					1650			
Glu	Ala	Ser	Gln	Leu	Lys	Gln	Gln	Val	Glu	Met	Leu	Gln	Asp	His
	1655					1660					1665			
Lys	Arg	Glu	Leu	Leu	Gly	Ser	Pro	Ser	Leu	Gly	Glu	Asn	Gly	Val
	1670					1675					1680			
Ala	Gly	Leu	Lys	Glu	Arg	Leu	Trp	Lys	Leu	Glu	Ser	Ser	Ala	Leu
	1685					1690					1695			
Glu	Gln	Gln	Lys	Ile	Gln	Ser	Gln	Gln	Glu	Asn	Thr	Ile	Lys	Gln
	1700					1705					1710			
Leu	Glu	Gln	Leu	Arg	Gln	Arg	Phe	Glu	Leu	Glu	Ile	Glu	Arg	Met
	1715					1720					1725			
Lys	Gln	Met	His	Gln	Lys	Asp	Arg	Glu	Asp	Gln	Glu	Glu	Glu	Leu
	1730					1735					1740			
Glu	Asp	Val	Arg	Gln	Ser	Cys	Gln	Lys	Arg	Leu	His	Gln	Leu	Glu
	1745					1750					1755			
Met	Gln	Leu	Glu	Gln	Glu	Tyr	Glu	Glu	Lys	Gln	Met	Val	Leu	His
	1760					1765					1770			
Glu	Lys	Gln	Asp	Leu	Glu	Gly	Leu	Ile	Gly	Thr	Leu	Cys	Asp	Gln
	1775					1780					1785			
Ile	Gly	His	Arg	Asp	Phe	Asp	Val	Glu	Lys	Arg	Leu	Arg	Arg	Asp
	1790					1795					1800			
Leu	Arg	Arg	Thr	His	Ala	Leu	Leu	Ser	Asp	Val	Gln	Leu	Leu	Leu
	1805					1810					1815			
Gly	Thr	Met	Glu	Asp	Gly	Lys	Thr	Ser	Val	Ser	Lys	Glu	Glu	Leu
	1820					1825					1830			
Glu	Lys	Val	His	Ser	Gln	Leu	Glu	Gln	Ser	Glu	Ala	Lys	Cys	Glu
	1835					1840					1845			
Glu	Ala	Leu	Lys	Thr	Gln	Lys	Val	Leu	Thr	Ala	Asp	Leu	Glu	Ser
	1850					1855					1860			
Met	His	Ser	Glu	Leu	Glu	Asn	Met	Thr	Arg	Asn	Lys	Ser	Leu	Val
	1865					1870					1875			
Asp	Glu	Gln	Leu	Tyr	Arg	Leu	Gln	Phe	Glu	Lys	Ala	Asp	Leu	Leu
	1880					1885					1890			

Lys Arg Ile Asp Glu Asp Gln Asp Asp Leu Asn Glu Leu Met Gln  
 1895 1900 1905  
 Lys His Lys Asp Leu Ile Ala Gln Ser Ala Ala Asp Ile Gly Gln  
 1910 1915 1920  
 Ile Gln Glu Leu Gln Leu Gln Leu Glu Glu Ala Lys Lys Glu Lys  
 1925 1930 1935  
 His Lys Leu Gln Glu Gln Leu Gln Val Ala Gln Met Arg Ile Glu  
 1940 1945 1950  
 Tyr Leu Glu Gln Ser Thr Val Asp Arg Ala Ile Val Ser Arg Gln  
 1955 1960 1965  
 Glu Ala Val Ile Cys Asp Leu Glu Asn Lys Thr Glu Phe Gln Lys  
 1970 1975 1980  
 Val Gln Ile Lys Arg Phe Glu Val Leu Val Ile Arg Leu Arg Asp  
 1985 1990 1995  
 Ser Leu Ile Lys Met Gly Glu Glu Leu Ser Gln Ala Ala Thr Ser  
 2000 2005 2010  
 Glu Ser Gln Gln Arg Glu Ser Ser Gln Tyr Tyr Gln Arg Arg Leu  
 2015 2020 2025  
 Glu Glu Leu Lys Ala Asp Met Glu Glu Leu Val Gln Arg Glu Ala  
 2030 2035 2040  
 Glu Ala Ser Arg Arg Cys Met Glu Leu Glu Lys Tyr Val Glu Glu  
 2045 2050 2055  
 Leu Ala Ala Val Arg Gln Thr Leu Gln Thr Asp Leu Glu Thr Ser  
 2060 2065 2070  
 Ile Arg Arg Ile Ala Asp Leu Gln Ala Ala Leu Glu Glu Val Ala  
 2075 2080 2085  
 Ser Ser Asp Ser Asp Thr Glu Ser Val Gln Thr Ala Val Asp Cys  
 2090 2095 2100  
 Gly Ser Ser Gly Arg Lys Glu Met Asp Asn Val Ser Ile Leu Ser  
 2105 2110 2115  
 Ser Gln Pro Glu Gly Ser Leu Gln Ser Trp Leu Ser Cys Thr Leu  
 2120 2125 2130  
 Ser Leu Ala Thr Asp Thr Met Arg Thr Pro Ser Arg Gln Ser Ala  
 2135 2140 2145  
 Thr Ser Ser Arg Ile Leu Ser Pro Arg Ile Asn Glu Glu Ala Gly

2150						2155						2160
Asp	Thr	Glu	Arg	Thr	Gln	Ser	Ala	Leu	Ala	Leu	Ser	Arg
2165						2170					2175	Ala Arg
Ser	Thr	Asn	Val	His	Ser	Lys	Thr	Ser	Gly	Asp	Lys	Pro
2180						2185					2190	Val Ser
Pro	His	Phe	Val	Arg	Arg	Gln	Lys	Tyr	Cys	His	Phe	Gly
2195						2200					2205	Asp Gly
Glu	Val	Leu	Ala	Val	Gln	Arg	Lys	Ser	Thr	Glu	Arg	Leu
2210						2215					2220	Glu Pro
Ala	Ser	Ser	Pro	Leu	Ala	Ser	Arg	Ser	Thr	Asn	Thr	Ser
2225						2230					2235	Pro Leu
Ser	Arg	Glu	Lys	Leu	Pro	Ser	Pro	Ser	Ala	Ala	Leu	Ser
2240						2245					2250	Glu Phe
Val	Glu	Gly	Leu	Arg	Arg	Lys	Arg	Ala	Gln	Arg	Gly	Gln
2255						2260					2265	Gly Ser
Thr	Leu	Gly	Leu	Glu	Asp	Trp	Pro	Thr	Leu	Pro	Ile	Tyr
2270						2275					2280	Gln Thr
Thr	Gly	Ala	Ser	Thr	Leu	Arg	Arg	Gly	Arg	Ala	Gly	Ser
2285						2290					2295	Asp Glu
Gly	Asn	Leu	Ser	Leu	Arg	Val	Gly	Ala	Lys	Ser	Pro	Leu
2300						2305					2310	Glu Ile
Glu	Gly	Ala	Ala	Gly	Gly	Leu	Leu	Arg	Ser	Thr	Ser	Leu
2315						2320					2325	Lys Cys
Ile	Ser	Ser	Asp	Gly	Val	Gly	Gly	Thr	Thr	Leu	Leu	Pro
2330						2335					2340	Glu Lys
Ser	Lys	Thr	Gln	Phe	Ser	Ser	Cys	Glu	Ser	Leu	Leu	Glu
2345						2350					2355	Ser Arg
Pro	Ser	Met	Gly	Arg	Lys	Leu	Ser	Ser	Pro	Thr	Thr	Pro
2360						2365					2370	Arg Asp
Met	Leu	Leu	Ser	Pro	Thr	Leu	Arg	Pro	Arg	Arg	Arg	Cys
2375						2380					2385	Leu Glu
Ser	Ser	Val	Asp	Asp	Ala	Gly	Cys	Pro	Asp	Leu	Gly	Lys
2390						2395					2400	Glu Pro
Leu	Val	Phe	Gln	Asn	Arg	Gln	Phe	Ala	His	Leu	Met	Glu
2405						2410					2415	Glu Pro

N3027PCT\_sequ.list.txt

Leu Gly Ser Asp Pro Phe Ser Trp Lys Leu Pro Ser Leu Asp Tyr  
 2420 2425 2430  
 Glu Arg Lys Thr Lys Val Asp Phe Asp Asp Phe Leu Pro Ala Ile  
 2435 2440 2445  
 Arg Lys Pro Gln Thr Pro Thr Ser Leu Ala Gly Ser Ala Lys Gly  
 2450 2455 2460  
 Gly Gln Asp Gly Ser Gln Arg Ser Ser Ile His Phe Glu Thr Glu  
 2465 2470 2475  
 Glu Ala Asn Arg Ser Phe Leu Ser Gly Ile Lys Thr Ile Leu Lys  
 2480 2485 2490  
 Lys Ser Pro Glu Pro Lys Glu Asp Pro Ala His Leu Ser Asp Ser  
 2495 2500 2505  
 Ser Ser Ser Ser Gly Ser Ile Val Ser Phe Lys Ser Ala Asp Ser  
 2510 2515 2520  
 Ile Lys Ser Arg Pro Gly Ile Pro Arg Leu Ala Gly Asp Gly Gly  
 2525 2530 2535  
 Glu Arg Thr Ser Pro Glu Arg Arg Glu Pro Gly Thr Gly Arg Lys  
 2540 2545 2550  
 Asp Asp Asp Val Ala Ser Ile Met Lys Lys Tyr Leu Gln Lys  
 2555 2560 2565

<210> 53  
 <211> 6038  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mi sc\_f eature  
 <222> (1)..(6038)  
 <223> myosin, heavy chain 1, skeletal muscle, adult (MYH1)

<400> 53  
 gtctctcctc ataaagcttc aagtctctgat ccactttaag gtcgcatctc tacgccaggg 60  
 tccttaactg ggctaccatc aataacctgc agccatgagt tccgactctg agatggccat 120  
 ttttggggag gctgctcctt tcctccgaaa gtctgaaagg gagcgaattg aagcccagaa 180  
 caagcctttt gatgccaaga catcagctctt tgtggaggac cct aaggagt cctttgtgaa 240  
 agcaacagtg cagagcaggg aaggggggaa ggtgacagct aagaccgaag ctggagctac 300  
 tgtaacagtg aaagatgacc aagctctccc catgaacctt cccaaat atg acaagatcga 360  
 ggacatggcc atgatgactc atctacacga gcctgctgtg ctgtacaacc tcaaagagcg 420  
 ctacgcagcc tggatgatct acacctactc aggcttgttc tgtgtcactg tcaaccct a 480

N3027PCT\_sequ. list . . txt

caagt ggt t g	ccagt gt at a	at gcagaggt	ggt gacagcc	t accgaggca	aaaagcgcca	540
ggaggcccca	ccccacat ct	t ct ccat ct c	t gacaat gcc	t at cagt t ca	t gct gact ga	600
t cgggagaat	cagt ct at ct	t gat caccgg	agaat ct ggc	gcagggaaga	ct gt gaacac	660
caagcgt gt c	at ccagt act	t t gcaacaat	t gcagt t act	ggggagaaga	agaaggaaga	720
agt t act t ct	ggcaaaat gc	aggggact ct	ggaagat caa	at cat cagt g	ccaaccccct	780
act ggaggcc	t t t ggcaacg	ccaagaccgt	gaggaat gac	aact cct ct c	gct t t ggt aa	840
at t cat cagg	at ccact t cg	gt accacagg	gaaact ggct	t ct gct gat a	t t gaaacat a	900
t ct t ct ggag	aagt ct agag	t t act t t cca	gct aaaggct	gaaagaagct	at cat at t t t	960
t t at cagat c	at gt ct aaca	agaagccaga	t ct aat t gaa	at gct cct ga	t caccacca	1020
cccat acgat	t at gcct t cg	t cagt caagg	ggagat caca	gt gccagca	t t gat gacca	1080
agaagagt t g	at ggct acag	at agt gccat	t gaaat t ct g	ggct t t act t	cagat gaaag	1140
agt gt ccat c	t at aagct ca	caggggct gt	gat gcat t at	gggaacat ga	aat t caagca	1200
aaagcagcgt	gaggagcaag	ct gagccaga	t ggcact gaa	gt t gct gaca	aggcagcct a	1260
t ct ccaaaat	ct gaact ct g	cagat ct gct	caaagccct c	t gct accct a	gggt caaggt	1320
cggcaat gag	t at gt cacca	aaggt caaac	t gt gcagcag	gt gt acaat g	cagt gggt gc	1380
t ct ggccaaa	gct gt ct acg	at aagat gt t	ct t gt ggat g	gt caccgcga	t caaccagca	1440
gct ggacacc	aagcagccca	ggcagt act t	cat t ggggt c	t t ggacat t g	ct ggct t t ga	1500
gat ct t t gat	t t caacagcc	t ggagcagct	gt gcat caac	t t caccaat g	agaaact gca	1560
acagt t t t t c	aaccaccaca	t gt t cgt gct	ggagcaggag	gagt acaaga	aggaaggcat	1620
t gagt ggacg	t t cat t gact	t t gggat gga	cct ggct gcc	t gcat cgagc	t cat cgagaa	1680
gcct at gggc	at ct t ct cca	t cct ggaaga	ggagt gcat g	t t ccccaagg	cgacagacac	1740
ct cct t caag	aacaagct gt	at gaacaaca	t ct t ggaaaa	t ccaat aact	t ccagaagcc	1800
caagcct gcc	aaaggcaagc	ct gaggccca	ct t ct ct t t g	at t cact at g	ct ggcaccgt	1860
ggact acaac	at t gccggct	ggct t gacaa	gaacaaggac	cccct gaat g	agact gt ggt	1920
ggggct gt ac	cagaagt ct g	caat gaagac	t ct ggct ct c	ct ct t t gt t g	gggcaacggg	1980
agcgggaagca	gaggct ggcg	gt ggaaagaa	aggt ggt aag	aagaagggt t	ct t ct t t cca	2040
gact gt gt ct	gct ct ct t ca	gggagaat t t	gaat aagct g	at gaccaact	t gaggagcac	2100
t cccccccac	t t t gt gcggt	gcat cat ccc	caat gaaact	aaaact cct g	gt gccat gga	2160
gcat gagct t	gt cct gcat c	agct gaggt g	t aacgggt gt g	ct ggaaggca	t ccgcat ct g	2220
caggaaaggc	t t cccaagca	gaat cct t t a	t gcagact t c	aaacagagat	acaaggt gt t	2280
aaat gcaagt	gct at ccct g	aaggacaat t	cat cgat agc	aagaaggct t	cagagaagct	2340
cct ggggt cc	at t gacat t g	accacacca	gt at aaat t t	ggg cacacca	aggt ct t t t t	2400
caaagct ggt	ct t ct ggggc	t cct agagga	gat gcgagat	gagaagct gg	cccagct gat	2460
t acccgaacc	caggccat gt	gcagagggt t	ct t ggcaaga	gt ggagt acc	agaaaat ggt	2520

N3027PCT\_sequ. list.txt

ggaaagaaga	gagtccatct	tctgcatcca	gtacaatgtc	cgtagccttca	tgaatgtgaa	2580
gcactggccc	tggatgaagc	tgtatttcaa	gatcaaacc	ctcctcaaaa	gtgcagagac	2640
agagaaggag	atggccaaca	tgaaggaaga	atttgagaaa	accaaagaag	agctggctaa	2700
gaccgaggca	aaaaggaaag	agctggaaga	aaaaatggtt	actctgatgc	aagaaaaaaaa	2760
tgacttgcaa	ctccaggttc	aagctgaagc	tgacagcttg	gctgatgcag	aggaaagggtg	2820
tgaccagcta	atcaaaacca	aaatccagct	agaagccaaa	atcaaagagg	tgactgagag	2880
agctgaggat	gaggaagaga	tcaatgctga	gctgacagcc	aagaagagga	aactggagga	2940
tgaatgttca	gaactcaaga	aagacattga	tgaccttgag	ctgacactgg	ccaagggttga	3000
gaaggagaaa	catgccacag	aaaacaaggt	gaaaaacctc	acagaagaga	tggcgggtct	3060
ggatgaaacc	attgctaagc	tgaccaagga	gaagaaggct	ctccaggagg	cccaccagca	3120
gacctggat	gacctgcagg	cagaggagga	caaagtcaac	accctgacca	aagctaaaat	3180
caaaacttgaa	caacaagtg	atgatcttga	aggatctttg	gaacaagaaa	agaaaatccg	3240
gatggatcta	gaaagagcaa	agagaaaact	agaggagagac	ctaaaattgg	ctcaagaatc	3300
cacaatggat	atagaaaatg	acaaacaaca	acttgatgaa	aagcttaaaa	agaaagagtt	3360
tgaaatgagc	ggtctgcaaa	gcaagattga	agatgaacaa	gcccttggta	tgcagctgca	3420
gaagaaaaatc	aaggagttac	aagcccgcat	tgaggagctg	gaggaggaaa	tcgaggcaga	3480
gcggggcctcc	cggggccaaag	cagagaagca	gcgctctgat	ctctcccggg	agctggagga	3540
gatcagcgag	aggctggaag	aagccgggtg	ggccacctca	gccagattg	agatgaacaa	3600
gaagcgggag	gctgagttcc	agaaaatgcg	caggggacctg	gaggaggcca	ccctacagca	3660
tgaagccacg	gcggccaccc	tgaggaagaa	gcatgcagat	agtgtggccg	agcttgggga	3720
gcagattgac	aacctgcagc	gagtgaagca	gaagctggag	aaggagaaga	gtgagatgaa	3780
gatggagatc	gatgaccttg	ctagtacat	ggagactgtc	tccaaagcca	agggaaacct	3840
tgaaaagatg	tgccgcgctc	tagaagatca	actgagtgaa	attaaacca	aggaagagga	3900
gcagcagcgg	ctgatcaatg	acctcacagc	acagagagcg	cgctgcaaa	cagaatcagg	3960
tgaatattca	cgccagctag	atgaaaagga	cacactagtt	tcacagctct	cgaggggcaa	4020
acaagccttt	acacaacaga	ttgaggaact	gaaaaggcaa	cttgaagagg	agataaaggc	4080
caagagtgcc	ctggcacatg	ccctgcagtc	ctccgccat	gactgtgacc	tgctgcggga	4140
acagtatgag	gaggagcagg	aagccaaggc	cgagctacag	agagcaatgt	ccaaggccaa	4200
cagtgaggtt	gcccagtgga	ggaccaaata	tgagacagat	gccatccagc	gcacagagga	4260
gctggaggag	gccaagaaga	agctggctca	gcgtctgcag	gatgctgagg	aacatgtaga	4320
agctgtgaat	gccaaatgtg	cttcccttga	gaagacgaag	cagaggctcc	agaatgaagt	4380
tgaggacctc	atgattgatg	ttgagaggac	aaatgctgcc	tgtgccgccc	tggacaaaaa	4440
gcaaaggaac	tttgataaga	tcctggcaga	atggaaacag	aagtgtgaag	aaactcatgc	4500
tgaacttgaa	gcttctcaaa	aggaatcccg	ctcactcagc	acagaactat	tttaagattaa	4560
gaatgcttat	gaggaatctt	tagaccaact	tgaaccttg	aaacgggaaa	ataagaattt	4620

N3027PCT\_sequ. list . . txt

gcaacaggag atttctgatc t cactgaaca gattgcagaa ggaggaaagc gcatccatga 4680  
 actggaaaaa ataaagaagc aagttgagca agaaaagct gaacttcagg ctgccttga 4740  
 ggaggcagag gcatctcttg aacatgaaga gggaaagatc ctgcgcatcc agcttgagt 4800  
 gaaccaagtc aagctgagg ttgataggaa aattgctgaa aaagatgagg aaattgacca 4860  
 gatgaagaga aaccacatt a gaatcgtgga gtccatgcag agcacactgg atgctgagat 4920  
 caggagcagg aatgatgcca ttaggctcaa gaagaagatg gagggagacc tcaatgaaat 4980  
 ggaaatccag ctgaaccatg ccaaccgcat ggctgctgag gccctgagga actataggaa 5040  
 caccaagcc atcctcaagg ataccagct ccacctggat gatgctctcc ggagccagga 5100  
 ggacctgaag gaacagctgg ctatggtgga gcgcagagcc aacctgctgc aggctgagat 5160  
 cgaggagctg cggggccactc tggaaacagac agagaggagc aggaaaatcg cagaacagga 5220  
 gctcctggat gccagtgagc gtgttcagct cctgcacacc cagaacacca gcctgatcaa 5280  
 caccaagaag aagctggaga cagacatttc ccaaatccag ggagagatgg aagacatcat 5340  
 ccaggaagcc cgcaatgcag aagagaaggc caagaaggcc atcactgatg ctgccatgat 5400  
 ggctgaggag ctgaagaagg aacaggacac cagcgcccat ctggagcgga tgaagaagaa 5460  
 cctggaacag acggtgaagg acctgcagca tcgtctggat gaggctgagc agctggccct 5520  
 gaagggtggg aagaagcaga tcagaaact ggaggccagg gtctcgtgaac ttgaaggatga 5580  
 agttgaaagt gaacagaagc gcaatgttga agctgtcaag ggtctacgca aacatgagag 5640  
 aaaagtgaag gaactcactt accaaactga ggaagaccgc aagaatattc tcaggctcca 5700  
 ggacctggtg gacaaactgc aagcaaaggt gaaatcctac aagagacaag ctgaagaagc 5760  
 ggaggaacaa tccaacgtca acctctccaa attccgcagg atccagcacg agctggagga 5820  
 ggccgaggaa cgggctgaca ttgctgagtc ccaggtcaac aagctgaggg tgaagagcag 5880  
 ggaggttcac aaaaaaatca taagtgaaga gtattttatc taactgctga aaggtgacca 5940  
 aagaaatgca caaaatgtga aaatctttgt cactccattt tgtacttatg acttttggag 6000  
 ataaaaatt tatctgccaa aaaaaaaaaa aaaaaaaa 6038

<210> 54  
 <211> 1939  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1939)  
 <223> myosin, heavy chain 1, skeletal muscle, adult (MYH1)  
 <400> 54

Met Ser Ser Asp Ser Glu Met Ala Ile Phe Gly Glu Ala Ala Pro Phe  
 1 5 10 15

Leu Arg Lys Ser Glu Arg Glu Arg Ile Glu Ala Gln Asn Lys Pro Phe  
 20 25 30

N3027PCT\_sequ.list.txt

Asp Ala Lys Thr Ser Val Phe Val Val Asp Pro Lys Glu Ser Phe Val  
 35 40 45  
 Lys Ala Thr Val Gln Ser Arg Glu Gly Gly Lys Val Thr Ala Lys Thr  
 50 55 60  
 Glu Ala Gly Ala Thr Val Thr Val Lys Asp Asp Gln Val Phe Pro Met  
 65 70 75 80  
 Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His  
 85 90 95  
 Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala  
 100 105 110  
 Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
 115 120 125  
 Tyr Lys Trp Leu Pro Val Tyr Asn Ala Glu Val Val Thr Ala Tyr Arg  
 130 135 140  
 Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
 145 150 155 160  
 Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu  
 165 170 175  
 Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val  
 180 185 190  
 Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu  
 195 200 205  
 Glu Val Thr Ser Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile  
 210 215 220  
 Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg  
 225 230 235 240  
 Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly  
 245 250 255  
 Thr Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu  
 260 265 270  
 Lys Ser Arg Val Thr Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile  
 275 280 285  
 Phe Tyr Gln Ile Met Ser Asn Lys Lys Pro Asp Leu Ile Glu Met Leu  
 290 295 300

N3027PCT\_sequ.list.txt

Leu Ile Thr Thr Asn Pro Tyr Asp Tyr Ala Phe Val Ser Gln Gly Glu  
 305 310 315 320  
 Ile Thr Val Pro Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp  
 325 330 335  
 Ser Ala Ile Glu Ile Leu Gly Phe Thr Ser Asp Glu Arg Val Ser Ile  
 340 345 350  
 Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys  
 355 360 365  
 Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala  
 370 375 380  
 Asp Lys Ala Ala Tyr Leu Gln Asn Leu Asn Ser Ala Asp Leu Leu Lys  
 385 390 395 400  
 Ala Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys  
 405 410 415  
 Gly Gln Thr Val Gln Gln Val Tyr Asn Ala Val Gly Ala Leu Ala Lys  
 420 425 430  
 Ala Val Tyr Asp Lys Met Phe Leu Trp Met Val Thr Arg Ile Asn Gln  
 435 440 445  
 Gln Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp  
 450 455 460  
 Ile Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys  
 465 470 475 480  
 Ile Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met  
 485 490 495  
 Phe Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr  
 500 505 510  
 Phe Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu  
 515 520 525  
 Lys Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro  
 530 535 540  
 Lys Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Glu Gln His Leu  
 545 550 555 560  
 Gly Lys Ser Asn Asn Phe Gln Lys Pro Lys Pro Ala Lys Gly Lys Pro  
 565 570 575

N3027PCT\_sequ.list.txt

G u A l a H i s P h e S e r L e u I l e H i s T y r A l a G y T h r V a l A s p T y r A s n  
 580 585 590  
 I l e A l a G y T r p L e u A s p L y s A s n L y s A s p P r o L e u A s n G l u T h r V a l  
 595 600 605  
 V a l G y L e u T y r G n L y s S e r A l a M e t L y s T h r L e u A l a L e u L e u P h e  
 610 615 620  
 V a l G y A l a T h r G y A l a G u A l a G u A l a G y G y G y L y s L y s G y  
 625 630 635 640  
 G y L y s L y s L y s G y S e r S e r P h e G n T h r V a l S e r A l a L e u P h e A r g  
 645 650 655  
 G u A s n L e u A s n L y s L e u M e t T h r A s n L e u A r g S e r T h r H i s P r o H i s  
 660 665 670  
 P h e V a l A r g C y s I l e I l e P r o A s n G u T h r L y s T h r P r o G y A l a M e t  
 675 680 685  
 G u H i s G u L e u V a l L e u H i s G n L e u A r g C y s A s n G y V a l L e u G u  
 690 695 700  
 G y I l e A r g I l e C y s A r g L y s G y P h e P r o S e r A r g I l e L e u T y r A l a  
 705 710 715 720  
 A s p P h e L y s G n A r g T y r L y s V a l L e u A s n A l a S e r A l a I l e P r o G u  
 725 730 735  
 G y G n P h e I l e A s p S e r L y s L y s A l a S e r G u L y s L e u L e u G y S e r  
 740 745 750  
 I l e A s p I l e A s p H i s T h r G n T y r L y s P h e G y H i s T h r L y s V a l P h e  
 755 760 765  
 P h e L y s A l a G y L e u L e u G y L e u L e u G u G u M e t A r g A s p G u L y s  
 770 775 780  
 L e u A l a G n L e u I l e T h r A r g T h r G n A l a M e t C y s A r g G y P h e L e u  
 785 790 795 800  
 A l a A r g V a l G u T y r G n L y s M e t V a l G u A r g A r g G u S e r I l e P h e  
 805 810 815  
 C y s I l e G n T y r A s n V a l A r g A l a P h e M e t A s n V a l L y s H i s T r p P r o  
 820 825 830  
 T r p M e t L y s L e u T y r P h e L y s I l e L y s P r o L e u L e u L y s S e r A l a G u  
 835 840 845  
 T h r G u L y s G u M e t A l a A s n M e t L y s G u G u P h e G u L y s T h r L y s  
 Page 245

850

855

860

G u G u L e u A l a L y s T h r G u A l a L y s A r g L y s G u L e u G u G u L y s  
865 870 875 880

M e t V a l T h r L e u M e t G n G u L y s A s n A s p L e u G n L e u G n V a l G n  
885 890 895

A l a G u A l a A s p S e r L e u A l a A s p A l a G u G u A r g O y s A s p G n L e u  
900 905 910

I l e L y s T h r L y s I l e G n L e u G u A l a L y s I l e L y s G u V a l T h r G u  
915 920 925

A r g A l a G u A s p G u G u G u I l e A s n A l a G u L e u T h r A l a L y s L y s  
930 935 940

A r g L y s L e u G u A s p G u O y s S e r G u L e u L y s L y s A s p I l e A s p A s p  
945 950 955 960

L e u G u L e u T h r L e u A l a L y s V a l G u L y s G u L y s H i s A l a T h r G u  
965 970 975

A s n L y s V a l L y s A s n L e u T h r G u G u M e t A l a G l y L e u A s p G u T h r  
980 985 990

I l e A l a L y s L e u T h r L y s G u L y s L y s A l a L e u G n G u A l a H i s G n  
995 1000 1005

G n T h r L e u A s p A s p L e u G n A l a G u G u A s p L y s V a l A s n T h r  
1010 1015 1020

L e u T h r L y s A l a L y s I l e L y s L e u G u G n G n V a l A s p A s p L e u  
1025 1030 1035

G u G l y S e r L e u G u G n G u L y s L y s I l e A r g M e t A s p L e u G u  
1040 1045 1050

A r g A l a L y s A r g L y s L e u G u G l y A s p L e u L y s L e u A l a G n G u  
1055 1060 1065

S e r T h r M e t A s p I l e G u A s n A s p L y s G n G n L e u A s p G u L y s  
1070 1075 1080

L e u L y s L y s L y s G u P h e G u M e t S e r G l y L e u G n S e r L y s I l e  
1085 1090 1095

G u A s p G u G n A l a L e u G l y M e t G n L e u G n L y s L y s I l e L y s  
1100 1105 1110

G u L e u G n A l a A r g I l e G u G u L e u G u G u G u I l e G u A l a  
1115 1120 1125

N3027PCT\_sequ.list.txt

G u A r g A l a S e r A r g A l a L y s A l a G u L y s G n A r g S e r A s p L e u  
 1130 1135 1140  
 S e r A r g G u L e u G u G u I l e S e r G u A r g L e u G u G u A l a G l y  
 1145 1150 1155  
 G l y A l a T h r S e r A l a G n I l e G u M e t A s n L y s L y s A r g G u A l a  
 1160 1165 1170  
 G u P h e G n L y s M e t A r g A r g A s p L e u G u G u A l a T h r L e u G n  
 1175 1180 1185  
 H i s G u A l a T h r A l a A l a T h r L e u A r g L y s L y s H i s A l a A s p S e r  
 1190 1195 1200  
 V a l A l a G u L e u G l y G u G n I l e A s p A s n L e u G n A r g V a l L y s  
 1205 1210 1215  
 G n L y s L e u G u L y s G u L y s S e r G u M e t L y s M e t G u I l e A s p  
 1220 1225 1230  
 A s p L e u A l a S e r A s n M e t G u T h r V a l S e r L y s A l a L y s G l y A s n  
 1235 1240 1245  
 L e u G u L y s M e t C y s A r g A l a L e u G u A s p G n L e u S e r G u I l e  
 1250 1255 1260  
 L y s T h r L y s G u G u G u G n G n A r g L e u I l e A s n A s p L e u T h r  
 1265 1270 1275  
 A l a G n A r g A l a A r g L e u G n T h r G u S e r G l y G u T y r S e r A r g  
 1280 1285 1290  
 G n L e u A s p G u L y s A s p T h r L e u V a l S e r G n L e u S e r A r g G l y  
 1295 1300 1305  
 L y s G n A l a P h e T h r G n G n I l e G u G u L e u L y s A r g G n L e u  
 1310 1315 1320  
 G u G u G u I l e L y s A l a L y s S e r A l a L e u A l a H i s A l a L e u G n  
 1325 1330 1335  
 S e r S e r A r g H i s A s p C y s A s p L e u L e u A r g G u G n T y r G u G u  
 1340 1345 1350  
 G u G n G u A l a L y s A l a G u L e u G n A r g A l a M e t S e r L y s A l a  
 1355 1360 1365  
 A s n S e r G u V a l A l a G n T r p A r g T h r L y s T y r G u T h r A s p A l a  
 1370 1375 1380

N3027PCT\_sequ.list.txt

I l e G n A r g T h r G u G u L e u G u G u A l a L y s L y s L y s L e u A l a  
1385 1390 1395

G n A r g L e u G n A s p A l a G u G u H i s V a l G u A l a V a l A s n A l a  
1400 1405 1410

L y s C y s A l a S e r L e u G u L y s T h r L y s G n A r g L e u G n A s n G u  
1415 1420 1425

V a l G u A s p L e u M e t I l e A s p V a l G u A r g T h r A s n A l a A l a C y s  
1430 1435 1440

A l a A l a L e u A s p L y s L y s G n A r g A s n P h e A s p L y s I l e L e u A l a  
1445 1450 1455

G u T r p L y s G n L y s C y s G u G u T h r H i s A l a G u L e u G u A l a  
1460 1465 1470

S e r G n L y s G u S e r A r g S e r L e u S e r T h r G u L e u P h e L y s I l e  
1475 1480 1485

L y s A s n A l a T y r G u G u S e r L e u A s p G n L e u G u T h r L e u L y s  
1490 1495 1500

A r g G u A s n L y s A s n L e u G n G n G u I l e S e r A s p L e u T h r G u  
1505 1510 1515

G n I l e A l a G u G y G y L y s A r g I l e H i s G u L e u G u L y s I l e  
1520 1525 1530

L y s L y s G n V a l G u G n G u L y s S e r G u L e u G n A l a A l a L e u  
1535 1540 1545

G u G u A l a G u A l a S e r L e u G u H i s G u G u G y L y s I l e L e u  
1550 1555 1560

A r g I l e G n L e u G u L e u A s n G n V a l L y s S e r G u V a l A s p A r g  
1565 1570 1575

L y s I l e A l a G u L y s A s p G u G u I l e A s p G n M e t L y s A r g A s n  
1580 1585 1590

H i s I l e A r g I l e V a l G u S e r M e t G n S e r T h r L e u A s p A l a G u  
1595 1600 1605

I l e A r g S e r A r g A s n A s p A l a I l e A r g L e u L y s L y s L y s M e t G u  
1610 1615 1620

G y A s p L e u A s n G u M e t G u I l e G n L e u A s n H i s A l a A s n A r g  
1625 1630 1635

Met Ala Ala Glu Ala Leu Arg Asn Tyr Arg Asn Thr Gln Ala Ile  
1640 1645 1650  
Leu Lys Asp Thr Gln Leu His Leu Asp Asp Ala Leu Arg Ser Gln  
1655 1660 1665  
Glu Asp Leu Lys Glu Gln Leu Ala Met Val Glu Arg Arg Ala Asn  
1670 1675 1680  
Leu Leu Gln Ala Glu Ile Glu Glu Leu Arg Ala Thr Leu Glu Gln  
1685 1690 1695  
Thr Glu Arg Ser Arg Lys Ile Ala Glu Gln Glu Leu Leu Asp Ala  
1700 1705 1710  
Ser Glu Arg Val Gln Leu Leu His Thr Gln Asn Thr Ser Leu Ile  
1715 1720 1725  
Asn Thr Lys Lys Lys Leu Glu Thr Asp Ile Ser Gln Ile Gln Gly  
1730 1735 1740  
Glu Met Glu Asp Ile Ile Gln Glu Ala Arg Asn Ala Glu Glu Lys  
1745 1750 1755  
Ala Lys Lys Ala Ile Thr Asp Ala Ala Met Met Ala Glu Glu Leu  
1760 1765 1770  
Lys Lys Glu Gln Asp Thr Ser Ala His Leu Glu Arg Met Lys Lys  
1775 1780 1785  
Asn Leu Glu Gln Thr Val Lys Asp Leu Gln His Arg Leu Asp Glu  
1790 1795 1800  
Ala Glu Gln Leu Ala Leu Lys Gly Gly Lys Lys Gln Ile Gln Lys  
1805 1810 1815  
Leu Glu Ala Arg Val Arg Glu Leu Glu Gly Glu Val Glu Ser Glu  
1820 1825 1830  
Gln Lys Arg Asn Val Glu Ala Val Lys Gly Leu Arg Lys His Glu  
1835 1840 1845  
Arg Lys Val Lys Glu Leu Thr Tyr Gln Thr Glu Glu Asp Arg Lys  
1850 1855 1860  
Asn Ile Leu Arg Leu Gln Asp Leu Val Asp Lys Leu Gln Ala Lys  
1865 1870 1875  
Val Lys Ser Tyr Lys Arg Gln Ala Glu Glu Ala Glu Glu Gln Ser  
1880 1885 1890  
Asn Val Asn Leu Ser Lys Phe Arg Arg Ile Gln His Glu Leu Glu

1895

1900

1905

Glu Ala Glu Glu Arg Ala Asp Ile Ala Glu Ser Gln Val Asn Lys  
 1910 1915 1920

Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Ile Ile Ser Glu  
 1925 1930 1935

Glu

<210> 55  
 <211> 6163  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(6163)  
 <223> myosin, heavy chain 2, skeletal muscle, adult (MYH2), transcript  
 variant 1

<400> 55  
 at agct at cc at at aaaaga gccct t ggaa t gaggct gac t cgt cct gct t t aaaaagct 60  
 ccaagaact g t ct cact ccc aggct acat c t t ct cact t g ct aacaagga cct ct gagt t 120  
 cagcagccat gagt t cagac t cagaat t gg ct gt t t t t gg ggaggct gct cct t t cct cc 180  
 gaaagt ct ga aagggagcgc at t gaggccc agaat aggcc ct t t gat gcc aaaacat ct g 240  
 t ct t t gt ggc ggagcccaaa gaat cct t t g t caaagggac cat ccagagc agagaaggag 300  
 gaaaagt gac ggt gaagact gaggaggag cgact ct gac agt gaaggat gat caggt ct 360  
 t ccccat gaa ccct cccaaa t at gacaaga t cgaggat at ggccat gat g act cat ct gc 420  
 at gagcct gc t gt gct gt ac aacct caaag aacgt t at gc agcct ggat g at ct acacct 480  
 at t caggt ct ct t ct gt gt c act gt caacc cct acaagt g gct gcct gt g t at aagcccg 540  
 aggt ggt gac agcct accga ggcaaaaagc gccaggaggc cccgccccac at ct t ct cca 600  
 t ct ct gacaa cgcct at cag t t cat gct ga ct gaccgaga gaat cagt ca at cct gat ca 660  
 ct ggagaat c t ggt gcaggg aagact gt ga acaccaagcg t gt cat ccag t act t t gcaa 720  
 caat t gcagt t act ggt gag aagaagaagg aagaaat t ac t t ct ggcaaa at acagggga 780  
 ct ct ggaaga t caaat cat c agt gccaac ccct act gga ggcct t t ggc aacgccaaga 840  
 ccgt gaggaa t gacaact cc t ct cgct t t g gt aaat t cat cagaat ccac t t t ggcact a 900  
 ct ggaaaact ggcct ct gct gat at t gaaa cat at ct gct agagaagt ct agagt t gt t t 960  
 t ccagct t aa ggct gagaga agt t at cat a t t t t t acca gat t acat cg aat aagaaac 1020  
 cagaact t at t gaaat gct t ct gat t acca cgaacccat a t gat t accca t t t gt cagt c 1080  
 aaggggagat cagt gt ggcc agcat cgat g at caggaaga act gat ggcc acagat agt g 1140  
 ct at t gat at t t t gggct t t act aat gaag aaaaggt ct c cat t t acaag ct cacggggg 1200  
 ct gt gat gca t t at gggaac ct aaaat t t a agcaaaagca gcgt gaggag caagcagagc 1260

N3027PCT\_sequ. list . . txt

cagat ggcac	agaagt t gct	gacaaggcgg	cct acct cca	gagt ct gaac	t ct gcagat c	1320
t gct caaagc	t ct ct gct ac	cccaggggt ca	aggt cggcaa	t gagt at gt c	accaaaggcc	1380
agact gt aga	acaggt gt cc	aacgcagt ag	gt gct ct ggc	caaagccgt c	t acgagaaga	1440
t gt t cct gt g	gat ggt t gcc	cgcat caacc	agcagct gga	caccaagcag	cccaggcagt	1500
act t cat cgg	ggt ct t ggac	at t gct ggt t	t t gagat t t t	t gat t t caac	agcct ggagc	1560
agct gt gcat	caact t cacc	aat gaaaaac	t gcaacagt t	t t t caaccac	cacat gt t cg	1620
t gct ggagca	ggaggagt ac	aagaaggaag	gcat cgagt g	gacgt t cat c	gact t cggga	1680
t ggacct ggc	t gcct gcat c	gagct cat cg	agaagcct at	gggcat ct t c	t ccat cct gg	1740
aagaggagt g	cat gt t ccct	aaggcaacag	acacct cct t	caagaacaag	ct gt at gacc	1800
agcacct ggg	caagt ct gcc	aact t ccaga	agcccaaggt	ggt caaaggc	aaggccgagg	1860
cccact t cgc	t ct gat t cac	t at gct ggt g	t t gt ggact a	caacat t act	ggct ggct gg	1920
agaagaacaa	ggacccccct g	aat gagaccg	t ggt t ggact	gt accagaag	t ct gcaat ga	1980
aaact ct agc	t cagct ct t c	t ct ggggct c	aaact gct ga	aggagagggga	gct ggt ggag	2040
gggccaagaa	aggt ggt aag	aagaagggct	ct t ct t t cca	gacagt gt ct	gccct t t t ca	2100
gagagaat t t	gaacaagct g	at gaccaacc	t caggagt ac	ccat cct cac	t t t gt gaggt	2160
gt at cat ccc	caat gagaca	aaaact cct g	gt gccat gga	gcat gagct t	gt cct ccacc	2220
agct gaggt g	t aacggt gt g	ct ggaaggca	t ccgcat ct g	t aggaaagga	t t t ccaagca	2280
gaat cct t t a	t gcagact t c	aaacagagat	acaaggt at t	aaat gcaagt	gcaat ccct g	2340
aagggaat t	cat t gat agc	aagaaggcct	ct gagaagct	cct t gcat cc	at cgacat t g	2400
accacaccca	gt at aaat t t	gggcacacca	aggt ct t t t t	caaagct ggt	ct t ct ggggc	2460
t cct agagga	gat gcgagat	gacaagct gg	cccagct gat	t acccgaacc	caggccaggt	2520
gcagaggggt t	ct t ggcaaga	gt ggagt acc	agaggat ggt	ggagagaagg	gaggccat ct	2580
t ct gt at cca	gt acaat at c	agat cct t ca	t gaat gt caa	gcact ggccc	t ggat gaaac	2640
t ct t ct t caa	gat caagcct	ct gt t gaaga	gt gcagaaac	t gagaaggag	at ggccacca	2700
t gaaggaaga	at t t cagaaa	at t aaagacg	aact t gccaa	gt cagaggca	aaaaggaagg	2760
aact ggaaga	aaagat ggt g	acgct gt t ga	aagaaaaaaa	t gact t gcag	ct ccaagt t c	2820
aggct gaagc	cgaaggct t g	gct gat gcag	aggaaaggt g	t gaccagct a	at caaaacca	2880
aaat ccagct	agaagccaaa	at caaagagg	t gact gagag	agct gaggat	gaggaagaga	2940
t caat gct ga	gct gacagcc	aagaagagga	aact ggagga	t gaat gt t ca	gaact caaga	3000
aagacat t ga	t gacct t gag	ct gacact gg	ccaaggt t ga	gaaggagaaa	cat gccacag	3060
aaaacaaggt	gaaaaacct c	acagaagaga	t ggcaggt ct	ggat gaaacc	at t gct aagc	3120
t gaccaagga	gaagaaggct	ct ccaggagg	cccaccagca	gaccct ggat	gacct gcagg	3180
cagaggagga	caaagt caac	accct gacca	aagct aaaat	caaact t gaa	caacaagt gg	3240
at gat ct t ga	agggt cct t g	gagcaagaaa	agaaact t cg	cat ggacct a	gaaagggct a	3300

N3027PCT\_sequ. list.txt

agaggaaact	t gagggt gac	t t gaagt t gg	cccaagaat c	cat aat ggac	at t gaaaat g	3360
agaaacagca	act t gat gaa	aagct caaaa	agaaagagt t	t gaaat cagc	aat ct gcaaa	3420
gcaagat t ga	agat gaacag	gcact t ggca	t t caat t gca	gaagaaaat t	aaagaat t gc	3480
aagcccgc	at t gaggagct g	gaggaggaaa	t cgaggcaga	gcgggcct cc	cgggccaaag	3540
cagagaagca	gcgct ct gac	ct ct cccggg	agct ggagga	gat cagcgag	aggct ggaag	3600
aagccggt gg	ggccact t ca	gcccagat t g	agat gaacaa	gaagcgggag	gct gagt t cc	3660
agaaaat gcg	cagggacct g	gaggaggcca	ccct acagca	t gaagccaca	gcggccaccc	3720
t gaggaagaa	gcat gcagat	agt gt ggccg	agct t gggga	gcagat t gac	aacct gcagc	3780
gagt gaagca	gaagct ggag	aaggagaaga	gt gagat gaa	gat ggagat t	gat gacct t g	3840
ct agt aat gt	agaaacggt c	t ccaaagcca	agggaaacct	agagaaaat g	t gccggact c	3900
t agaggacca	act gagt gaa	ct gaaat caa	aggaagagga	gcagcagcgg	ct gat caat g	3960
acct gact gc	gcagagggggg	cgct gcaga	ct gaat ct gg	t gagt t t t ca	cgccagct t g	4020
at gaaaagga	agct ct ggt g	t ct cagt t at	caagaggcaa	acaagcct t t	act caacaga	4080
t t gaagaat t	aaagaggcaa	ct t gaagagg	agat aaaagc	caagaacgcc	ct ggcgc	4140
ccct gcagt c	t t cccgccac	gact gt gacc	t gct gcggga	acagt at gag	gaggagcagg	4200
aat ccaaggc	cgagct gcag	agagcact gt	ccaaggccaa	caccgaggt t	gccaat gga	4260
ggaccaa	at a cgagacggac	gccat ccagc	gcacagagga	gct ggaggag	gccaagaaga	4320
agct ggcca	gcggct gcag	gcagct gagg	aacat gt aga	agct gt gaac	gccaat gt g	4380
ct t ccct cga	aaagacgaag	cagcggct gc	agaat gaggt	cgaggacct c	at gct t gat g	4440
t ggagaggac	aaat gccgcc	t gt gccgcc	t t gacaaaaa	gcaaaggaac	t t cgat aaga	4500
t cct ggcaga	at ggaaacag	aaat gt gagg	aaacgc	at gc t gag	gcct cccaga	4560
aggaggccccg	t t ccct t ggc	act gagct gt	t caagat aaa	gaat gcct at	gaggaat ct t	4620
t ggat cagct	agaaaccct g	aagcgagaga	acaaaaact t	acagcaggag	at t t ct gacc	4680
t cacggaaca	gat t gcagaa	ggagggaac	gt at ccat ga	act ggagaaa	at aaagaac	4740
aagt ggaaca	agaaaagt gt	gaact t cagg	ct gct t t aga	agaagcagag	gcat ct ct t g	4800
aacat gaaga	gggaaagat c	ct gcgc	at cc agct t g	agt t gat t	gaaccaagt c	4860
t t gat aggaa	aat t gct gaa	aaagat gagg	aaat t gacca	gct gaagaga	aaccacat t a	4920
gaat cgt gga	gt ccat gcag	agcacgct gg	at gct gagat	caggagt agg	aat gat gcca	4980
t t aggct caa	gaagaagat g	gaggagacc	t caat gaaat	ggaaat ccag	ct gaacct g	5040
ccaaccgc	at ggct gct gag	gccct gagga	act acaggaa	caccaaggc	at cct caagg	5100
at acccagat	ccacct ggat	gat gct ct cc	ggagccagga	ggacct gaag	gaacagct gg	5160
ccat ggt gga	gcgcagagcc	aacct gct gc	aggct gagat	cgaggagct g	cgggccact c	5220
t ggaacagac	agagaggagc	agaaaaat cg	cagaacagga	gct cct ggat	gccagt gagg	5280
gt gt t cagct	act gcacacc	cagaacacca	gcct gat caa	caccaagaag	aagct ggaga	5340
cagat at t t c	ccaaat gcaa	ggagagat gg	aggacat t ct	ccaggaagcc	cgcaat gcag	5400

N3027PCT\_sequ.list.txt

```

aagaaaaggc caagaaggcc at cact gat g ccgccat gat ggct gaggag ct gaagaagg 5460
agcaggacac cagcgccac ct ggagcgga t gaagaagaa cat ggagcag accgt gaagg 5520
at ct gcagct ccgt ct ggat gaggct gagc agct ggccct gaagggt ggg aagaagcaga 5580
t ccagaaact ggaggccagg gt acgggagc t ggaaggaga ggt t gagagt gagcaaaagc 5640
gt aat gct ga ggct gt caaa ggt ct gcgca aacat gagag gcgagt gaag gaact cact t 5700
accagacgga agaagat aga aagaat at t c t caggct t ca agat t t ggt a gat aaact t c 5760
aggcaaaagt gaaat ct t at aagagacaag ct gaggaggc t gaggaacaa t ccaacacca 5820
at ct agct aa at t ccgcaag ct ccagcat g agct ggagga ggccgaggaa cgggct gaca 5880
t t gct gagt c ccaggt gaac aaact gcggg t gaagagccg ggaggt t cac acaaaagt ca 5940
t aagt gaaga gt gat cat gt cct gat gcca t ggaat gact gaagacaggc acaaaat gt g 6000
acat ct t t gg t cat t t ccct ct gt aat t at t gt gt at t ct accct gt t gc aaaggaaat a 6060
aagcat aggg t agt t t gcaa acaat aaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 6120
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 6163

```

<210> 56  
 <211> 1941  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> M SC\_FEATURE  
 <222> (1)..(1941)  
 <223> myosin, heavy chain 2, skeletal muscle, adult (MYH2), transcript variant 1

<400> 56

Met Ser Ser Asp Ser Glu Leu Ala Val Phe Gly Glu Ala Ala Pro Phe  
1 5 10 15

Leu Arg Lys Ser Glu Arg Glu Arg Ile Glu Ala Glu Asn Arg Pro Phe  
20 25 30

Asp Ala Lys Thr Ser Val Phe Val Ala Glu Pro Lys Glu Ser Phe Val  
35 40 45

Lys Gly Thr Ile Glu Ser Arg Glu Gly Gly Lys Val Thr Val Lys Thr  
50 55 60

Glu Gly Gly Ala Thr Leu Thr Val Lys Asp Asp Glu Val Phe Pro Met  
65 70 75 80

Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His  
85 90 95

Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala  
100 105 110

N3027PCT\_sequ.list.txt

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
 115 120 125  
 Tyr Lys Trp Leu Pro Val Tyr Lys Pro Glu Val Val Thr Ala Tyr Arg  
 130 135 140  
 Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
 145 150 155 160  
 Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu  
 165 170 175  
 Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val  
 180 185 190  
 Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu  
 195 200 205  
 Glu Ile Thr Ser Gly Lys Ile Gln Gly Thr Leu Glu Asp Gln Ile Ile  
 210 215 220  
 Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg  
 225 230 235 240  
 Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly  
 245 250 255  
 Thr Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu  
 260 265 270  
 Lys Ser Arg Val Val Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile  
 275 280 285  
 Phe Tyr Gln Ile Thr Ser Asn Lys Lys Pro Glu Leu Ile Glu Met Leu  
 290 295 300  
 Leu Ile Thr Thr Asn Pro Tyr Asp Tyr Pro Phe Val Ser Gln Gly Glu  
 305 310 315 320  
 Ile Ser Val Ala Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp  
 325 330 335  
 Ser Ala Ile Asp Ile Leu Gly Phe Thr Asn Glu Glu Lys Val Ser Ile  
 340 345 350  
 Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Leu Lys Phe Lys  
 355 360 365  
 Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala  
 370 375 380

N3027PCT\_sequ.list.txt

Asp 385 Lys Ala Ala Tyr Leu 390 Gln Ser Leu Asn 395 Ser Ala Asp Leu Leu Lys 400  
 Ala Leu Cys Tyr Pro 405 Arg Val Lys Val Gly 410 Asn Glu Tyr Val Thr 415 Lys  
 Gly Gln Thr Val 420 Glu Gln Val Ser Asn 425 Ala Val Gly Ala Leu 430 Ala Lys  
 Ala Val Tyr 435 Glu Lys Met Phe Leu 440 Trp Met Val Ala Arg 445 Ile Asn Gln  
 Gln Leu 450 Asp Thr Lys Gln Pro 455 Arg Gln Tyr Phe Ile 460 Gly Val Leu Asp  
 Ile 465 Ala Gly Phe Glu Ile 470 Phe Asp Phe Asn Ser 475 Leu Glu Gln Leu Cys 480  
 Ile Asn Phe Thr Asn 485 Glu Lys Leu Gln Gln 490 Phe Phe Asn His 495 His Met  
 Phe Val Leu Glu 500 Gln Glu Glu Tyr Lys 505 Lys Glu Gly Ile Glu 510 Trp Thr  
 Phe Ile Asp 515 Phe Gly Met Asp Leu 520 Ala Ala Cys Ile Glu 525 Leu Ile Glu  
 Lys Pro 530 Met Gly Ile Phe Ser 535 Ile Leu Glu Glu Glu 540 Cys Met Phe Pro  
 Lys 545 Ala Thr Asp Thr Ser 550 Phe Lys Asn Lys Leu 555 Tyr Asp Gln His 560 Leu  
 Gly Lys Ser Ala Asn 565 Phe Gln Lys Pro Lys 570 Val Val Lys Gly Lys 575 Ala  
 Glu Ala His Phe 580 Ala Leu Ile His Tyr 585 Ala Gly Val Val Asp 590 Tyr Asn  
 Ile Thr Gly 595 Trp Leu Glu Lys Asn 600 Lys Asp Pro Leu Asn 605 Glu Thr Val  
 Val Gly 610 Leu Tyr Gln Lys Ser 615 Ala Met Lys Thr Leu 620 Ala Gln Leu Phe  
 Ser 625 Gly Ala Gln Thr Ala 630 Glu Gly Glu Gly Ala 635 Gly Gly Gly Ala Lys 640  
 Lys Gly Gly Lys Lys 645 Lys Gly Ser Ser Phe 650 Gln Thr Val Ser Ala 655 Leu  
 Phe Arg Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His

660

665

670

Pro His Phe Val Arg Cys Ile Ile Pro Asn Glu Thr Lys Thr Pro Gly  
 675 680 685  
 Ala Met Glu His Glu Leu Val Leu His Gln Leu Arg Cys Asn Gly Val  
 690 700  
 Leu Glu Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu  
 705 710 715 720  
 Tyr Ala Asp Phe Lys Gln Arg Tyr Lys Val Leu Asn Ala Ser Ala Ile  
 725 730 735  
 Pro Glu Gly Gln Phe Ile Asp Ser Lys Lys Ala Ser Glu Lys Leu Leu  
 740 745 750  
 Ala Ser Ile Asp Ile Asp His Thr Gln Tyr Lys Phe Gly His Thr Lys  
 755 760 765  
 Val Phe Phe Lys Ala Gly Leu Leu Gly Leu Leu Glu Glu Met Arg Asp  
 770 775 780  
 Asp Lys Leu Ala Gln Leu Ile Thr Arg Thr Gln Ala Arg Cys Arg Gly  
 785 790 795 800  
 Phe Leu Ala Arg Val Glu Tyr Gln Arg Met Val Glu Arg Arg Glu Ala  
 805 810 815  
 Ile Phe Cys Ile Gln Tyr Asn Ile Arg Ser Phe Met Asn Val Lys His  
 820 825 830  
 Trp Pro Trp Met Lys Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser  
 835 840 845  
 Ala Glu Thr Glu Lys Glu Met Ala Thr Met Lys Glu Glu Phe Gln Lys  
 850 855 860  
 Ile Lys Asp Glu Leu Ala Lys Ser Glu Ala Lys Arg Lys Glu Leu Glu  
 865 870 875 880  
 Glu Lys Met Val Thr Leu Leu Lys Glu Lys Asn Asp Leu Gln Leu Gln  
 885 890 895  
 Val Gln Ala Glu Ala Glu Gly Leu Ala Asp Ala Glu Glu Arg Cys Asp  
 900 905 910  
 Gln Leu Ile Lys Thr Lys Ile Gln Leu Glu Ala Lys Ile Lys Glu Val  
 915 920 925  
 Thr Glu Arg Ala Glu Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala  
 930 935 940

N3027PCT\_sequ.list.txt

Lys Lys Arg Lys Leu Glu Asp Glu Oys Ser Glu Leu Lys Lys Asp Ile  
 945 950 955 960  
 Asp Asp Leu Glu Leu Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala  
 965 970 975  
 Thr Glu Asn Lys Val Lys Asn Leu Thr Glu Glu Met Ala Gly Leu Asp  
 980 985 990  
 Glu Thr Ile Ala Lys Leu Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala  
 995 1000 1005  
 His Gln Gln Thr Leu Asp Asp Leu Gln Ala Glu Glu Asp Lys Val  
 1010 1015 1020  
 Asn Thr Leu Thr Lys Ala Lys Ile Lys Leu Glu Gln Gln Val Asp  
 1025 1030 1035  
 Asp Leu Glu Gly Ser Leu Glu Gln Glu Lys Lys Leu Arg Met Asp  
 1040 1045 1050  
 Leu Glu Arg Ala Lys Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala  
 1055 1060 1065  
 Gln Glu Ser Ile Met Asp Ile Glu Asn Glu Lys Gln Gln Leu Asp  
 1070 1075 1080  
 Glu Lys Leu Lys Lys Lys Glu Phe Glu Ile Ser Asn Leu Gln Ser  
 1085 1090 1095  
 Lys Ile Glu Asp Glu Gln Ala Leu Gly Ile Gln Leu Gln Lys Lys  
 1100 1105 1110  
 Ile Lys Glu Leu Gln Ala Arg Ile Glu Glu Leu Glu Glu Glu Ile  
 1115 1120 1125  
 Glu Ala Glu Arg Ala Ser Arg Ala Lys Ala Glu Lys Gln Arg Ser  
 1130 1135 1140  
 Asp Leu Ser Arg Glu Leu Glu Glu Ile Ser Glu Arg Leu Glu Glu  
 1145 1150 1155  
 Ala Gly Gly Ala Thr Ser Ala Gln Ile Glu Met Asn Lys Lys Arg  
 1160 1165 1170  
 Glu Ala Glu Phe Gln Lys Met Arg Arg Asp Leu Glu Glu Ala Thr  
 1175 1180 1185  
 Leu Gln His Glu Ala Thr Ala Ala Thr Leu Arg Lys Lys His Ala  
 1190 1195 1200

N3027PCT\_sequ.list.txt

Asp	Ser	Val	Ala	Glu	Leu	Gly	Glu	Gln	Ile	Asp	Asn	Leu	Gln	Arg
1205						1210					1215			
Val	Lys	Gln	Lys	Leu	Glu	Lys	Glu	Lys	Ser	Glu	Met	Lys	Met	Glu
1220						1225					1230			
Ile	Asp	Asp	Leu	Ala	Ser	Asn	Val	Glu	Thr	Val	Ser	Lys	Ala	Lys
1235						1240					1245			
Gly	Asn	Leu	Glu	Lys	Met	Cys	Arg	Thr	Leu	Glu	Asp	Gln	Leu	Ser
1250						1255					1260			
Glu	Leu	Lys	Ser	Lys	Glu	Glu	Glu	Gln	Gln	Arg	Leu	Ile	Asn	Asp
1265						1270					1275			
Leu	Thr	Ala	Gln	Arg	Gly	Arg	Leu	Gln	Thr	Glu	Ser	Gly	Glu	Phe
1280						1285					1290			
Ser	Arg	Gln	Leu	Asp	Glu	Lys	Glu	Ala	Leu	Val	Ser	Gln	Leu	Ser
1295						1300					1305			
Arg	Gly	Lys	Gln	Ala	Phe	Thr	Gln	Gln	Ile	Glu	Glu	Leu	Lys	Arg
1310						1315					1320			
Gln	Leu	Glu	Glu	Glu	Ile	Lys	Ala	Lys	Asn	Ala	Leu	Ala	His	Ala
1325						1330					1335			
Leu	Gln	Ser	Ser	Arg	His	Asp	Cys	Asp	Leu	Leu	Arg	Glu	Gln	Tyr
1340						1345					1350			
Glu	Glu	Glu	Gln	Glu	Ser	Lys	Ala	Glu	Leu	Gln	Arg	Ala	Leu	Ser
1355						1360					1365			
Lys	Ala	Asn	Thr	Glu	Val	Ala	Gln	Trp	Arg	Thr	Lys	Tyr	Glu	Thr
1370						1375					1380			
Asp	Ala	Ile	Gln	Arg	Thr	Glu	Glu	Leu	Glu	Glu	Ala	Lys	Lys	Lys
1385						1390					1395			
Leu	Ala	Gln	Arg	Leu	Gln	Ala	Ala	Glu	Glu	His	Val	Glu	Ala	Val
1400						1405					1410			
Asn	Ala	Lys	Cys	Ala	Ser	Leu	Glu	Lys	Thr	Lys	Gln	Arg	Leu	Gln
1415						1420					1425			
Asn	Glu	Val	Glu	Asp	Leu	Met	Leu	Asp	Val	Glu	Arg	Thr	Asn	Ala
1430						1435					1440			
Ala	Cys	Ala	Ala	Leu	Asp	Lys	Lys	Gln	Arg	Asn	Phe	Asp	Lys	Ile
1445						1450					1455			

Leu Ala 1460 Glu Trp Lys Gln Lys 1465 Cys Glu Glu Thr His 1470 Ala Glu Leu  
 Glu Ala 1475 Ser Gln Lys Glu Ala 1480 Arg Ser Leu Gly Thr 1485 Glu Leu Phe  
 Lys Ile 1490 Lys Asn Ala Tyr Glu 1495 Glu Ser Leu Asp Gln 1500 Leu Glu Thr  
 Leu Lys 1505 Arg Glu Asn Lys Asn 1510 Leu Gln Gln Glu Ile 1515 Ser Asp Leu  
 Thr Glu 1520 Gln Ile Ala Glu Gly 1525 Gly Lys Arg Ile His 1530 Glu Leu Glu  
 Lys Ile 1535 Lys Lys Gln Val Glu 1540 Gln Glu Lys Cys Glu 1545 Leu Gln Ala  
 Ala Leu 1550 Glu Glu Ala Glu Ala 1555 Ser Leu Glu His Glu 1560 Glu Gly Lys  
 Ile Leu 1565 Arg Ile Gln Leu Glu 1570 Leu Asn Gln Val Lys 1575 Ser Glu Val  
 Asp Arg 1580 Lys Ile Ala Glu Lys 1585 Asp Glu Glu Ile Asp 1590 Gln Leu Lys  
 Arg Asn 1595 His Ile Arg Ile Val 1600 Glu Ser Met Gln Ser 1605 Thr Leu Asp  
 Ala Glu 1610 Ile Arg Ser Arg Asn 1615 Asp Ala Ile Arg Leu 1620 Lys Lys Lys  
 Met Glu 1625 Gly Asp Leu Asn Glu 1630 Met Glu Ile Gln Leu 1635 Asn His Ala  
 Asn Arg 1640 Met Ala Ala Glu Ala 1645 Leu Arg Asn Tyr Arg 1650 Asn Thr Gln  
 Gly Ile 1655 Leu Lys Asp Thr Gln 1660 Ile His Leu Asp Asp 1665 Ala Leu Arg  
 Ser Gln 1670 Glu Asp Leu Lys Glu 1675 Gln Leu Ala Met Val 1680 Glu Arg Arg  
 Ala Asn 1685 Leu Leu Gln Ala Glu 1690 Ile Glu Glu Leu Arg 1695 Ala Thr Leu  
 Glu Gln 1700 Thr Glu Arg Ser Arg 1705 Lys Ile Ala Glu Gln 1710 Glu Leu Leu  
 Asp Ala Ser Glu Arg Val Gln Leu Leu His Thr Gln Asn Thr Ser

1715

1720

1725

Leu Ile Asn Thr Lys Lys Lys Leu Glu Thr Asp Ile Ser Glu Met  
 1730 1735 1740  
 Glu Gly Glu Met Glu Asp Ile Leu Glu Glu Ala Arg Asn Ala Glu  
 1745 1750 1755  
 Glu Lys Ala Lys Lys Ala Ile Thr Asp Ala Ala Met Met Ala Glu  
 1760 1765 1770  
 Glu Leu Lys Lys Glu Glu Asp Thr Ser Ala His Leu Glu Arg Met  
 1775 1780 1785  
 Lys Lys Asn Met Glu Glu Thr Val Lys Asp Leu Glu Leu Arg Leu  
 1790 1795 1800  
 Asp Glu Ala Glu Glu Leu Ala Leu Lys Gly Gly Lys Lys Glu Ile  
 1805 1810 1815  
 Glu Lys Leu Glu Ala Arg Val Arg Glu Leu Glu Gly Glu Val Glu  
 1820 1825 1830  
 Ser Glu Glu Lys Arg Asn Ala Glu Ala Val Lys Gly Leu Arg Lys  
 1835 1840 1845  
 His Glu Arg Arg Val Lys Glu Leu Thr Tyr Glu Thr Glu Glu Asp  
 1850 1855 1860  
 Arg Lys Asn Ile Leu Arg Leu Glu Asp Leu Val Asp Lys Leu Glu  
 1865 1870 1875  
 Ala Lys Val Lys Ser Tyr Lys Arg Glu Ala Glu Glu Ala Glu Glu  
 1880 1885 1890  
 Glu Ser Asn Thr Asn Leu Ala Lys Phe Arg Lys Leu Glu His Glu  
 1895 1900 1905  
 Leu Glu Glu Ala Glu Glu Arg Ala Asp Ile Ala Glu Ser Glu Val  
 1910 1915 1920  
 Asn Lys Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Val Ile  
 1925 1930 1935  
 Ser Glu Glu  
 1940

<210> 57  
 <211> 6163  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6163)

&lt;223&gt; myosin, heavy chain 2, skeletal muscle, adult (MYH2), transcript variant 2

&lt;400&gt; 57

```

aggacgggcc tttcaagagg gacactggtc acaccgccca gtgtcagcag cagctgctag      60
ttctgaactg tctcactccc aggctacatc ttctcacttg ctacaagga cctctgagtt      120
cagcagccat gaggttcagac tcagaattgg ctgtttttgg ggaggctgct cctttcctcc      180
gaaagtctga aaggggagcgc attgaggccc agaataggcc ctttgatgcc aaaacatctg      240
tctttgtggc ggagcccaaa gaatcctttg tcaaagggac catccagagc agagaaggag      300
gaaaagtgac ggtgaagact gagggaggag cgactctgac agtgaaggat gatcaggtct      360
tccccatgaa ccctcccaa t atgacaaga t cgaggat at ggccat gat g actcatctgc      420
atgagcctgc tgtgctgtac aacctcaaag aacgttatgc agcctggatg atctacacct      480
attcaggtct cttctgtgtc actgtcaacc cctacaagt g gctgcctgtg tat aagcccg      540
aggtggtgac agcctaccga ggcaaaaagc gccaggaggc cccgccccac atcttctcca      600
tctctgacaa cgcctatcag ttcatgctga ctgaccgaga gaatcagtc a atcctgatca      660
ctggagaatc tgggagagg aagactgtga acaccaagcg tgtcatccag tactttgcaa      720
caattgcagt tactggtgag aagaagaagg aagaaattac ttctggcaa atacagggga      780
ctctggaaga tcaaatcatc agtgccaacc ccctactgga ggcctttggc aacgccaaga      840
ccgtgaggaa tgacaactcc tctcgctttg gtaaatcatc cagaatccac tttggcacta      900
ctggaaaact ggcatctgct gatattgaaa catatctgct agagaagtct agagttgttt      960
tccagcttaa ggctgagaga agttatcata ttttttacc a gat tacatcg aat aagaaac      1020
cagaacttat tgaaatgctt ctgattacca cgaacccata tgattacca tttgtcagtc      1080
aaggggagat cagtggtggc agcatcgatg atcaggaaga actgatggcc acagatagt g      1140
ctattgatat tttgggcttt actaatgaag aaaaggtctc cat t tacaag ct cagggggg      1200
ctgtgatgca ttatgggaac ctaaaattta agcaaaagca gcgtgaggag caagcagagc      1260
cagatggcac agaagt t gct gacaaggcgg cctacctcca gagtctgaac tctgcagatc      1320
tgctcaaagc tctctgctac cccagggtca aggtcggcaa tgagtatgtc accaaaggcc      1380
agactgtaga acaggtgtcc aacgcagt ag gtgctctggc caaagccgtc t acgagaaga      1440
tgttctgtg gatggttggc cgcatcaacc agcagctgga caccaagcag cccaggcagt      1500
acttcatcgg ggtcttggac attgctggtt ttgagat ttt tgatttcaac agcctggagc      1560
agctgtgcat caacttcacc aatgagaaac tgcaacagtt tttcaaccac cacatgttgc      1620
tgctggagca ggaggagtac aagaaggaag gcatcgagt g gacgttcatc gacttcggga      1680
tggacctggc tgcctgcatc gagctcatcg agaagcctat gggcatcttc tccatcctgg      1740
aagaggagt g catgttccct aaggcaacag acacctcctt caagaacaag ctgtatgacc      1800
agcacctggg caagtctgcc aacttccaga agcccaaggt ggtcaaaggc aaggccgagg      1860

```

N3027PCT\_sequ. list.txt

cccact t cgc t ct gat t cac t at gct ggt g t t gt ggact a caacat t act ggct ggct gg	1920
agaagaacaa ggacccccct g aat gagaccg t ggt t ggact gt accagaag t ct gcaat ga	1980
aaact ct agc t cagct ct t c t ct ggggct c aaact gct ga aggagaggga gct ggt ggag	2040
gggccaagaa aggt ggt aag aagaagggt ct t ct t t cca gacagt gt ct gccct t t t ca	2100
gagagaat t t gaacaagct g at gaccaacc t caggagt ac ccat cct cac t t t gt gaggt	2160
gt at cat ccc caat gagaca aaaact cct g gt gccat gga gcat gagct t gt cct ccacc	2220
agct gaggt g t aacggt gt g ct ggaaggca t ccgcat ct g t aggaaagga t t t ccaagca	2280
gaat cct t t a t gcagact t c aaacagagat acaagggt at t aaat gcaagt gcaat ccct g	2340
aagggaat t cat t gat agc aagaaggcct ct gagaagct cct t gcat cc at cgacat t g	2400
accacacca gt at aaat t t gggcacacca aggt ct t t t t caaagct ggt ct t ct ggggc	2460
t cct agagga gat gcgagat gacaagct gg cccagct gat t acccgaacc caggccaggt	2520
gcagagggt t ct t ggcaaga gt ggagt acc agaggat ggt ggagagaagg gaggccat ct	2580
t ct gt at cca gt acaat at c agat cct t ca t gaat gt caa gcaact ggccc t ggat gaaac	2640
t ct t ct t caa gat caagcct ct gt t gaaga gt gcagaaac t gagaaggag at ggccacca	2700
t gaaggaaga at t t cagaaa at t aaagacg aact t gccaa gt cagaggca aaaaggaagg	2760
aact ggaaga aaagat ggt g acgct gt t ga aagaaaaaaa t gact t gcag ct ccaagt t c	2820
aggct gaagc cgaaggct t g gct gat gcag aggaaagggt g t gaccagct a at caaaacca	2880
aaat ccagct agaagccaaa at caaagagg t gact gagag agct gaggat gaggaagaga	2940
t caat gct ga gct gacagcc aagaagagga aact ggagga t gaat gt t ca gaact caaga	3000
aagacat t ga t gacct t gag ct gacact gg ccaagggt t ga gaaggagaaa cat gccacag	3060
aaaacaagggt gaaaaacct c acagaagaga t ggcagggt ct ggat gaaacc at t gct aagc	3120
t gaccaagga gaagaaggct ct ccaggagg cccaccagca gacct ggat gacct gcagg	3180
cagaggagga caaagt caac accct gacca aagct aaaat caaact t gaa caacaagt gg	3240
at gat ct t ga aggt cct t g gagcaagaaa agaaact t cg cat ggacct a gaaagggt a	3300
agaggaaact t gagggt gac t t gaagt t gg cccaagaat c cat aat ggac at t gaaaat g	3360
agaaacagca act t gat gaa aagct caaaa agaaagagt t t gaaat cagc aat ct gcaaa	3420
gcaagat t ga agat gaacag gcaact t ggca t t caat t gca gaagaaaat t aaagaat t gc	3480
aagcccgcct t gaggagct g gaggaggaaa t cgaggcaga gcgggcct cc cgggccaag	3540
cagagaagca gcgct ct gac ct ct cccggg agct ggagga gat cagcgag aggct ggaag	3600
aagccggt gg ggccact t ca gccagat t g agat gaacaa gaagcgggag gct gagt t cc	3660
agaaaat gcg caggacct g gaggaggcca ccct acagca t gaagccaca gcggccaccc	3720
t gaggaagaa gcat gcagat agt gt ggccg agct t gggga gcagat t gac aacct gcagc	3780
gagt gaagca gaagct ggag aaggagaaga gt gagat gaa gat ggagat t gat gacct t g	3840
ct agt aat gt agaaacggt c t ccaaagcca agggaaacct agagaaaat g t gccggact c	3900
t agaggacca act gagt gaa ct gaaat caa aggaagagga gcagcagcg ct gat caat g	3960

N3027PCT\_sequ. list . . txt

acct gact gc	gcagaggggg	cgcct gcaga	ct gaat ct gg	t gagt t t t ca	cgccagct t g	4020
at gaaaagga	agct ct ggt g	t ct cagt t at	caagaggcaa	acaagcct t t	act caacaga	4080
t t gaagaat t	aaagaggcaa	ct t gaagagg	agat aaaagc	caagaacgcc	ct ggcgcat g	4140
ccct gcagt c	t t cccgccac	gact gt gacc	t gct gcggga	acagt at gag	gaggagcagg	4200
aat ccaaggc	cgagct gcag	agagcact gt	ccaaggccaa	caccgaggt t	gccaat gga	4260
ggaccaaata	cgagacggac	gccat ccagc	gcacagagga	gct ggaggag	gccaagaaga	4320
agct ggccca	gcggct gcag	gcagct gagg	aacat gt aga	agct gt gaac	gccaat gt g	4380
ct t ccct cga	aaagacgaag	cagcggct gc	agaat gaggt	cgaggacct c	at gct t gat g	4440
t ggagaggac	aaat gccgcc	t gt gccgcc	t t gacaaaaa	gcaaaggaac	t t cgat aaga	4500
t cct ggcaga	at ggaaacag	aaat gt gagg	aaacgcat gc	t gagct t gag	gcct cccaga	4560
aggaggcccg	t t ccct t ggc	act gagct gt	t caagat aaa	gaat gcct at	gaggaat ct t	4620
t ggat cagct	agaaaccct g	aagcgagaga	acaaaaact t	acagcaggag	at t t ct gacc	4680
t cacggaaca	gat t gcagaa	ggagggaaac	gt at ccat ga	act ggagaaa	at aaagaaac	4740
aagt ggaaca	agaaaagt gt	gaact t cagg	ct gct t t aga	agaagcagag	gcat ct ct t g	4800
aacat gaaga	gggaaagat c	ct gcgcat cc	agct t gagt t	gaaccaagt c	aagt ct gagg	4860
t t gat aggaa	aat t gct gaa	aaagat gagg	aaat t gacca	gct gaagaga	aaccacat t a	4920
gaat cgt gga	gt ccat gcag	agcacgct gg	at gct gagat	caggagt agg	aat gat gcca	4980
t t aggct caa	gaagaagat g	gaggagacc	t caat gaaat	ggaaat ccag	ct gaacat g	5040
ccaaccgcat	ggct gct gag	gccct gagga	act acaggaa	cacccaaggc	at cct caagg	5100
at acccagat	ccacct ggat	gat gct ct cc	ggagccagga	ggacct gaag	gaacagct gg	5160
ccat ggt gga	gcgcagagcc	aacct gct gc	aggct gagat	cgaggagct g	cgggccact c	5220
t ggaacagac	agagaggagc	agaaaaat cg	cagaacagga	gct cct ggat	gccagt gagg	5280
gt gt t cagct	act gcacacc	cagaacacca	gcct gat caa	caccaagaag	aagct ggaga	5340
cagat at t t c	ccaaat gcaa	ggagagat gg	aggacat t ct	ccaggaagcc	cgcaat gcag	5400
aagaaaaggc	caagaaggcc	at cact gat g	ccgccat gat	ggct gaggag	ct gaagaagg	5460
agcaggacac	cagcgcccac	ct ggagcggg	t gaagaagaa	cat ggagcag	accgt gaagg	5520
at ct gcagct	ccgt ct ggat	gaggct gagg	agct ggccct	gaagggg ggg	aagaagcaga	5580
t ccagaaaact	ggaggccagg	gt acgggagc	t ggaaggaga	ggg t gagagt	gagcaaaaagc	5640
gt aat gct ga	ggct gt caaa	ggc ct gcgca	aacat gagag	gcgagt gaag	gaact cact t	5700
accagacgga	agaagat aga	aagaat at t c	t caggct t ca	agat t t ggt a	gat aaact t c	5760
aggcaaaaagt	gaaat ct t at	aagagacaag	ct gaggaggc	t gaggaacaa	t ccaacacca	5820
at ct agct aa	at t ccgcaag	ct ccagcat g	agct ggagga	ggccgaggaa	cgggct gaca	5880
t t gct gagt c	ccaggt gaac	aaact gcggg	t gaagagccg	ggaggt t cac	acaaaagt ca	5940
t aagt gaaga	gt gat cat gt	cct gat gcca	t ggaat gact	gaagacaggc	acaaaat gt g	6000

N3027PCT\_sequ.list.txt

acatctttgg tcatttccct ctgtaattat tgtgtattct accctgttgc aaaggaaat a 6060  
aagcataggg tagtttgcaa acaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 6120  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 6163

<210> 58  
<211> 1941  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1941)  
<223> myosin, heavy chain 2, skeletal muscle, adult (MYH2), transcript  
variant 2

<400> 58

Met Ser Ser Asp Ser Glu Leu Ala Val Phe Gly Glu Ala Ala Pro Phe  
1 5 10 15

Leu Arg Lys Ser Glu Arg Glu Arg Ile Glu Ala Gln Asn Arg Pro Phe  
20 25 30

Asp Ala Lys Thr Ser Val Phe Val Ala Glu Pro Lys Glu Ser Phe Val  
35 40 45

Lys Gly Thr Ile Gln Ser Arg Glu Gly Gly Lys Val Thr Val Lys Thr  
50 55 60

Glu Gly Gly Ala Thr Leu Thr Val Lys Asp Asp Gln Val Phe Pro Met  
65 70 75 80

Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His  
85 90 95

Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala  
100 105 110

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
115 120 125

Tyr Lys Trp Leu Pro Val Tyr Lys Pro Glu Val Val Thr Ala Tyr Arg  
130 135 140

Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
145 150 155 160

Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu  
165 170 175

Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val  
180 185 190

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu  
 195 200 205  
 Glu Ile Thr Ser Gly Lys Ile Gln Gly Thr Leu Glu Asp Gln Ile Ile  
 210 215 220  
 Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg  
 225 230 235 240  
 Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly  
 245 250 255  
 Thr Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu  
 260 265 270  
 Lys Ser Arg Val Val Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile  
 275 280 285  
 Phe Tyr Gln Ile Thr Ser Asn Lys Lys Pro Glu Leu Ile Glu Met Leu  
 290 295 300  
 Leu Ile Thr Thr Asn Pro Tyr Asp Tyr Pro Phe Val Ser Gln Gly Glu  
 305 310 315 320  
 Ile Ser Val Ala Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp  
 325 330 335  
 Ser Ala Ile Asp Ile Leu Gly Phe Thr Asn Glu Glu Lys Val Ser Ile  
 340 345 350  
 Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Leu Lys Phe Lys  
 355 360 365  
 Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala  
 370 375 380  
 Asp Lys Ala Ala Tyr Leu Gln Ser Leu Asn Ser Ala Asp Leu Leu Lys  
 385 390 395 400  
 Ala Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys  
 405 410 415  
 Gly Gln Thr Val Glu Gln Val Ser Asn Ala Val Gly Ala Leu Ala Lys  
 420 425 430  
 Ala Val Tyr Glu Lys Met Phe Leu Trp Met Val Ala Arg Ile Asn Gln  
 435 440 445  
 Gln Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp  
 450 455 460  
 Ile Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys  
 Page 265

```

465                               470                               475                               480
I l e A s n P h e T h r A s n G l u L y s L e u G l n G l n P h e P h e A s n H i s H i s M e t
485                               490
P h e V a l L e u G l u G l n G l u G l u T y r L y s L y s G l u G l y I l e G l u T r p T h r
500                               505                               510
P h e I l e A s p P h e G l y M e t A s p L e u A l a A l a C y s I l e G l u L e u I l e G l u
515                               520                               525
L y s P r o M e t G l y I l e P h e S e r I l e L e u G l u G l u G l u C y s M e t P h e P r o
530                               535                               540
L y s A l a T h r A s p T h r S e r P h e L y s A s n L y s L e u T y r A s p G l n H i s L e u
545                               550                               555                               560
G l y L y s S e r A l a A s n P h e G l n L y s P r o L y s V a l V a l L y s G l y L y s A l a
565                               570                               575
G l u A l a H i s P h e A l a L e u I l e H i s T y r A l a G l y V a l V a l A s p T y r A s n
580                               585                               590
I l e T h r G l y T r p L e u G l u L y s A s n L y s A s p P r o L e u A s n G l u T h r V a l
595                               600                               605
V a l G l y L e u T y r G l n L y s S e r A l a M e t L y s T h r L e u A l a G l n L e u P h e
610                               615                               620
S e r G l y A l a G l n T h r A l a G l u G l y G l u G l y A l a G l y G l y G l y A l a L y s
625                               630                               635                               640
L y s G l y G l y L y s L y s L y s G l y S e r S e r P h e G l n T h r V a l S e r A l a L e u
645                               650                               655
P h e A r g G l u A s n L e u A s n L y s L e u M e t T h r A s n L e u A r g S e r T h r H i s
660                               665                               670
P r o H i s P h e V a l A r g C y s I l e I l e P r o A s n G l u T h r L y s T h r P r o G l y
675                               680                               685
A l a M e t G l u H i s G l u L e u V a l L e u H i s G l n L e u A r g C y s A s n G l y V a l
690                               695                               700
L e u G l u G l y I l e A r g I l e C y s A r g L y s G l y P h e P r o S e r A r g I l e L e u
705                               710                               715                               720
T y r A l a A s p P h e L y s G l n A r g T y r L y s V a l L e u A s n A l a S e r A l a I l e
725                               730                               735
P r o G l u G l y G l n P h e I l e A s p S e r L y s L y s A l a S e r G l u L y s L e u L e u
740                               745                               750

```

N3027PCT\_sequ.list.txt

Ala Ser Ile Asp Ile Asp His Thr Gln Tyr Lys Phe Gly His Thr Lys  
755 760 765

Val Phe Phe Lys Ala Gly Leu Leu Gly Leu Leu Glu Glu Met Arg Asp  
770 775 780

Asp Lys Leu Ala Gln Leu Ile Thr Arg Thr Gln Ala Arg Cys Arg Gly  
785 790 795 800

Phe Leu Ala Arg Val Glu Tyr Gln Arg Met Val Glu Arg Arg Glu Ala  
805 810 815

Ile Phe Cys Ile Gln Tyr Asn Ile Arg Ser Phe Met Asn Val Lys His  
820 825 830

Trp Pro Trp Met Lys Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser  
835 840 845

Ala Glu Thr Glu Lys Glu Met Ala Thr Met Lys Glu Glu Phe Gln Lys  
850 855 860

Ile Lys Asp Glu Leu Ala Lys Ser Glu Ala Lys Arg Lys Glu Leu Glu  
865 870 875 880

Glu Lys Met Val Thr Leu Leu Lys Glu Lys Asn Asp Leu Gln Leu Gln  
885 890 895

Val Gln Ala Glu Ala Glu Gly Leu Ala Asp Ala Glu Glu Arg Cys Asp  
900 905 910

Gln Leu Ile Lys Thr Lys Ile Gln Leu Glu Ala Lys Ile Lys Glu Val  
915 920 925

Thr Glu Arg Ala Glu Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala  
930 935 940

Lys Lys Arg Lys Leu Glu Asp Glu Cys Ser Glu Leu Lys Lys Asp Ile  
945 950 955 960

Asp Asp Leu Glu Leu Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala  
965 970 975

Thr Glu Asn Lys Val Lys Asn Leu Thr Glu Glu Met Ala Gly Leu Asp  
980 985 990

Glu Thr Ile Ala Lys Leu Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala  
995 1000 1005

His Gln Gln Thr Leu Asp Asp Leu Gln Ala Glu Glu Asp Lys Val  
1010 1015 1020

N3027PCT\_sequ.list.txt

Asn	Thr	Leu	Thr	Lys	Ala	Lys	Ile	Lys	Leu	Glu	Gln	Gln	Val	Asp
1025						1030					1035			
Asp	Leu	Glu	Gly	Ser	Leu	Glu	Gln	Glu	Lys	Lys	Leu	Arg	Met	Asp
1040						1045					1050			
Leu	Glu	Arg	Ala	Lys	Arg	Lys	Leu	Glu	Gly	Asp	Leu	Lys	Leu	Ala
1055						1060					1065			
Gln	Glu	Ser	Ile	Met	Asp	Ile	Glu	Asn	Glu	Lys	Gln	Gln	Leu	Asp
1070						1075					1080			
Glu	Lys	Leu	Lys	Lys	Lys	Glu	Phe	Glu	Ile	Ser	Asn	Leu	Gln	Ser
1085						1090					1095			
Lys	Ile	Glu	Asp	Glu	Gln	Ala	Leu	Gly	Ile	Gln	Leu	Gln	Lys	Lys
1100						1105					1110			
Ile	Lys	Glu	Leu	Gln	Ala	Arg	Ile	Glu	Glu	Leu	Glu	Glu	Glu	Ile
1115						1120					1125			
Glu	Ala	Glu	Arg	Ala	Ser	Arg	Ala	Lys	Ala	Glu	Lys	Gln	Arg	Ser
1130						1135					1140			
Asp	Leu	Ser	Arg	Glu	Leu	Glu	Glu	Ile	Ser	Glu	Arg	Leu	Glu	Glu
1145						1150					1155			
Ala	Gly	Gly	Ala	Thr	Ser	Ala	Gln	Ile	Glu	Met	Asn	Lys	Lys	Arg
1160						1165					1170			
Glu	Ala	Glu	Phe	Gln	Lys	Met	Arg	Arg	Asp	Leu	Glu	Glu	Ala	Thr
1175						1180					1185			
Leu	Gln	His	Glu	Ala	Thr	Ala	Ala	Thr	Leu	Arg	Lys	Lys	His	Ala
1190						1195					1200			
Asp	Ser	Val	Ala	Glu	Leu	Gly	Glu	Gln	Ile	Asp	Asn	Leu	Gln	Arg
1205						1210					1215			
Val	Lys	Gln	Lys	Leu	Glu	Lys	Glu	Lys	Ser	Glu	Met	Lys	Met	Glu
1220						1225					1230			
Ile	Asp	Asp	Leu	Ala	Ser	Asn	Val	Glu	Thr	Val	Ser	Lys	Ala	Lys
1235						1240					1245			
Gly	Asn	Leu	Glu	Lys	Met	Cys	Arg	Thr	Leu	Glu	Asp	Gln	Leu	Ser
1250						1255					1260			
Glu	Leu	Lys	Ser	Lys	Glu	Glu	Glu	Gln	Gln	Arg	Leu	Ile	Asn	Asp
1265						1270					1275			

Leu Thr Ala Gln Arg Gly Arg Leu Gln Thr Glu Ser Gly Glu Phe  
 1280 1285 1290  
 Ser Arg Gln Leu Asp Glu Lys Glu Ala Leu Val Ser Gln Leu Ser  
 1295 1300 1305  
 Arg Gly Lys Gln Ala Phe Thr Gln Gln Ile Glu Glu Leu Lys Arg  
 1310 1315 1320  
 Gln Leu Glu Glu Glu Ile Lys Ala Lys Asn Ala Leu Ala His Ala  
 1325 1330 1335  
 Leu Gln Ser Ser Arg His Asp Cys Asp Leu Leu Arg Glu Gln Tyr  
 1340 1345 1350  
 Glu Glu Glu Gln Glu Ser Lys Ala Glu Leu Gln Arg Ala Leu Ser  
 1355 1360 1365  
 Lys Ala Asn Thr Glu Val Ala Gln Trp Arg Thr Lys Tyr Glu Thr  
 1370 1375 1380  
 Asp Ala Ile Gln Arg Thr Glu Glu Leu Glu Glu Ala Lys Lys Lys  
 1385 1390 1395  
 Leu Ala Gln Arg Leu Gln Ala Ala Glu Glu His Val Glu Ala Val  
 1400 1405 1410  
 Asn Ala Lys Cys Ala Ser Leu Glu Lys Thr Lys Gln Arg Leu Gln  
 1415 1420 1425  
 Asn Glu Val Glu Asp Leu Met Leu Asp Val Glu Arg Thr Asn Ala  
 1430 1435 1440  
 Ala Cys Ala Ala Leu Asp Lys Lys Gln Arg Asn Phe Asp Lys Ile  
 1445 1450 1455  
 Leu Ala Glu Trp Lys Gln Lys Cys Glu Glu Thr His Ala Glu Leu  
 1460 1465 1470  
 Glu Ala Ser Gln Lys Glu Ala Arg Ser Leu Gly Thr Glu Leu Phe  
 1475 1480 1485  
 Lys Ile Lys Asn Ala Tyr Glu Glu Ser Leu Asp Gln Leu Glu Thr  
 1490 1495 1500  
 Leu Lys Arg Glu Asn Lys Asn Leu Gln Gln Glu Ile Ser Asp Leu  
 1505 1510 1515  
 Thr Glu Gln Ile Ala Glu Gly Gly Lys Arg Ile His Glu Leu Glu  
 1520 1525 1530  
 Lys Ile Lys Lys Gln Val Glu Gln Glu Lys Cys Glu Leu Gln Ala  
 1535 1540 1545

1535						1540						1545
Ala	Leu	Glu	Glu	Ala	Glu	Ala	Ser	Leu	Glu	His	Glu	Glu
1550						1555					1560	Gly Lys
Ile	Leu	Arg	Ile	Gln	Leu	Glu	Leu	Asn	Gln	Val	Lys	Ser
1565						1570					1575	Glu Val
Asp	Arg	Lys	Ile	Ala	Glu	Lys	Asp	Glu	Glu	Ile	Asp	Gln
1580						1585					1590	Leu Lys
Arg	Asn	His	Ile	Arg	Ile	Val	Glu	Ser	Met	Gln	Ser	Thr
1595						1600					1605	Leu Asp
Ala	Glu	Ile	Arg	Ser	Arg	Asn	Asp	Ala	Ile	Arg	Leu	Lys
1610						1615					1620	Lys Lys
Met	Glu	Gly	Asp	Leu	Asn	Glu	Met	Glu	Ile	Gln	Leu	Asn
1625						1630					1635	His Ala
Asn	Arg	Met	Ala	Ala	Glu	Ala	Leu	Arg	Asn	Tyr	Arg	Asn
1640						1645					1650	Thr Gln
Gly	Ile	Leu	Lys	Asp	Thr	Gln	Ile	His	Leu	Asp	Asp	Ala
1655						1660					1665	Leu Arg
Ser	Gln	Glu	Asp	Leu	Lys	Glu	Gln	Leu	Ala	Met	Val	Glu
1670						1675					1680	Arg Arg
Ala	Asn	Leu	Leu	Gln	Ala	Glu	Ile	Glu	Glu	Leu	Arg	Ala
1685						1690					1695	Thr Leu
Glu	Gln	Thr	Glu	Arg	Ser	Arg	Lys	Ile	Ala	Glu	Gln	Glu
1700						1705					1710	Leu Leu
Asp	Ala	Ser	Glu	Arg	Val	Gln	Leu	Leu	His	Thr	Gln	Asn
1715						1720					1725	Thr Ser
Leu	Ile	Asn	Thr	Lys	Lys	Lys	Leu	Glu	Thr	Asp	Ile	Ser
1730						1735					1740	Gln Met
Gln	Gly	Glu	Met	Glu	Asp	Ile	Leu	Gln	Glu	Ala	Arg	Asn
1745						1750					1755	Ala Glu
Glu	Lys	Ala	Lys	Lys	Ala	Ile	Thr	Asp	Ala	Ala	Met	Met
1760						1765					1770	Ala Glu
Glu	Leu	Lys	Lys	Glu	Gln	Asp	Thr	Ser	Ala	His	Leu	Glu
1775						1780					1785	Arg Met
Lys	Lys	Asn	Met	Glu	Gln	Thr	Val	Lys	Asp	Leu	Gln	Leu
1790						1795					1800	Arg Leu

N3027PCT\_sequ.list.txt

Asp Glu Ala Glu Gln Leu Ala Leu Lys Gly Gly Lys Lys Gln Ile  
1805 1810 1815

Gln Lys Leu Glu Ala Arg Val Arg Glu Leu Glu Gly Glu Val Glu  
1820 1825 1830

Ser Glu Gln Lys Arg Asn Ala Glu Ala Val Lys Gly Leu Arg Lys  
1835 1840 1845

His Glu Arg Arg Val Lys Glu Leu Thr Tyr Gln Thr Glu Glu Asp  
1850 1855 1860

Arg Lys Asn Ile Leu Arg Leu Gln Asp Leu Val Asp Lys Leu Gln  
1865 1870 1875

Ala Lys Val Lys Ser Tyr Lys Arg Gln Ala Glu Glu Ala Glu Glu  
1880 1885 1890

Gln Ser Asn Thr Asn Leu Ala Lys Phe Arg Lys Leu Gln His Glu  
1895 1900 1905

Leu Glu Glu Ala Glu Glu Arg Ala Asp Ile Ala Glu Ser Gln Val  
1910 1915 1920

Asn Lys Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Val Ile  
1925 1930 1935

Ser Glu Glu  
1940

<210> 59  
<211> 6037  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc \_ feat ure  
<222> (1)..(6037)  
<223> myosin, heavy chain 3, skeletal muscle, embryonic, (MYH3)

<400> 59  
gtggcgagg gtctgggatc tcttggtgt tgcctgtctc tgcctctcatc ctgcaggtgg 60  
gactctcagc tgacaccatg agtagtgaca ctgaaatgga agtgttcggc atagctgctc 120  
ctttcctccg gaagtcagaa aaggagagga tgcaggctca gaaccagccc tttgatgcc 180  
agacgtattg cttcgtggtg gactcaaagg aagaatatgc caaggggaaa atcaagagt 240  
ctcaggatgg gaaggtcact gtggaaactg aggacaacag gaccctggtg gtcaaaccag 300  
aggatgtgta cgccatgaac ccccccaagt tgcacaggat cgaagacatg gccatgctga 360  
cgcacctgaa tgagccagcc gtgctgtaca acctgaagga ccgttacaca tcttggatga 420  
tctatacct a ctcaggcctc ttctgtgtca ctgtcaacc ctacaagtgg ctgccggtgt 480

N3027PCT\_sequ. list . . txt

acaacccccga	ggt ggt ggaa	ggct accgag	gcaaaaagcg	ccaggaggcc	ccacccccaca	540
t c t t c t c c a t	c t c t g a c a a c	g c c t a t c a g t	t c a t g c t g a c	t g a t c g t g a a	a a c c a g t c c a	600
t t c t g a t c a c	c g g a g a a t c c	g g g g c a g g a a	a g a c t g t g a a	c a c c a a a c g g	g t c a t c c a g t	660
a c t t t g c a a c	a a t t g c a g c t	a c t g g g g a c c	t g g c c a a g a a	g a a g g a c t c c	a a a a t g a a g g	720
g g a c t c t g g a	a g a t c a a a t c	a t c a g t g c c a	a t c c c c t g c t	g g a g g c c t t t	g g g a a c g c c a	780
a g a c t g t g a g	g a a t g a c a a c	t c c t c c c g t t	t t g g c a a g t t	c a t c c g a a t c	c a t t t t g g a a	840
c c a c t g g g a a	g c t g g c c t c t	g c a g a t a t t g	a a a c t t a t c t	t c t g g a a a a a	t c a a g a g t c a	900
c t t t c c a g c t	g a a g g c t g a a	a g a a g c t a c c	a c a t c t t c t a	c c a g a t t c t t	t c t a a c a a g a	960
a g c c t g a g c t	c a t a g a g c t g	c t g c t t a t t a	c g a c c a a c c c	t t a c g a c t a c	c c g t t c a t t a	1020
g c c a g g g g g a	g a t c c t g g t g	g c c a g c a t a g	a t g a t g c a g a	g g a g c t g c t g	g c t a c a g a c a	1080
g c g c c a t t g a	c a t c c t g g g c	t t c a c c c c a g	a a g a g a a a t c	t g g g c t c t a c	a a g c t g a c g g	1140
g a g c c g t g a t	g c a c t a c g g g	a a c a t g a a g t	t c a a g c a g a a	g c a g c g a g a g	g a g c a g g c c g	1200
a g c c g g a t g g	c a c a g a a g t g	g c t g a c a a a a	c a g c c t a t c t	g a t g g g c c t g	a a c t c t t c g g	1260
a c c t c c t a a a	a g c t t t g t g c	t t t c c t a g a g	t g a a a g t t g g	g a a t g a g t a c	g t t a c c a a a g	1320
g t c a a a c t g t	g g a t c a g g t t	c a c c a t g c t g	t g a a t g c t c t	t t c a a a a t c a	g t t t a t g a a a	1380
a g t t g t t c t t	g t g g a t g g t c	a c t c g c a t t a	a c c a g c a a c t	g g a t a c g a a g	c t t c c a a g a c	1440
a a c a c t t c a t	t g g t g t t t t g	g a c a t t g c a g	g c t t t g a a a t	c t t t g a g t a t	a a c a g c c t g g	1500
a g c a g c t g t g	c a t c a a c t t c	a c c a a t g a g a	a a c t g c a a c a	g t t t t t c a a c	c a c c a c a t g t	1560
t c g t g c t g g a	g c a g g a g g a g	t a c a a g a a g g	a a g g c a t c g a	g t g g a c g t t c	a t t g a c t t c g	1620
g g a t g g a c c t	g g c t g c c t g c	a t c g a g c t c a	t c g a g a a g c c	t a t g g g c a t c	t t c t c c a t c c	1680
t g g a a g a g g a	g t g c a t g t t c	c c c a a g g c a a	c a g a c a c c t c	c t t c a a g a a c	a a g c t g t a t g	1740
a c c a g c a t c t	t g g a a a g t c c	a a c a a c t t c c	a g a a g c c c a a	g g t g g t c a a a	g g c a g g g c c g	1800
a g g c t c a c t t	c t c a c t g a t c	c a c t a t g c g g	g c a c c g t g g a	c t a c a g t g t c	t c a g g t t g g c	1860
t g g a g a a g a a	c a a g g a c c c t	c t g a a c g a g a	c t g t g g t t g g	g c t g t a c c a g	a a g t c t t c c a	1920
a c a g g c t c c t	g g c a c a c c t c	t a t g c c a c g t	t t g c c a c g g c	g g a t g c t g a c	a g t g g a a a g a	1980
a g a a a g t t g c	c a a g a a g a a g	g g t t c t t c c t	t c c a a a c t g t	c t c t g c c c t t	t t c a g g g a a a	2040
a c c t g a a c a a	g c t g a t g t c a	a a t t t a a g a a	c t a c t c a c c c	t c a t t t t g t g	c g t t g t a t a a	2100
t t c c c a a t g a	a a c c a a a a c t	c c a g g g g c t a	t g g a a c a c a g	c c t t g t t c t g	c a c c a g c t g c	2160
g g t g t a a c g g	t g t c c t g g a g	g g c a t c c g c a	t c t g c a g g a a	a g g g t t c c c a	a a c a g g a t t c	2220
t c t a t g g c g a	t t t t a a a c a a	a g a t a c c g a g	t g c t g a a t g c	c a g t g c a a t c	c c t g a g g g a c	2280
a a t t c a t t g a	c a g c a a g a a a	g c c t g t g a a a	a g c t t c t g g c	a t c c a t t g a t	a t t g a c c a c a	2340
c t c a g t a c a a	a t t t g g a c a t	a c c a a g g t g t	t c t t c a a g g c	t g g c t t g c t g	g g a a c c c t g g	2400
a a g a g a t g c g	g g a t g a c c g c	c t g g c c a a a c	t a a t c a c c c g	g a c a c a a g c t	g t g t g c a g a g	2460
g g t t c c t c a t	g c g t g t g g a a	t t c c a g a a g a	t g g t g c a g a g	g a g g g a g t c c	a t c t t c t g c a	2520

N3027PCT\_sequ. list . txt

t ccagt acaa cat t cgct ca t t cat gaacg t caagcact g gccct ggat g aaact ct t ct	2580
t caagat caa gccct cct c aagagt gcag agact gagaa agagat ggcc accat gaagg	2640
aagaat t cca gaaaacaaaa gat gaact cg ccaagt cgga ggcaaaaagg aaggagct ag	2700
aggaaaaact ggt gact ct g gt ccaagaga agaat gacct gcagct ccaa gt acaagct g	2760
aaagcgaaaa t t t gt t ggat gct gaggaaa gat gcgat ca gct gat caaa gccaaat t cc	2820
agct cgaggc caagat caag gaggt gacag agagagct ga agat gaggag gagat caat g	2880
ct gagct gac ggccaagaag aggaaact gg aggat gaat g ct cagagct c aagaaagaca	2940
t t gat gacct t gagt t gacc ct ggccaagg t t gagaagga gaagcat gcc acagagaaca	3000
aggt t aaaaa cct t act gag gaact ct ct g ggt t agat ga aacaat t gca aagt t aacca	3060
gagagaagaa gccct ccaa gaggcgcacc agcaggcct t ggat gacct c caagct gaag	3120
aagacaaagt caat t ct t t g aacaaaacca agagcaaact ggaacagcaa gt ggaagacc	3180
t ggaaagct c cct agaacaa gaaaagaagc t ccgagt aga cct ggaaagg aacaaaagga	3240
aat t ggaagg agact t gaag ct t gct caag agt ccat at t agat ct ggag aat gacaagc	3300
aacagct gga cgaaaggct c aagaagaaag at t t t gaat a t t gt caact t caaagcaaag	3360
t ggaagat ga gcagacact g gccct ccagt t t cagaagaa aat caaagag t t gcaggct c	3420
gaat t gagga gct ggaagag gagat agagg cggagagggc caccgcgcg aagacagaga	3480
aacagcgcag cgact at gcc cgggagct gg aggagct gag cgagcggct g gaggaggcgg	3540
gaggcgt cac ct ccacgcag at agagct ca acaagaagcg ggaggcggag t t cct gaagc	3600
t gcgcaggga cct ggaggag gccacact gc agcacgaagc cat ggt ggcc gcgct gagga	3660
agaagcat gc ggat agt gt g gccgagct t g gggagcagat t gacaacct g cagcgggt ca	3720
agcagaagct ggagaaggag aagagcgagt t caagct gga gat cgat gac ct ct ccagca	3780
gcat ggagag t gt gt cgaaa t ct aaggcaa at ct ggaaaa aat ct gccga accct ggagg	3840
at cagt t aag t gaggccagg ggcaagaat g aggaaat t ca gaggagcct g agcgagct ga	3900
ccacacagaa gt ct cgt t t g cagaccgagg ct ggt gagct gagt cgt cag ct ggaagaaa	3960
aagaaagcat agt at ccaa ct t t ccagga gcaagcaagc ct t t acccag caaacagaag	4020
agct caagag gcagct ggag gaagagaaca aggccaagaa cgccct ggcg cagccct gc	4080
agt cct cccg ccacgact gt gacct gct gc gggaacagt a t gaggaggag caggaaggca	4140
aagct gagct gcagagggcg ct gt ccaagg ccaat agt ga ggt t gccag t ggagaacca	4200
aat acgagac ggacgccat c cagcgcacag aagagct gga ggaggccaag aaaaaact t g	4260
ct cagcgct t caagat t cc gaggaacagg t t gaggcagt gaat gct aaa t gt gct t cac	4320
t ggagaagac caagcagagg ct gcaaggag aggt ggagga t ct gat ggt t gat gt t gaaa	4380
gagccaat t c ct t ggccgcc gct ct ggaca agaagcagag gaact t t gac aaggt gt t gg	4440
cagagt ggaa gacaaagt gt gaggagagcc aagcagagct ggaggcat cc ct gaaggagt	4500
cccgct cct t gagcact gag ct ct t caaac t gaaaaat gc ct acgaggaa gcct t agat c	4560
aact t gaaac t gt gaaacgg gaaaat aaga act t agagca ggagat agca gat ct cacag	4620

N3027PCT\_sequ. l i s t . . t x t

```

aacaaat tgc t gaaaat ggc aaaacccat cc at gaact gga gaaat caaga aagcagat t g 4680
agct ggaaaa ggct gat at c cagct ggct c t cgaggaagc agaggct gct ct t gagcat g 4740
aagaagccaa gat cct ccga at ccagct t g aat t gacaca agt gaaat ca gaaat t gat a 4800
gaaagat cgc cgagaaggat gaagagat cg agcagct gaa gaggaact ac cagagaacag 4860
t ggaaacccat gcagagcgcc ct ggacgccg aggt gcggag caggaat gaa gccat ccggc 4920
t caagaagaa gat ggagggg gacct gaat g aaat cgagat ccagct gagg cagccaacc 4980
gccaggcggc ggagaccct c aaacacct ca ggagt gt cca gggacagct g aaggat acgc 5040
agct ccacct ggat gat gcc ct ccggggcc aggaggacct gaaggagcag ct ggcat t g 5100
t ggagcgcag agccaacct g ct gcaggccg aggt ggagga gct gcgggct act ct ggagc 5160
agacggagag ggcccggaaa ct ggcggaac aggagct cct ggact ccaac gagagggt gc 5220
agct gct gca t acccagaac accagcct ca t ccacaccaa gaagaagct g gagacagacc 5280
t cat gcagct ccagagt gag gt agaagat g ccagcagga t gcaaggaac gct gaggaga 5340
aggccaagaa ggccat cagc gacgct gcca t gat ggcgga ggagct gaag aaggagcagg 5400
acaccagcgc ccacct t gag cggat gaaga agaacct gga acagacggt g aaggacct gc 5460
agcat cgt ct agat gaggcc gagcagct gg cgct gaaggg cgggaagaag cagat ccaga 5520
aact ggagac caggat ccga gagct ggagt t t gaact t ga gggagagcag aagaagaaca 5580
cagagt ct gt t aagggcct g aggaagt at g agcggagggt caaggagct g acgt accaga 5640
gt gaagagga caggaagaat gt gct gagat t gcaggat ct ggt ggat aaa ct gcaagt ga 5700
aagt caagt c ct acaagagg caggcggagg aggt gat ga acaagccaat gct cat ct ca 5760
ccaaat t ccg aaaggct cag cat gagct gg aggaggccga ggaacgt gcg gat at cgcag 5820
aat ct caagt caacaagct c cgcgct aaga ct cgagact t cacct ccagc aggat ggt gg 5880
t ccacgagag t gaagagt ga gccagccct t ct ggagcagg acagaagat a t gcaaaat gt 5940
at at t t t ct t gat t cct gac cat t gat act t aat gt ccat gt gact ct t t t t cacat gca 6000
at aaact t t g ct t t gt t t ca at ct gggaaa aaaaaa 6037

```

```

<210> 60
<211> 1940
<212> PRT
<213> Homo sapi ens

```

```

<220>
<221> M SC_FEATURE
<222> (1)..(1940)
<223> myosi n, heavy chai n 3, skel et al muscl e, emb ryoni c, ( MYH3)
<400> 60

```

```

Met Ser Ser Asp Thr Gl u Met Gl u Val Phe Gly Ile Ala Ala Pro Phe
1          5          10          15

```

```

Leu Arg Lys Ser Gl u Lys Gl u Arg Ile Gl u Ala Gl n Asn Gl n Pro Phe
20          25          30

```

N3027PCT\_sequ.list.txt

Asp Ala Lys Thr Tyr Cys Phe Val Val Asp Ser Lys Glu Glu Tyr Ala  
 35 40 45  
 Lys Gly Lys Ile Lys Ser Ser Gln Asp Gly Lys Val Thr Val Glu Thr  
 50 55 60  
 Glu Asp Asn Arg Thr Leu Val Val Lys Pro Glu Asp Val Tyr Ala Met  
 65 70 75 80  
 Asn Pro Pro Lys Phe Asp Arg Ile Glu Asp Met Ala Met Leu Thr His  
 85 90 95  
 Leu Asn Glu Pro Ala Val Leu Tyr Asn Leu Lys Asp Arg Tyr Thr Ser  
 100 105 110  
 Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
 115 120 125  
 Tyr Lys Trp Leu Pro Val Tyr Asn Pro Glu Val Val Glu Gly Tyr Arg  
 130 135 140  
 Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
 145 150 155 160  
 Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu  
 165 170 175  
 Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val  
 180 185 190  
 Ile Gln Tyr Phe Ala Thr Ile Ala Ala Thr Gly Asp Leu Ala Lys Lys  
 195 200 205  
 Lys Asp Ser Lys Met Lys Gly Thr Leu Glu Asp Gln Ile Ile Ser Ala  
 210 215 220  
 Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asp  
 225 230 235 240  
 Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Thr Thr  
 245 250 255  
 Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys Ser  
 260 265 270  
 Arg Val Thr Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile Phe Tyr  
 275 280 285  
 Gln Ile Leu Ser Asn Lys Lys Pro Glu Leu Ile Glu Leu Leu Leu Ile  
 290 295 300

N3027PCT\_sequ.list.txt

Thr 305	Thr	Asn	Pro	Tyr	Asp 310	Tyr	Pro	Phe	Ile	Ser 315	Gln	Gly	Glu	Ile	Leu 320
Val	Ala	Ser	Ile	Asp 325	Asp	Ala	Glu	Glu	Leu 330	Leu	Ala	Thr	Asp	Ser 335	Ala
Ile	Asp	Ile	Leu 340	Gly	Phe	Thr	Pro	Glu 345	Glu	Lys	Ser	Gly	Leu 350	Tyr	Lys
Leu	Thr	Gly 355	Ala	Val	Met	His	Tyr 360	Gly	Asn	Met	Lys	Phe 365	Lys	Gln	Lys
Gln	Arg 370	Glu	Glu	Gln	Ala	Glu 375	Pro	Asp	Gly	Thr	Glu 380	Val	Ala	Asp	Lys
Thr 385	Ala	Tyr	Leu	Met	Gly 390	Leu	Asn	Ser	Ser	Asp 395	Leu	Leu	Lys	Ala	Leu 400
Cys	Phe	Pro	Arg	Val 405	Lys	Val	Gly	Asn	Glu 410	Tyr	Val	Thr	Lys	Gly 415	Gln
Thr	Val	Asp	Gln 420	Val	His	His	Ala	Val 425	Asn	Ala	Leu	Ser	Lys 430	Ser	Val
Tyr	Glu	Lys 435	Leu	Phe	Leu	Trp	Met 440	Val	Thr	Arg	Ile	Asn 445	Gln	Gln	Leu
Asp	Thr 450	Lys	Leu	Pro	Arg	Gln 455	His	Phe	Ile	Gly	Val 460	Leu	Asp	Ile	Ala
Gly 465	Phe	Glu	Ile	Phe	Glu 470	Tyr	Asn	Ser	Leu	Glu 475	Gln	Leu	Cys	Ile	Asn 480
Phe	Thr	Asn	Glu 485	Lys	Leu	Gln	Gln	Phe	Phe 490	Asn	His	His	Met	Phe 495	Val
Leu	Glu	Gln	Glu 500	Glu	Tyr	Lys	Lys	Glu 505	Gly	Ile	Glu	Trp	Thr 510	Phe	Ile
Asp	Phe	Gly 515	Met	Asp	Leu	Ala	Ala 520	Cys	Ile	Glu	Leu	Ile 525	Glu	Lys	Pro
Met 530	Gly	Ile	Phe	Ser	Ile	Leu 535	Glu	Glu	Glu	Cys	Met 540	Phe	Pro	Lys	Ala
Thr 545	Asp	Thr	Ser	Phe	Lys 550	Asn	Lys	Leu	Tyr	Asp 555	Gln	His	Leu	Gly	Lys 560
Ser	Asn	Asn	Phe	Gln 565	Lys	Pro	Lys	Val	Val 570	Lys	Gly	Arg	Ala	Glu 575	Ala

H i s P h e S e r L e u I l e H i s T y r A l a G l y T h r V a l A s p T y r S e r V a l S e r  
 580 585 590  
 G l y T r p L e u G l u L y s A s n L y s A s p P r o L e u A s n G l u T h r V a l V a l G l y  
 595 600 605  
 L e u T y r G l n L y s S e r S e r A s n A r g L e u L e u A l a H i s L e u T y r A l a T h r  
 610 615 620  
 P h e A l a T h r A l a A s p A l a A s p S e r G l y L y s L y s L y s V a l A l a L y s L y s  
 625 630 635 640  
 L y s G l y S e r S e r P h e G l n T h r V a l S e r A l a L e u P h e A r g G l u A s n L e u  
 645 650 655  
 A s n L y s L e u M e t S e r A s n L e u A r g T h r T h r H i s P r o H i s P h e V a l A r g  
 660 665 670  
 C y s I l e I l e P r o A s n G l u T h r L y s T h r P r o G l y A l a M e t G l u H i s S e r  
 675 680 685  
 L e u V a l L e u H i s G l n L e u A r g C y s A s n G l y V a l L e u G l u G l y I l e A r g  
 690 695 700  
 I l e C y s A r g L y s G l y P h e P r o A s n A r g I l e L e u T y r G l y A s p P h e L y s  
 705 710 715 720  
 G l n A r g T y r A r g V a l L e u A s n A l a S e r A l a I l e P r o G l u G l y G l n P h e  
 725 730 735  
 I l e A s p S e r L y s L y s A l a C y s G l u L y s L e u L e u A l a S e r I l e A s p I l e  
 740 745 750  
 A s p H i s T h r G l n T y r L y s P h e G l y H i s T h r L y s V a l P h e P h e L y s A l a  
 755 760 765  
 G l y L e u L e u G l y T h r L e u G l u G l u M e t A r g A s p A s p A r g L e u A l a L y s  
 770 775 780  
 L e u I l e T h r A r g T h r G l n A l a V a l C y s A r g G l y P h e L e u M e t A r g V a l  
 785 790 795 800  
 G l u P h e G l n L y s M e t V a l G l n A r g A r g G l u S e r I l e P h e C y s I l e G l n  
 805 810 815  
 T y r A s n I l e A r g S e r P h e M e t A s n V a l L y s H i s T r p P r o T r p M e t L y s  
 820 825 830  
 L e u P h e P h e L y s I l e L y s P r o L e u L e u L y s S e r A l a G l u T h r G l u L y s  
 835 840 845  
 G l u M e t A l a T h r M e t L y s G l u G l u P h e G l n L y s T h r L y s A s p G l u L e u  
 Page 277

850

855

860

Ala Lys Ser Glu Ala Lys Arg Lys Glu Leu Glu Glu Lys Leu Val Thr  
 865 870 875 880  
 Leu Val Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln Ala Glu Ser  
 885 890 895  
 Glu Asn Leu Leu Asp Ala Glu Glu Arg Cys Asp Gln Leu Ile Lys Ala  
 900 905 910  
 Lys Phe Gln Leu Glu Ala Lys Ile Lys Glu Val Thr Glu Arg Ala Glu  
 915 920 925  
 Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala Lys Lys Arg Lys Leu  
 930 935 940  
 Glu Asp Glu Cys Ser Glu Leu Lys Lys Asp Ile Asp Asp Leu Glu Leu  
 945 950 955 960  
 Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu Asn Lys Val  
 965 970 975  
 Lys Asn Leu Thr Glu Glu Leu Ser Gly Leu Asp Glu Thr Ile Ala Lys  
 980 985 990  
 Leu Thr Arg Glu Lys Lys Ala Leu Gln Glu Ala His Gln Gln Ala Leu  
 995 1000 1005  
 Asp Asp Leu Gln Ala Glu Glu Asp Lys Val Asn Ser Leu Asn Lys  
 1010 1015 1020  
 Thr Lys Ser Lys Leu Glu Gln Gln Val Glu Asp Leu Glu Ser Ser  
 1025 1030 1035  
 Leu Glu Gln Glu Lys Lys Leu Arg Val Asp Leu Glu Arg Asn Lys  
 1040 1045 1050  
 Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala Gln Glu Ser Ile Leu  
 1055 1060 1065  
 Asp Leu Glu Asn Asp Lys Gln Gln Leu Asp Glu Arg Leu Lys Lys  
 1070 1075 1080  
 Lys Asp Phe Glu Tyr Cys Gln Leu Gln Ser Lys Val Glu Asp Glu  
 1085 1090 1095  
 Gln Thr Leu Gly Leu Gln Phe Gln Lys Lys Ile Lys Glu Leu Gln  
 1100 1105 1110  
 Ala Arg Ile Glu Glu Leu Glu Glu Glu Ile Glu Ala Glu Arg Ala  
 1115 1120 1125

N3027PCT\_sequ.list.txt

Thr	Arg	Ala	Lys	Thr	Glu	Lys	Gln	Arg	Ser	Asp	Tyr	Ala	Arg	Glu
	1130					1135					1140			
Leu	Glu	Glu	Leu	Ser	Glu	Arg	Leu	Glu	Glu	Ala	Gly	Gly	Val	Thr
	1145					1150					1155			
Ser	Thr	Gln	Ile	Glu	Leu	Asn	Lys	Lys	Arg	Glu	Ala	Glu	Phe	Leu
	1160					1165					1170			
Lys	Leu	Arg	Arg	Asp	Leu	Glu	Glu	Ala	Thr	Leu	Gln	His	Glu	Ala
	1175					1180					1185			
Met	Val	Ala	Ala	Leu	Arg	Lys	Lys	His	Ala	Asp	Ser	Val	Ala	Glu
	1190					1195					1200			
Leu	Gly	Glu	Gln	Ile	Asp	Asn	Leu	Gln	Arg	Val	Lys	Gln	Lys	Leu
	1205					1210					1215			
Glu	Lys	Glu	Lys	Ser	Glu	Phe	Lys	Leu	Glu	Ile	Asp	Asp	Leu	Ser
	1220					1225					1230			
Ser	Ser	Met	Glu	Ser	Val	Ser	Lys	Ser	Lys	Ala	Asn	Leu	Glu	Lys
	1235					1240					1245			
Ile	Cys	Arg	Thr	Leu	Glu	Asp	Gln	Leu	Ser	Glu	Ala	Arg	Gly	Lys
	1250					1255					1260			
Asn	Glu	Glu	Ile	Gln	Arg	Ser	Leu	Ser	Glu	Leu	Thr	Thr	Gln	Lys
	1265					1270					1275			
Ser	Arg	Leu	Gln	Thr	Glu	Ala	Gly	Glu	Leu	Ser	Arg	Gln	Leu	Glu
	1280					1285					1290			
Glu	Lys	Glu	Ser	Ile	Val	Ser	Gln	Leu	Ser	Arg	Ser	Lys	Gln	Ala
	1295					1300					1305			
Phe	Thr	Gln	Gln	Thr	Glu	Glu	Leu	Lys	Arg	Gln	Leu	Glu	Glu	Glu
	1310					1315					1320			
Asn	Lys	Ala	Lys	Asn	Ala	Leu	Ala	His	Ala	Leu	Gln	Ser	Ser	Arg
	1325					1330					1335			
His	Asp	Cys	Asp	Leu	Leu	Arg	Glu	Gln	Tyr	Glu	Glu	Glu	Gln	Glu
	1340					1345					1350			
Gly	Lys	Ala	Glu	Leu	Gln	Arg	Ala	Leu	Ser	Lys	Ala	Asn	Ser	Glu
	1355					1360					1365			
Val	Ala	Gln	Trp	Arg	Thr	Lys	Tyr	Glu	Thr	Asp	Ala	Ile	Gln	Arg
	1370					1375					1380			

N3027PCT\_sequ.list.txt

Thr	G u	G u	Leu	G u	G u	Al a	Lys	Lys	Lys	Leu	Al a	G n	Arg	Leu
	1385					1390					1395			
G n	Asp	Ser	G u	G u	G n	Val	G u	Al a	Val	Asn	Al a	Lys	Cys	Al a
	1400					1405					1410			
Ser	Leu	G u	Lys	Thr	Lys	G n	Arg	Leu	G n	G y	G u	Val	G u	Asp
	1415					1420					1425			
Leu	Met	Val	Asp	Val	G u	Arg	Al a	Asn	Ser	Leu	Al a	Al a	Al a	Leu
	1430					1435					1440			
Asp	Lys	Lys	G n	Arg	Asn	Phe	Asp	Lys	Val	Leu	Al a	G u	Trp	Lys
	1445					1450					1455			
Thr	Lys	Cys	G u	G u	Ser	G n	Al a	G u	Leu	G u	Al a	Ser	Leu	Lys
	1460					1465					1470			
G u	Ser	Arg	Ser	Leu	Ser	Thr	G u	Leu	Phe	Lys	Leu	Lys	Asn	Al a
	1475					1480					1485			
Tyr	G u	G u	Al a	Leu	Asp	G n	Leu	G u	Thr	Val	Lys	Arg	G u	Asn
	1490					1495					1500			
Lys	Asn	Leu	G u	G n	G u	I le	Al a	Asp	Leu	Thr	G u	G n	I le	Al a
	1505					1510					1515			
G u	Asn	G y	Lys	Thr	I le	His	G u	Leu	G u	Lys	Ser	Arg	Lys	G n
	1520					1525					1530			
I le	G u	Leu	G u	Lys	Al a	Asp	I le	G n	Leu	Al a	Leu	G u	G u	Al a
	1535					1540					1545			
G u	Al a	Al a	Leu	G u	His	G u	G u	Al a	Lys	I le	Leu	Arg	I le	G n
	1550					1555					1560			
Leu	G u	Leu	Thr	G n	Val	Lys	Ser	G u	I le	Asp	Arg	Lys	I le	Al a
	1565					1570					1575			
G u	Lys	Asp	G u	G u	I le	G u	G n	Leu	Lys	Arg	Asn	Tyr	G n	Arg
	1580					1585					1590			
Thr	Val	G u	Thr	Met	G n	Ser	Al a	Leu	Asp	Al a	G u	Val	Arg	Ser
	1595					1600					1605			
Arg	Asn	G u	Al a	I le	Arg	Leu	Lys	Lys	Lys	Met	G u	G y	Asp	Leu
	1610					1615					1620			
Asn	G u	I le	G u	I le	G n	Leu	Ser	His	Al a	Asn	Arg	G n	Al a	Al a
	1625					1630					1635			

G u	Thr	Leu	Lys	His	Leu	Arg	Ser	Val	G n	G y	G n	Leu	Lys	Asp
1640						1645					1650			
Thr	G n	Leu	His	Leu	Asp	Asp	Al a	Leu	Arg	G y	G n	G u	Asp	Leu
1655						1660					1665			
Lys	G u	G n	Leu	Al a	I l e	Val	G u	Arg	Arg	Al a	Asn	Leu	Leu	G n
1670						1675					1680			
Al a	G u	Val	G u	G u	Leu	Arg	Al a	Thr	Leu	G u	G n	Thr	G u	Arg
1685						1690					1695			
Al a	Arg	Lys	Leu	Al a	G u	G n	G u	Leu	Leu	Asp	Ser	Asn	G u	Arg
1700						1705					1710			
Val	G n	Leu	Leu	His	Thr	G n	Asn	Thr	Ser	Leu	I l e	His	Thr	Lys
1715						1720					1725			
Lys	Lys	Leu	G u	Thr	Asp	Leu	Met	G n	Leu	G n	Ser	G u	Val	G u
1730						1735					1740			
Asp	Al a	Ser	Arg	Asp	Al a	Arg	Asn	Al a	G u	G u	Lys	Al a	Lys	Lys
1745						1750					1755			
Al a	I l e	Thr	Asp	Al a	Al a	Met	Met	Al a	G u	G u	Leu	Lys	Lys	G u
1760						1765					1770			
G n	Asp	Thr	Ser	Al a	His	Leu	G u	Arg	Met	Lys	Lys	Asn	Leu	G u
1775						1780					1785			
G n	Thr	Val	Lys	Asp	Leu	G n	His	Arg	Leu	Asp	G u	Al a	G u	G n
1790						1795					1800			
Leu	Al a	Leu	Lys	G y	G y	Lys	Lys	G n	I l e	G n	Lys	Leu	G u	Thr
1805						1810					1815			
Arg	I l e	Arg	G u	Leu	G u	Phe	G u	Leu	G u	G y	G u	G n	Lys	Lys
1820						1825					1830			
Asn	Thr	G u	Ser	Val	Lys	G y	Leu	Arg	Lys	Tyr	G u	Arg	Arg	Val
1835						1840					1845			
Lys	G u	Leu	Thr	Tyr	G n	Ser	G u	G u	Asp	Arg	Lys	Asn	Val	Leu
1850						1855					1860			
Arg	Leu	G n	Asp	Leu	Val	Asp	Lys	Leu	G n	Val	Lys	Val	Lys	Ser
1865						1870					1875			
Tyr	Lys	Arg	G n	Al a	G u	G u	Al a	Asp	G u	G n	Al a	Asn	Al a	His
1880						1885					1890			
Leu	Thr	Lys	Phe	Arg	Lys	Al a	G n	His	G u	Leu	G u	G u	Al a	G u

1895

1900

1905

G u A r g A l a A s p I l e A l a G u S e r G l n V a l A s n L y s L e u A r g A l a  
 1910 1915 1920

L y s T h r A r g A s p P h e T h r S e r S e r A r g M e t V a l V a l H i s G l u S e r  
 1925 1930 1935

G u G u  
 1940

<210> 61  
 <211> 6016  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> (1)..(6016)  
 <223> myosin, heavy chain 4, skeletal muscle (MYH4)

<400> 61  
 at cct t cct c aaaat t ct t g aagt agt t gt ct gct t t gag cct gccacct t ct t cat ct g 60  
 at aat acaag aggt at acct agt ccagt ac t gccat caat aacct gcagc cat gagt t ct 120  
 gact ct gaga t ggccat t t t t ggggaggct gct cct t t cc t ccgaaagt c t gaaaaggag 180  
 cgaat t gaag ct cagaacaa gcct t t t gat gccaaagacat cagt ct t t gt ggt ggaccct 240  
 aaggagt cct acgt gaaagc aat agt gcag agcagggag gggggaagg gacagccaag 300  
 accgaagct g gagct act gt aact gt gaaa gaagaccaag t ct t ct ccat gaaccct ccc 360  
 aaat at gaca agat cgagga cat ggccat g at gact cacc t gcat gagcc t gct gt gct g 420  
 t at aacct ca aagagcgt t a cgcagcct gg at gat ct aca cct act cggg cct ct t ct gt 480  
 gt caccgt ca acccct acaa gt ggct gccg gt gt acaacc ct gaggt ggt gacagcct ac 540  
 cgaggcaaaa agcgccagga ggccccaccc cat at ct t ct ccat ct ct ga caat gcct at 600  
 cagt t cat gc t aact gat cg t gaaaaccag t caat ct t ga t t act ggaga at ct ggt gca 660  
 gggaagact g t gaacacgaa gcgt gt cat c cagt act t t g caacaat t gc agt t act gga 720  
 gagaagaaaa aagaggaacc t gcct ct ggc aaaat gcagg ggaccct t ga agat caaat c 780  
 at cagt gct a accccct act ggaagcct t c ggcaat gcca agaccgt gag gaat gacaac 840  
 t cct ct cgct t t ggt aaat t cat caggat c cat t t t ggt g ccacaggcaa act ggct t ct 900  
 gcagat at t g aaacat at ct gct agagaag t cccgagt t a ct t t t cagct aaaggct gaa 960  
 agaagct acc acat at t t t a t caaat cct g t ccaat aaga aaccagagct cat t gaaat g 1020  
 ct t ct gat ca ccaccaaccc at at gact t c gcat t t gt ca gccaaagggga aat t act gt g 1080  
 cccagcat t g at gaccagga agagct gat g gccacagat a gt gct gt gga cat cct ggg 1140  
 t t cact gct g at gaaaagg ggcatt t ac aagct cact g gagccgt gat gcat t at ggg 1200  
 aacat gaaat t caagcaaaa gcaaagggaa gagcaggcag agccagat gg cacggaagt t 1260

N3027PCT\_sequ. list.txt

gct gacaaag ct gct t at ct gacaagt ct g aact ct gct g acct gct caa at ct ct ct gc	1320
t at cccagag t caaggt cgg caat gagt t c gt aaccaaag gccagact gt gcagcaggt g	1380
t acaat gcag t ggggt gct ct ggccaaagcc at ct acgaga agat gt t cct gt ggat ggt c	1440
acccgcat ca accagcagct ggacaccaag cagcccaggc agt act t cat cgggggt ct t g	1500
gacat t gct g gct t t gagat ct t t gat t t c aacagcct gg agcagct gt g cat caact t c	1560
accaacgaga aact gcaaca gt t t t t caac caccacat gt t cgt gct gga gcaggaagag	1620
t acaagaagg aaggcat cga gt gggagt t c at t gact t cg ggat ggacct ggct gcct gc	1680
at cgagct ca t cgagaagcc t at gggcat c t t ct ccat cc t agaagagga gt gcat gt t c	1740
cccaaggcaa cagacacct c ct t caagaac aagct gt at g aacaacat ct t ggaaaat cc	1800
aacaact t cc agaagcccaa gcct gccaaa ggcaagcct g aggct cact t ct cact ggt g	1860
cact at gccg gcaccgt gga ct acaacat c gccggct ggc t ggacaaaaa caaggacccc	1920
ct gaat gaga ct gt ggt ggg gct gt accag aagt ct gcaa t gaagact ct ggct t t cct c	1980
t t ct ct gggg cacaaact gc t gaagcagag ggt ggt ggt g gaaagaaagg t ggcaaaaag	2040
aaggggt t ct t ct t t ccagac agt gt cagct ct t t t caggg agaat t t gaa t aagct gat g	2100
accaact t ga ggagcact ca cccccact t t gt gcgggt gca t cat ccccaa t gaaact aaa	2160
act cct ggt g ccat ggagca t gagct t gt c ct gcat cagc t gaggt gt aa cggt gt gct g	2220
gaaggcat cc gcat ct gcag gaaaggct t c ccaagcagaa t cct t t at gc agact t caaa	2280
cagagat aca aggt t ct aaa t gcgagt gct at cccagagg gt cagt t cat t gacagcaag	2340
aaggct t ct g agaaact t ct aggggt ct at t gaaat t gacc acaccagt a caaat t cggt	2400
cat accaagg t t t t ct t caa agct ggcct g ct gggaact c t agaggaaat gcgagat gaa	2460
aagct agct c aact cat cac gcgcact caa gccat at gca gaggggt t cct gat gagagt g	2520
gagt t cagaa agat gat gga gaggagagag t ccat ct t ct gcat t cagt a caacat ccgt	2580
gct t t cat ga at gt gaagca ct ggccct gg at gaagct gt at t t caagat caagcccct c	2640
ct caagagt g cagagacaga gaaggagat g gccaacat ga aggaagaat t t gagaaaacc	2700
aaagaagagc t ggct aagac agaggcaaaa aggaagaac t agaagaaaa gat ggt gacg	2760
ct aat gcaag agaaaaat ga ct t acaact c caagt t caag ct gaagcaga t gcct t ggct	2820
gat gcagagg aaagat gt ga t cagt t gat t aaaacaaaa t ccaact t ga ggccaaaat c	2880
aaagaggt aa ct gaaagagc t gaggat gag gaagagat ca at gct gagct gacagccaag	2940
aagaggaaac t ggaggat ga at gt t cagag ct caagaaag acat t gat ga cct t gagct g	3000
acact ggcca aggt t gagaa ggagaaacat gccacagaga acaaggt gaa aaacct caca	3060
gaagagat gg caggt ct gga t gaaaccat t gct aagct ga ccaaggagaa gaaggct ct c	3120
caggaggccc accagcagac cct ggat gac ct gcagat gg aggaggacaa agt caacacc	3180
ct gaccaaag ct aaaaccaa gct agaacag caagt ggacg at ct t gaagg at ct ct ggaa	3240
caagaaaaga aact t t gcat ggact t agaa agagccaaga gaaaact gga ggggt gacct a	3300
aaat t ggccc aagaat ccac aat ggat aca gaaaat gaca aacagcaact t aat gagaaa	3360

N3027PCT\_sequ. list . . txt

ct caaaaaga	aagagt t t ga	aat gagcaat	ct gcaaggca	agat t gaaga	t gaacaagcc	3420
ct t gcaat ac	agct acaaaa	gaagat caaa	gaat t acagg	cccgc at t ga	ggagct ggag	3480
gaggaaaat cg	aggcagagcg	ggcct cccgg	gccaaagcag	agaagcagcg	ct ct gacct c	3540
t cccgggagc	t ggaggagat	cagt gagagg	ct ggaagaag	ccggt ggggc	cact t cagcc	3600
cagat t gaga	t gaacaagaa	gcgggaggct	gagt t ccaga	aaat gcgcag	ggacct ggaa	3660
gagt ccaccc	t gcagcacga	agccacggca	gct gct ct t c	ggaagaagca	cgcagat agt	3720
gt ggct gagc	t t ggggagca	gat t gacagc	ct t cagcggg	t caagcagaa	gct ggagaag	3780
gaaaagagt g	agct gaagat	ggagat caat	gacct t gct a	gt aacat gga	gact gt ct cc	3840
aaagccaagg	caaact t t ga	gaaaat gt gc	cgcaccct ag	aggaccagct	t agt gaaat a	3900
aaaacaaaagg	aagaagagca	acaacgct t a	at aaat gagt	t gt cagccca	gaaggcacgt	3960
t t acacacag	aat caggt ga	gt t t t cacga	cagct agat g	aaaaagat gc	t at ggt t t ct	4020
cagct at ccc	gaggcaaaca	agcat t t aca	caacagat t g	aagaat t aaa	gaggcagct a	4080
gaagaggaga	ct aaggccaa	gagcact ct g	gccc at gcc	t gcagt cagc	ccgccc at gac	4140
t gt gacct gc	t gcgggaaca	gt at gaggag	gagcaggaag	ccaaggct ga	gct gcagagg	4200
ggaat gt cca	aggccaacag	t gaggt t gcc	cagt ggagga	ccaagt acga	gacggacgcc	4260
at ccagcgca	cagaggagct	ggaggaggcc	aagaagaagc	t agcccagcg	t ct gcaggat	4320
gcagaagaac	at gt agaagc	t gt gaat t cc	aaat gt gct t	ct ct t gaaaa	gacaaagcag	4380
aggct acaga	at gaagt aga	ggacct cat g	at t gat gt gg	aacgat ct aa	t gct gcct gc	4440
at agct ct cg	at aagaagca	aagaaact t t	gacaaggt t c	t ggcagaat g	gaaacagaag	4500
t at gaggaaa	ct caggct ga	act t gaggcc	t cccagaagg	agt cgcgt t c	t ct cagcact	4560
gagct gt t ca	aggt gaagaa	t gcct acgag	gaat ccct gg	at cat ct t ga	aact ct aaag	4620
cgagagaat a	agaact t aca	acaggagat t	t ct gacct ga	cagagcaa at	t gcagagggt	4680
ggaaagcat a	t ccat gaact	ggagaaaagt a	aagaaacaac	t t gat cat ga	gaagagt gaa	4740
ct acagact t	ccct agagga	agcagaggca	t ct ct t gagg	at gaagaagg	caaaat t ct t	4800
cgc at t caac	t t gagct aaa	t caggt gaaa	t ct gagat t g	accgaaaaat	t gct gaaaaa	4860
gat gaagaac	t cgat cagct	aaagaggaac	cat ct cagag	t t gt ggagt c	aat gcagagt	4920
acact ggat g	ct gagat cag	gagcagaaat	gat gct ct ga	ggat caagaa	gaagat ggag	4980
ggagat ct t a	at gaaat gga	aat ccagct g	aaccat gcc	accgccaggc	t gct gaggca	5040
ct aaggaat c	t t agaaacac	acaaggaat a	ct gaaggaca	ct cagct aca	t t t ggat gat	5100
gccat cagag	gccaaagat ga	cct t aaggaa	caact ggcaa	t ggt t gagcg	cagagct aac	5160
ct gat gcagg	ct gaagt t ga	agagct cagg	gcat ccct gg	aacggact ga	gagaggcagg	5220
aaaat ggcag	agcaagagct	t ct ggat gcc	agt gaacgt g	t gcaact t ct	gcacact cag	5280
aacaccagcc	t gat caacac	caagaagaag	ct ggaaacag	acat t t ccca	aat ccaggga	5340
gagat ggagg	acat cgt cca	ggaagcccgc	aat gcagagg	agaaggccaa	gaaggccat c	5400

N3027PCT\_sequ.list.txt

act gat gct g ccat gat ggc t gaggagct g aagaaggaac aggacaccag cgcccacct g 5460  
gagcggat ga agaagaacat ggagcagacc gt gaaggat c t gcagct ccg t ct ggat gag 5520  
gct gagcagc t ggcgct gaa ggggt gggaag aagcagat cc agaaact gga ggccagggt g 5580  
agagagct t g aaagt gaggt ggaaagt gaa cagaagcaca at gt t gaggc t gt caagggt 5640  
ct t cgcaaac at gagagaag agt gaaggaa ct cact t acc agact gagga ggaccgcaag 5700  
aat at t ct ca ggct gcagga ct t ggt ggac aaat t gcaaa ccaaagt caa agct t acaag 5760  
agacaagct g aagaggct ga ggaacaat cc aat gt caacc t t gccaaagt t ccgcaagct c 5820  
cagcacgagc t ggaggaggc caaggaacgg gct gacat t g ct gagt ccca agt caacaag 5880  
ct gagagt ga agagt cgga ggt t cacaca aaagt cat aa gt gaagagt a at t cat t ct a 5940  
at gaaagaaa at gt gaccaa agaaat gcac gaaat gt gaa gt t ct t t gt c act gt cct gt 6000  
at at caagga aat aaa 6016

<210> 62  
<211> 1939  
<212> PRT  
<213> Homo sapi ens

<220>  
<221> M SC FEATURE  
<222> (1)..(1939)  
<223> myosin, heavy chain 4, skeletal muscle (MYH4)

<400> 62

Met Ser Ser Asp Ser Gl u Met Ala Ile Phe Gly Gl u Ala Ala Pro Phe  
1 5 10 15

Leu Arg Lys Ser Gl u Lys Gl u Arg Ile Gl u Ala Gl n Asn Lys Pro Phe  
20 25 30

Asp Ala Lys Thr Ser Val Phe Val Val Asp Pro Lys Gl u Ser Tyr Val  
35 40 45

Lys Ala Ile Val Gl n Ser Arg Gl u Gly Gly Lys Val Thr Ala Lys Thr  
50 55 60

Gl u Ala Gly Ala Thr Val Thr Val Lys Gl u Asp Gl n Val Phe Ser Met  
65 70 75 80

Asn Pro Pro Lys Tyr Asp Lys Ile Gl u Asp Met Ala Met Met Thr His  
85 90 95

Leu His Gl u Pro Ala Val Leu Tyr Asn Leu Lys Gl u Arg Tyr Ala Ala  
100 105 110

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
115 120 125

Tyr Lys Trp Leu Pro Val Tyr Asn Pro Gl u Val Val Thr Ala Tyr Arg

130

135

140

Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
145 150 155 160

Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu  
165 170 175

Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val  
180 185 190

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu  
195 200 205

Glu Pro Ala Ser Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile  
210 215 220

Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg  
225 230 235 240

Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly  
245 250 255

Ala Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu  
260 265 270

Lys Ser Arg Val Thr Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile  
275 280 285

Phe Tyr Gln Ile Leu Ser Asn Lys Lys Pro Glu Leu Ile Glu Met Leu  
290 295 300

Leu Ile Thr Thr Asn Pro Tyr Asp Phe Ala Phe Val Ser Gln Gly Glu  
305 310 315 320

Ile Thr Val Pro Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp  
325 330 335

Ser Ala Val Asp Ile Leu Gly Phe Thr Ala Asp Glu Lys Val Ala Ile  
340 345 350

Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys  
355 360 365

Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala  
370 375 380

Asp Lys Ala Ala Tyr Leu Thr Ser Leu Asn Ser Ala Asp Leu Leu Lys  
385 390 395 400

Ser Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Phe Val Thr Lys  
405 410 415

N3027PCT\_sequ.list.txt

G l y   G n   T h r   V a l   G n   G n   V a l   T y r   A s n   A l a   V a l   G l y   A l a   L e u   A l a   L y s  
                     420                                    425                                    430

A l a   I l e   T y r   G u   L y s   M e t   P h e   L e u   T r p   M e t   V a l   T h r   A r g   I l e   A s n   G n  
                     435                                    440                                    445

G n   L e u   A s p   T h r   L y s   G n   P r o   A r g   G n   T y r   P h e   I l e   G l y   V a l   L e u   A s p  
                     450                                    455                                    460

I l e   A l a   G l y   P h e   G u   I l e   P h e   A s p   P h e   A s n   S e r   L e u   G u   G n   L e u   C y s  
                     465                                    470                                    475                                    480

I l e   A s n   P h e   T h r   A s n   G u   L y s   L e u   G n   G n   P h e   P h e   A s n   H i s   H i s   M e t  
                                     485                                    490                                    495

P h e   V a l   L e u   G u   G n   G u   G u   T y r   L y s   L y s   G u   G l y   I l e   G u   T r p   G u  
                     500                                    505                                    510

P h e   I l e   A s p   P h e   G l y   M e t   A s p   L e u   A l a   A l a   C y s   I l e   G u   L e u   I l e   G u  
                     515                                    520                                    525

L y s   P r o   M e t   G l y   I l e   P h e   S e r   I l e   L e u   G u   G u   G u   C y s   M e t   P h e   P r o  
                     530                                    535                                    540

L y s   A l a   T h r   A s p   T h r   S e r   P h e   L y s   A s n   L y s   L e u   T y r   G u   G n   H i s   L e u  
                     545                                    550                                    555                                    560

G l y   L y s   S e r   A s n   A s n   P h e   G n   L y s   P r o   L y s   P r o   A l a   L y s   G l y   L y s   P r o  
                                     565                                    570                                    575

G u   A l a   H i s   P h e   S e r   L e u   V a l   H i s   T y r   A l a   G l y   T h r   V a l   A s p   T y r   A s n  
                     580                                    585                                    590

I l e   A l a   G l y   T r p   L e u   A s p   L y s   A s n   L y s   A s p   P r o   L e u   A s n   G u   T h r   V a l  
                     595                                    600                                    605

V a l   G l y   L e u   T y r   G n   L y s   S e r   A l a   M e t   L y s   T h r   L e u   A l a   P h e   L e u   P h e  
                     610                                    615                                    620

S e r   G l y   A l a   G n   T h r   A l a   G u   A l a   G u   G l y   G l y   G l y   G l y   L y s   L y s   G l y  
                     625                                    630                                    635                                    640

G l y   L y s   L y s   L y s   G l y   S e r   S e r   P h e   G n   T h r   V a l   S e r   A l a   L e u   P h e   A r g  
                     645                                    650                                    655

G u   A s n   L e u   A s n   L y s   L e u   M e t   T h r   A s n   L e u   A r g   S e r   T h r   H i s   P r o   H i s  
                     660                                    665                                    670

P h e   V a l   A r g   C y s   I l e   I l e   P r o   A s n   G u   T h r   L y s   T h r   P r o   G l y   A l a   M e t  
                     675                                    680                                    685

N3027PCT\_sequ.list.txt

G u H i s G u L e u V a l L e u H i s G n L e u A r g C y s A s n G l y V a l L e u G u  
 690 695 700  
 G l y I l e A r g I l e C y s A r g L y s G l y P h e P r o S e r A r g I l e L e u T y r A l a  
 705 710 715 720  
 A s p P h e L y s G n A r g T y r L y s V a l L e u A s n A l a S e r A l a I l e P r o G u  
 725 730 735  
 G l y G n P h e I l e A s p S e r L y s L y s A l a S e r G u L y s L e u L e u G l y S e r  
 740 745 750  
 I l e G u I l e A s p H i s T h r G n T y r L y s P h e G l y H i s T h r L y s V a l P h e  
 755 760 765  
 P h e L y s A l a G l y L e u L e u G l y T h r L e u G u G u M e t A r g A s p G u L y s  
 770 775 780  
 L e u A l a G n L e u I l e T h r A r g T h r G n A l a I l e C y s A r g G l y P h e L e u  
 785 790 795 800  
 M e t A r g V a l G u P h e A r g L y s M e t M e t G u A r g A r g G u S e r I l e P h e  
 805 810 815  
 C y s I l e G n T y r A s n I l e A r g A l a P h e M e t A s n V a l L y s H i s T r p P r o  
 820 825 830  
 T r p M e t L y s L e u T y r P h e L y s I l e L y s P r o L e u L e u L y s S e r A l a G u  
 835 840 845  
 T h r G u L y s G u M e t A l a A s n M e t L y s G u G u P h e G u L y s T h r L y s  
 850 855 860  
 G u G u L e u A l a L y s T h r G u A l a L y s A r g L y s G u L e u G u G u L y s  
 865 870 875 880  
 M e t V a l T h r L e u M e t G n G u L y s A s n A s p L e u G n L e u G n V a l G n  
 885 890 895  
 A l a G u A l a A s p A l a L e u A l a A s p A l a G u G u A r g C y s A s p G n L e u  
 900 905 910  
 I l e L y s T h r L y s I l e G n L e u G u A l a L y s I l e L y s G u V a l T h r G u  
 915 920 925  
 A r g A l a G u A s p G u G u G u I l e A s n A l a G u L e u T h r A l a L y s L y s  
 930 935 940  
 A r g L y s L e u G u A s p G u C y s S e r G u L e u L y s L y s A s p I l e A s p A s p  
 945 950 955 960

N3027PCT\_sequ.list.txt

Leu G u Leu Thr Leu Ala Lys Val G u Lys G u Lys His Ala Thr G u  
 965 970 975  
 Asn Lys Val Lys Asn Leu Thr G u G u Met Ala Gly Leu Asp G u Thr  
 980 985 990  
 Ile Ala Lys Leu Thr Lys G u Lys Lys Ala Leu G n G u Ala His G n  
 995 1000 1005  
 G n Thr Leu Asp Asp Leu G n Met G u G u Asp Lys Val Asn Thr  
 1010 1015 1020  
 Leu Thr Lys Ala Lys Thr Lys Leu G u G n G n Val Asp Asp Leu  
 1025 1030 1035  
 G u Gly Ser Leu G u G n G u Lys Lys Leu Cys Met Asp Leu G u  
 1040 1045 1050  
 Arg Ala Lys Arg Lys Leu G u Gly Asp Leu Lys Leu Ala G n G u  
 1055 1060 1065  
 Ser Thr Met Asp Thr G u Asn Asp Lys G n G n Leu Asn G u Lys  
 1070 1075 1080  
 Leu Lys Lys Lys G u Phe G u Met Ser Asn Leu G n Gly Lys Ile  
 1085 1090 1095  
 G u Asp G u G n Ala Leu Ala Ile G n Leu G n Lys Lys Ile Lys  
 1100 1105 1110  
 G u Leu G n Ala Arg Ile G u G u Leu G u G u G u Ile G u Ala  
 1115 1120 1125  
 G u Arg Ala Ser Arg Ala Lys Ala G u Lys G n Arg Ser Asp Leu  
 1130 1135 1140  
 Ser Arg G u Leu G u G u Ile Ser G u Arg Leu G u G u Ala Gly  
 1145 1150 1155  
 Gly Ala Thr Ser Ala G n Ile G u Met Asn Lys Lys Arg G u Ala  
 1160 1165 1170  
 G u Phe G n Lys Met Arg Arg Asp Leu G u G u Ser Thr Leu G n  
 1175 1180 1185  
 His G u Ala Thr Ala Ala Ala Leu Arg Lys Lys His Ala Asp Ser  
 1190 1195 1200  
 Val Ala G u Leu Gly G u G n Ile Asp Ser Leu G n Arg Val Lys  
 1205 1210 1215  
 G n Lys Leu G u Lys G u Lys Ser G u Leu Lys Met G u Ile Asn  
 Page 289

1220

1225

1230

Asp	Leu	Ala	Ser	Asn	Met	Glu	Thr	Val	Ser	Lys	Ala	Lys	Ala	Asn
1235						1240					1245			
Phe	Glu	Lys	Met	Cys	Arg	Thr	Leu	Glu	Asp	Gln	Leu	Ser	Glu	Ile
1250						1255					1260			
Lys	Thr	Lys	Glu	Glu	Glu	Gln	Gln	Arg	Leu	Ile	Asn	Glu	Leu	Ser
1265						1270					1275			
Ala	Gln	Lys	Ala	Arg	Leu	His	Thr	Glu	Ser	Gly	Glu	Phe	Ser	Arg
1280						1285					1290			
Gln	Leu	Asp	Glu	Lys	Asp	Ala	Met	Val	Ser	Gln	Leu	Ser	Arg	Gly
1295						1300					1305			
Lys	Gln	Ala	Phe	Thr	Gln	Gln	Ile	Glu	Glu	Leu	Lys	Arg	Gln	Leu
1310						1315					1320			
Glu	Glu	Glu	Thr	Lys	Ala	Lys	Ser	Thr	Leu	Ala	His	Ala	Leu	Gln
1325						1330					1335			
Ser	Ala	Arg	His	Asp	Cys	Asp	Leu	Leu	Arg	Glu	Gln	Tyr	Glu	Glu
1340						1345					1350			
Glu	Gln	Glu	Ala	Lys	Ala	Glu	Leu	Gln	Arg	Gly	Met	Ser	Lys	Ala
1355						1360					1365			
Asn	Ser	Glu	Val	Ala	Gln	Trp	Arg	Thr	Lys	Tyr	Glu	Thr	Asp	Ala
1370						1375					1380			
Ile	Gln	Arg	Thr	Glu	Glu	Leu	Glu	Glu	Ala	Lys	Lys	Lys	Leu	Ala
1385						1390					1395			
Gln	Arg	Leu	Gln	Asp	Ala	Glu	Glu	His	Val	Glu	Ala	Val	Asn	Ser
1400						1405					1410			
Lys	Cys	Ala	Ser	Leu	Glu	Lys	Thr	Lys	Gln	Arg	Leu	Gln	Asn	Glu
1415						1420					1425			
Val	Glu	Asp	Leu	Met	Ile	Asp	Val	Glu	Arg	Ser	Asn	Ala	Ala	Cys
1430						1435					1440			
Ile	Ala	Leu	Asp	Lys	Lys	Gln	Arg	Asn	Phe	Asp	Lys	Val	Leu	Ala
1445						1450					1455			
Glu	Trp	Lys	Gln	Lys	Tyr	Glu	Glu	Thr	Gln	Ala	Glu	Leu	Glu	Ala
1460						1465					1470			
Ser	Gln	Lys	Glu	Ser	Arg	Ser	Leu	Ser	Thr	Glu	Leu	Phe	Lys	Val
1475						1480					1485			

N3027PCT\_sequ.list.txt

Lys	Asn	Ala	Tyr	Glu	Glu	Ser	Leu	Asp	His	Leu	Glu	Thr	Leu	Lys
	1490					1495					1500			
Arg	Glu	Asn	Lys	Asn	Leu	Gln	Gln	Glu	Ile	Ser	Asp	Leu	Thr	Glu
	1505					1510					1515			
Gln	Ile	Ala	Glu	Gly	Gly	Lys	His	Ile	His	Glu	Leu	Glu	Lys	Val
	1520					1525					1530			
Lys	Lys	Gln	Leu	Asp	His	Glu	Lys	Ser	Glu	Leu	Gln	Thr	Ser	Leu
	1535					1540					1545			
Glu	Glu	Ala	Glu	Ala	Ser	Leu	Glu	His	Glu	Glu	Gly	Lys	Ile	Leu
	1550					1555					1560			
Arg	Ile	Gln	Leu	Glu	Leu	Asn	Gln	Val	Lys	Ser	Glu	Ile	Asp	Arg
	1565					1570					1575			
Lys	Ile	Ala	Glu	Lys	Asp	Glu	Glu	Leu	Asp	Gln	Leu	Lys	Arg	Asn
	1580					1585					1590			
His	Leu	Arg	Val	Val	Glu	Ser	Met	Gln	Ser	Thr	Leu	Asp	Ala	Glu
	1595					1600					1605			
Ile	Arg	Ser	Arg	Asn	Asp	Ala	Leu	Arg	Ile	Lys	Lys	Lys	Met	Glu
	1610					1615					1620			
Gly	Asp	Leu	Asn	Glu	Met	Glu	Ile	Gln	Leu	Asn	His	Ala	Asn	Arg
	1625					1630					1635			
Gln	Ala	Ala	Glu	Ala	Leu	Arg	Asn	Leu	Arg	Asn	Thr	Gln	Gly	Ile
	1640					1645					1650			
Leu	Lys	Asp	Thr	Gln	Leu	His	Leu	Asp	Asp	Ala	Ile	Arg	Gly	Gln
	1655					1660					1665			
Asp	Asp	Leu	Lys	Glu	Gln	Leu	Ala	Met	Val	Glu	Arg	Arg	Ala	Asn
	1670					1675					1680			
Leu	Met	Gln	Ala	Glu	Val	Glu	Glu	Leu	Arg	Ala	Ser	Leu	Glu	Arg
	1685					1690					1695			
Thr	Glu	Arg	Gly	Arg	Lys	Met	Ala	Glu	Gln	Glu	Leu	Leu	Asp	Ala
	1700					1705					1710			
Ser	Glu	Arg	Val	Gln	Leu	Leu	His	Thr	Gln	Asn	Thr	Ser	Leu	Ile
	1715					1720					1725			
Asn	Thr	Lys	Lys	Lys	Leu	Glu	Thr	Asp	Ile	Ser	Gln	Ile	Gln	Gly
	1730					1735					1740			

N3027PCT\_sequ.list.txt

[illegible]

```
<210> 63
<211> 5937
<212> DNA
<213> Homo sapiens
```

```

<220>
<221>   m i s c _ f e a t u r e
<222>   ( 1 ) . . ( 5 9 3 7 )
<223>   m y o s i n , h e a v y c h a i n 6 , c a r d i a c m u s c l e , a l p h a , ( c a r d i o m y o p a t h y ,
        h y p e r t r o p h i c 1 ) ( M Y H 6 )

```

N3027PCT\_sequ. list . . txt

```

<400> 63
agagagact c ct gcggccca gat t ct t cag gat t ct ccgt gaagggat aa ccaggggaag 60
caccaagat g accgat gccc agat ggct ga ct t t ggggca gcggcccagt acct ccgcaa 120
gt cagagaag gagcgt ct ag aggcccagac ccggccct t t gacat t cgca ct gagt gct t 180
cgt gcccgat gacaaggaag agt t t gt caa agccaagat t t t gt cccggg agggaggcaa 240
ggg cat t gct gaaaccgaga at gggaagac ggt gact gt g aaggaggacc aggt gt t gca 300
gcagaaccca cccaagt t cg acaagat t ga ggacat ggcc at gct gacct t cct gcacga 360
gcccgcggt g ct t t t caacc t caaggagcg ct acgcggcc t ggat gat at at acct act c 420
gggcct ct t c t gt gt cact g t caaccct a caagt ggct g ccgt gt aca at gccgaggt 480
ggg ggccgcc t accggggca agaagaggag t gagggcccg cccacat ct t ct ccat ct c 540
cgacaacgcc t at cagt aca t gct gacaga t cgggagaac cagt ccat cc t cat cacggg 600
agaat ccggg gcggggaaga ct gt gaacac caagcgt gt c at ccagt act t t gccagcat 660
t gcagccat a ggt gaccgt g gcaagaagga caat gccaat gcgaacaagg gcaccct gga 720
ggaccagat c at ccaggcca accccgct ct ggaggcct t c ggcaat gcca agact gt ccg 780
gaacgacaac t cct cccgct t t gggaaat t cat t aggat c cact t t gggg ccact ggaaa 840
gct ggct t ct gcagacat ag agacct acct gct ggagaag t cccgggt ga t ct t ccagct 900
gaaagct gag agaaact acc acat ct t ct a ccagat t ct g t ccaacaaga agccggagt t 960
gct ggacat g ct gct ggt ca ccaacaat cc ct acgact ac gcct t cgt gt ct cagggaga 1020
ggg gt ccgt g gcct ccat t g at gact ccga ggagct cat g gccaccgat a gt gcct t t ga 1080
cgt gct gggc t t cact t cag aggagaaagc t ggcgt ct ac aagct gacgg gagccat cat 1140
gcact acggg aacat gaagt t caagcagaa gcagcgggag gagcaggcgg agccagacgg 1200
caccgaagat gct gacaagt cggcct acct cat ggggct g aact cagct g acct gct caa 1260
ggggct gt gc caccct cggg t gaaagt ggg caacgagt at gt caccaagg ggcagagcgt 1320
gcagcaggt g t act act cca t cggggct ct ggccaaggca gt gt at gaga agat gt t caa 1380
ct ggat ggt g acgcgcat ca acgccacct ggagaccaag cagccacgcc agt act t cat 1440
aggagt cct g gacat cgct g gct t cgagat ct t cgact t c aacagct t t g agcagct ct g 1500
cat caact t c accaacgaga agct gcagca gt t ct t caac caccacat gt t cgt gct gga 1560
gcaggaggag t acaagaagg agggcat t ga gt ggacat t c at t gact t t g gcat ggacct 1620
gcaggcct gc at t gacct ca t cgagaagcc cat gggcat c at gt ccat cc t ggaggagga 1680
gt gcat gt t c cccaaggcca ct gacat gac ct t caaggcc aagct gt acg acaaccacct 1740
gggcaagt cc aacaat t t cc agaagccacg caacat caag gggaagcagg aagcccact t 1800
ct ccct gat c cact acgccg gcact gt gga ct acaacat c ct gggct ggc t ggaaaaaaa 1860
caaggat cct ct caacgaga ct gt t gt ggc cct gt accag aagt cct ccc t caagct cat 1920
ggccact ct c t t ct cct cct acgcaact gc cgat act ggg gacagt ggt a aaagcaaagg 1980
aggcaagaaa aagggt cat cct t ccagac ggt gt cggct ct ccaccggg aaaat ct caa 2040

```

N3027PCT\_sequ. list .txt

caagct aat g accaacct ga ggaccacca t cct cact t t gt gcgt t gca t cat ccccaa	2100
t gagcggaag gct ccagggg t gat ggacaa cccct ggt c at gcaccagc t gcgt gcaa	2160
t gggt gct g gagggcat cc gcat ct gcag gaagggt t c cccaaccgca t cct ct acgg	2220
ggact t ccgg cagaggt at c gcat cct gaa cccagt ggcc at cct gagg gacagt t cat	2280
t gat agcagg aaggggacag agaagct gct cagct ct ct g gacat t gat c acaaccagt a	2340
caagt t t ggc cacaccaagg t gt t ct t caa ggcagggt g ct t gggct gc t ggaggagat	2400
gcgggat gag aggct gagcc gcat cat cac gcgcat gcag gcccaagccc ggggccagct	2460
cat gcgcat t gagt t caaga agat agt gga acgcagggt gccct gct gg t aat ccagt g	2520
gaacat t cgg gcct t cat gg ggg t caagaa t t ggccct gg at gaagct ct act t caagat	2580
caagccgct g ct gaagagcg cagagacgga gaaggagat g gccacat ga aggaagagt t	2640
cgggcgcat c aaagagacgc t ggagaagt c cgaggct cgc cgcaaggagc t ggaggagaa	2700
gat ggt gt cc ct gct gcagg agaagaat ga cct gcagct c caagt gcagg cggaacaaga	2760
caacct caat gat gct gagg agcgt gcga ccagct gat c aaaaacaaga t t cagct gga	2820
ggccaaagt a aaggagat ga at gagaggct ggaggat gag gaggagat ga acgcggagct	2880
cact gccaaag aagcgcaagc t ggaagacga gt gct cagag ct caagaagg acat t gat ga	2940
cct ggagct g acact ggcca aggt ggagaa ggagaagcat gcaacagaga acaaggt gaa	3000
gaacct aaca gaggagat gg ct gggct gga t gaaat cat c gct aagct ga ccaaggagaa	3060
gaaagct ct a caagaggccc at cagcaggc cct ggat gac ct t caggt t g aggaagacaa	3120
ggt caacagc ct gt ccaagt ct aaggt caa gct ggagcag caggt ggat g at ct ggaggg	3180
at cct agag caagagaaga aggt gcgcat ggacct ggag cgagcaaagc ggaaact gga	3240
ggcgacct g aagct gaccc aggagagcat cat ggacct g gaaaat gat a aact gcagct	3300
ggaagaaaag ct t aagaaga aggagt t t ga cat t aat cag cagaacagt a agat t gagga	3360
t gagcaggt g ct ggccct t c aact acagaa gaaact gaag gaaaaccagg cacgcat cga	3420
ggagct ggag gaggagct gg aggccgagcg caccgccagg gct aaggt gg agaagct gcg	3480
ct cagacct g t ct cgggagc t ggaggagat cagcgagcgg ct ggaagagg ccggcggggc	3540
cacgt ccgt g cagat cgaga t gaacaagaa gcgcgaggcc gagt t ccaga agat gcggcg	3600
ggacct ggag gaggccacgc t gcagcacga ggccact gcc gcggccct gc gcaagaagca	3660
cgccgacagc gt ggccgagc t gggcgagca gat cgacaac ct gcagcggg t gaagcagaa	3720
gct ggagaag gagaagagcg agt t caagct ggagct ggat gacgt cacct ccaacat gga	3780
gcagat cat c aaggccaagg caaacct gga gaaagt gt ct cggacgct gg aggaccaggc	3840
caat gagt ac cgcgt gaagc t agaagaggc ccaacgct cc ct caat gat t t caccacca	3900
gcgagccaag ct gcagaccg agaat ggaga gt t ggcccgg cagct agagg aaaaggaggc	3960
gct aat ct cg cagct gaccc gggggaagct ct ct t at acc cagcaaat gg aggacct caa	4020
aaggcagct g gaggaggagg gcaaggcgaa gaacgccct g gcccat gcac t gcagt cggc	4080
ccggcat gac t gcgacct gc t gcgggagca gt acgaggag gagacagagg ccaaggccga	4140

N3027PCT\_sequ. list . . txt

gct gcagcgc	gt cct gt cca	aggccaact c	ggaggt ggcc	cagt ggagga	ccaagt at ga	4200
gacggacgcc	at t cagcgga	ct gaggagct	cgaagaggcc	aaaaagaagc	t ggcccagcg	4260
gct gcaggat	gccgaggagg	ccgt ggaggc	t gt t aat gcc	aagt gct cct	cact ggagaa	4320
gaccaagcac	cggct acaga	at gagat aga	ggact t gat g	gt ggacgt ag	agcgct ccaa	4380
t gct gct gct	gcagccct gg	acaagaagca	gagaaact t t	gacaagat cc	t ggccgagt g	4440
gaagcagaag	t at gaggagt	cgcagt ct ga	gct ggagt cc	t cacagaagg	aggct cgct c	4500
cct cagcaca	gagct ct t ca	agct caagaa	cgcct acgag	gagt ccct gg	agcacct aga	4560
gacct t caag	cgggagaaca	agaacct t ca	ggaggaaat c	t cggacct t a	ct gacgagct	4620
aggagaagga	ggaaagaat g	t gcat gagct	ggagaagg t c	cgcaaacagc	t ggaggt gga	4680
gaagct ggag	ct gcagt cag	ccct ggagga	ggcagaggcc	t ccct ggagc	acgaggaggg	4740
caagat cct c	cgggcccagc	t agagt t caa	ccagat caag	gcagagat cg	agcggaagct	4800
ggcagagaag	gacgaggaga	t ggaacaggc	caagcgcaac	caccagcggg	t ggt ggact c	4860
gct gcagacc	t ccct ggat g	cagagacacg	cagccgcaac	gaggt cct ga	gggt gaagaa	4920
gaagat ggaa	ggagacct ca	at gagat gga	gat ccagct c	agccacgcca	accgcat ggc	4980
t gccgaggcc	cagaagcaag	t caagagcct	ccagagct t g	ct gaaggaca	cccagat cca	5040
gct ggacgat	gcggt ccgt g	ccaacgacga	cct gaaggag	aacat cgcca	t cgt ggagcg	5100
gcgcaacaac	ct gct gcagg	ct gagct gga	ggagct gcgt	gccgt ggt gg	agcagacaga	5160
gcggt cccgg	aagct ggcg	agcaggagct	gat t gagacc	agcgagcggg	t gcagct gct	5220
gcat t cccag	aacaccagcc	t cat caacca	gaagaagaag	at ggagt cgg	at ct gaccca	5280
gct ccagt cg	gaagt ggagg	aggcagt gca	ggagt gcaga	aacgccgagg	agaaggccaa	5340
gaaggccat c	acggat gccg	ccat gat ggc	agaggagct g	aagaaggagc	aggacaccag	5400
cgcccacct g	gagcgcat ga	agaagaacat	ggagcagacc	at t aaggacc	t gcagcaccg	5460
gct ggacgag	gccgagcaga	t cgccct caa	gggaggcaag	aagcagct gc	agaagct gga	5520
agcgcggggt g	cgggagct gg	aggggt gagct	ggaggccgag	cagaagcgca	acgcagagt c	5580
ggt gaagggc	at gaggaaga	gcgagcggcg	cat caaggag	ct cacct acc	agacagagga	5640
agacaaaaag	aacct gct gc	ggct acagga	cct ggt ggac	aagct gcaac	t gaaggt caa	5700
ggcct acaag	cgccaggccg	aggaggcgga	ggagcaagcc	aacaccaacc	t gt ccaagt t	5760
ccgcaaggt g	cagcat gagg	t ggat gaggc	agaggagcgg	gcggacat cg	ct gagt ccca	5820
ggt caacaag	ct t cgagcca	agagccgt ga	cat t ggt gcc	aagcaaaaaa	t gcacgat ga	5880
ggagt gacac	t gcct cggga	acct cact ct	t gccaacct g	t aat aaat at	gagt gcc	5937

<210> 64  
 <211> 1939  
 <212> PRT  
 <213> Homo sapi ens

<220>

&lt;221&gt; M SC\_FEATURE

&lt;222&gt; (1)..(1939)

&lt;223&gt; myosin, heavy chain 6, cardiac muscle, alpha, (cardiomyopathy, hypertrophic 1) (MYH6)

&lt;400&gt; 64

Met Thr Asp Ala Gln Met Ala Asp Phe Gly Ala Ala Ala Gln Tyr Leu  
1 5 10 15Arg Lys Ser Glu Lys Glu Arg Leu Glu Ala Gln Thr Arg Pro Phe Asp  
20 25 30Ile Arg Thr Glu Cys Phe Val Pro Asp Asp Lys Glu Glu Phe Val Lys  
35 40 45Ala Lys Ile Leu Ser Arg Glu Gly Gly Lys Val Ile Ala Glu Thr Glu  
50 55 60Asn Gly Lys Thr Val Thr Val Lys Glu Asp Gln Val Leu Gln Gln Asn  
65 70 75 80Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Leu Thr Phe Leu  
85 90 95His Glu Pro Ala Val Leu Phe Asn Leu Lys Glu Arg Tyr Ala Ala Trp  
100 105 110Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro Tyr  
115 120 125Lys Trp Leu Pro Val Tyr Asn Ala Glu Val Val Ala Ala Tyr Arg Gly  
130 135 140Lys Lys Arg Ser Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp Asn  
145 150 155 160Ala Tyr Gln Tyr Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu Ile  
165 170 175Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val Ile  
180 185 190Gln Tyr Phe Ala Ser Ile Ala Ala Ile Gly Asp Arg Gly Lys Lys Asp  
195 200 205Asn Ala Asn Ala Asn Lys Gly Thr Leu Glu Asp Gln Ile Ile Gln Ala  
210 215 220Asn Pro Ala Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asp  
225 230 235 240Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala Thr  
245 250 255

N3027PCT\_sequ.list.txt

Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys Ser  
 260 265 270  
 Arg Val Ile Phe Gln Leu Lys Ala Glu Arg Asn Tyr His Ile Phe Tyr  
 275 280 285  
 Gln Ile Leu Ser Asn Lys Lys Pro Glu Leu Leu Asp Met Leu Leu Val  
 290 295 300  
 Thr Asn Asn Pro Tyr Asp Tyr Ala Phe Val Ser Gln Gly Glu Val Ser  
 305 310 315 320  
 Val Ala Ser Ile Asp Asp Ser Glu Glu Leu Met Ala Thr Asp Ser Ala  
 325 330 335  
 Phe Asp Val Leu Gly Phe Thr Ser Glu Glu Lys Ala Gly Val Tyr Lys  
 340 345 350  
 Leu Thr Gly Ala Ile Met His Tyr Gly Asn Met Lys Phe Lys Gln Lys  
 355 360 365  
 Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Asp Ala Asp Lys  
 370 375 380  
 Ser Ala Tyr Leu Met Gly Leu Asn Ser Ala Asp Leu Leu Lys Gly Leu  
 385 390 395 400  
 Cys His Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly Gln  
 405 410 415  
 Ser Val Gln Gln Val Tyr Tyr Ser Ile Gly Ala Leu Ala Lys Ala Val  
 420 425 430  
 Tyr Glu Lys Met Phe Asn Trp Met Val Thr Arg Ile Asn Ala Thr Leu  
 435 440 445  
 Glu Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile Ala  
 450 455 460  
 Gly Phe Glu Ile Phe Asp Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn  
 465 470 475 480  
 Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe Val  
 485 490 495  
 Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr Phe Ile  
 500 505 510  
 Asp Phe Gly Met Asp Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro  
 515 520 525

N3027PCT\_sequ.list.txt

Met Gly Ile Met Ser Ile Leu Gu Gu Gu Cys Met Phe Pro Lys Ala  
530 535 540

Thr Asp Met Thr Phe Lys Ala Lys Leu Tyr Asp Asn His Leu Gly Lys  
545 550 555 560

Ser Asn Asn Phe Gln Lys Pro Arg Asn Ile Lys Gly Lys Gln Gu Ala  
565 570 575

His Phe Ser Leu Ile His Tyr Ala Gly Thr Val Asp Tyr Asn Ile Leu  
580 585 590

Gly Trp Leu Gu Lys Asn Lys Asp Pro Leu Asn Gu Thr Val Val Ala  
595 600 605

Leu Tyr Gln Lys Ser Ser Leu Lys Leu Met Ala Thr Leu Phe Ser Ser  
610 615 620

Tyr Ala Thr Ala Asp Thr Gly Asp Ser Gly Lys Ser Lys Gly Gly Lys  
625 630 635 640

Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Leu His Arg Gu Asn  
645 650 655

Leu Asn Lys Leu Met Thr Asn Leu Arg Thr Thr His Pro His Phe Val  
660 665 670

Arg Cys Ile Ile Pro Asn Gu Arg Lys Ala Pro Gly Val Met Asp Asn  
675 680 685

Pro Leu Val Met His Gln Leu Arg Cys Asn Gly Val Leu Gu Gly Ile  
690 695 700

Arg Ile Cys Arg Lys Gly Phe Pro Asn Arg Ile Leu Tyr Gly Asp Phe  
705 710 715 720

Arg Gln Arg Tyr Arg Ile Leu Asn Pro Val Ala Ile Pro Gu Gly Gln  
725 730 735

Phe Ile Asp Ser Arg Lys Gly Thr Gu Lys Leu Leu Ser Ser Leu Asp  
740 745 750

Ile Asp His Asn Gln Tyr Lys Phe Gly His Thr Lys Val Phe Phe Lys  
755 760 765

Ala Gly Leu Leu Gly Leu Leu Gu Gu Met Arg Asp Gu Arg Leu Ser  
770 775 780

Arg Ile Ile Thr Arg Met Gln Ala Gln Ala Arg Gly Gln Leu Met Arg  
785 790 795 800

N3027PCT\_sequ.list.txt

I l e G u P h e L y s L y s I l e V a l G u A r g A r g A s p A l a L e u L e u V a l I l e  
805 810 815

G n T r p A s n I l e A r g A l a P h e M e t G l y V a l L y s A s n T r p P r o T r p M e t  
820 825 830

L y s L e u T y r P h e L y s I l e L y s P r o L e u L e u L y s S e r A l a G l u T h r G l u  
835 840 845

L y s G l u M e t A l a T h r M e t L y s G l u G l u P h e G l y A r g I l e L y s G l u T h r  
850 855 860

L e u G l u L y s S e r G l u A l a A r g A r g L y s G l u L e u G l u G l u L y s M e t V a l  
865 870 875 880

S e r L e u L e u G n G l u L y s A s n A s p L e u G n L e u G n V a l G n A l a G l u  
885 890 895

G n A s p A s n L e u A s n A s p A l a G l u G l u A r g C y s A s p G n L e u I l e L y s  
900 905 910

A s n L y s I l e G n L e u G l u A l a L y s V a l L y s G l u M e t A s n G l u A r g L e u  
915 920 925

G l u A s p G l u G l u G l u M e t A s n A l a G l u L e u T h r A l a L y s L y s A r g L y s  
930 935 940

L e u G l u A s p G l u C y s S e r G l u L e u L y s L y s A s p I l e A s p A s p L e u G l u  
945 950 955 960

L e u T h r L e u A l a L y s V a l G l u L y s G l u L y s H i s A l a T h r G l u A s n L y s  
965 970 975

V a l L y s A s n L e u T h r G l u G l u M e t A l a G l y L e u A s p G l u I l e I l e A l a  
980 985 990

L y s L e u T h r L y s G l u L y s L y s A l a L e u G n G l u A l a H i s G n G n A l a  
995 1000 1005

L e u A s p A s p L e u G n V a l G l u G l u A s p L y s V a l A s n S e r L e u S e r  
1010 1015 1020

L y s S e r L y s V a l L y s L e u G l u G n G n V a l A s p A s p L e u G l u G l y  
1025 1030 1035

S e r L e u G l u G n G l u L y s L y s V a l A r g M e t A s p L e u G l u A r g A l a  
1040 1045 1050

L y s A r g L y s L e u G l u G l y A s p L e u L y s L e u T h r G n G l u S e r I l e  
1055 1060 1065

M e t A s p L e u G l u A s n A s p L y s L e u G n L e u G l u G l u L y s L e u L y s  
Page 299

1070

1075

1080

Lys	Lys	G u	Phe	Asp	I l e	Asn	G n	G n	Asn	Ser	Lys	I l e	G u	Asp
	1085					1090					1095			
G u	G n	Val	Leu	Al a	Leu	G n	Leu	G n	Lys	Lys	Leu	Lys	G u	Asn
	1100					1105					1110			
G n	Al a	Arg	I l e	G u	G u	Leu	G u	G u	G u	Leu	G u	Al a	G u	Arg
	1115					1120					1125			
Thr	Al a	Arg	Al a	Lys	Val	G u	Lys	Leu	Arg	Ser	Asp	Leu	Ser	Arg
	1130					1135					1140			
G u	Leu	G u	G u	I l e	Ser	G u	Arg	Leu	G u	G u	Al a	G y	G y	Al a
	1145					1150					1155			
Thr	Ser	Val	G n	I l e	G u	Met	Asn	Lys	Lys	Arg	G u	Al a	G u	Phe
	1160					1165					1170			
G n	Lys	Met	Arg	Arg	Asp	Leu	G u	G u	Al a	Thr	Leu	G n	Hi s	G u
	1175					1180					1185			
Al a	Thr	Al a	Al a	Al a	Leu	Arg	Lys	Lys	Hi s	Al a	Asp	Ser	Val	Al a
	1190					1195					1200			
G u	Leu	G y	G u	G n	I l e	Asp	Asn	Leu	G n	Arg	Val	Lys	G n	Lys
	1205					1210					1215			
Leu	G u	Lys	G u	Lys	Ser	G u	Phe	Lys	Leu	G u	Leu	Asp	Asp	Val
	1220					1225					1230			
Thr	Ser	Asn	Met	G u	G n	I l e	I l e	Lys	Al a	Lys	Al a	Asn	Leu	G u
	1235					1240					1245			
Lys	Val	Ser	Arg	Thr	Leu	G u	Asp	G n	Al a	Asn	G u	Tyr	Arg	Val
	1250					1255					1260			
Lys	Leu	G u	G u	Al a	G n	Arg	Ser	Leu	Asn	Asp	Phe	Thr	Thr	G n
	1265					1270					1275			
Arg	Al a	Lys	Leu	G n	Thr	G u	Asn	G y	G u	Leu	Al a	Arg	G n	Leu
	1280					1285					1290			
G u	G u	Lys	G u	Al a	Leu	I l e	Ser	G n	Leu	Thr	Arg	G y	Lys	Leu
	1295					1300					1305			
Ser	Tyr	Thr	G n	G n	Met	G u	Asp	Leu	Lys	Arg	G n	Leu	G u	G u
	1310					1315					1320			
G u	G y	Lys	Al a	Lys	Asn	Al a	Leu	Al a	Hi s	Al a	Leu	G n	Ser	Al a
	1325					1330					1335			

N3027PCT\_sequ.list.txt

Arg His 1340	Asp Cys	Asp Leu	Leu 1345	Arg Glu	Gln Tyr	Glu 1350	Glu Glu	Thr
Glu Ala 1355	Lys Ala	Glu Leu	Gln 1360	Arg Val	Leu Ser	Lys 1365	Ala Asn	Ser
Glu Val 1370	Ala Gln	Trp Arg	Thr 1375	Lys Tyr	Glu Thr	Asp 1380	Ala Ile	Gln
Arg Thr 1385	Glu Glu	Leu Glu	Glu 1390	Ala Lys	Lys Lys	Leu 1395	Ala Gln	Arg
Leu Gln 1400	Asp Ala	Glu Glu	Ala 1405	Val Glu	Ala Val	Asn 1410	Ala Lys	Cys
Ser Ser 1415	Leu Glu	Lys Thr	Lys 1420	His Arg	Leu Gln	Asn 1425	Glu Ile	Glu
Asp Leu 1430	Met Val	Asp Val	Glu 1435	Arg Ser	Asn Ala	Ala 1440	Ala Ala	Ala
Leu Asp 1445	Lys Lys	Gln Arg	Asn 1450	Phe Asp	Lys Ile	Leu 1455	Ala Glu	Trp
Lys Gln 1460	Lys Tyr	Glu Glu	Ser 1465	Gln Ser	Glu Leu	Glu 1470	Ser Ser	Gln
Lys Glu 1475	Ala Arg	Ser Leu	Ser 1480	Thr Glu	Leu Phe	Lys 1485	Leu Lys	Asn
Ala Tyr 1490	Glu Glu	Ser Leu	Glu 1495	His Leu	Glu Thr	Phe 1500	Lys Arg	Glu
Asn Lys 1505	Asn Leu	Gln Glu	Glu 1510	Ile Ser	Asp Leu	Thr 1515	Glu Gln	Leu
Gly Glu 1520	Gly Gly	Lys Asn	Val 1525	His Glu	Leu Glu	Lys 1530	Val Arg	Lys
Gln Leu 1535	Glu Val	Glu Lys	Leu 1540	Glu Leu	Gln Ser	Ala 1545	Leu Glu	Glu
Ala Glu 1550	Ala Ser	Leu Glu	His 1555	Glu Glu	Gly Lys	Ile 1560	Leu Arg	Ala
Gln Leu 1565	Glu Phe	Asn Gln	Ile 1570	Lys Ala	Glu Ile	Glu 1575	Arg Lys	Leu
Ala Glu 1580	Lys Asp	Glu Glu	Met 1585	Glu Gln	Ala Lys	Arg 1590	Asn His	Gln

N3027PCT\_sequ.list.txt

Arg	Val	Val	Asp	Ser	Leu	Gln	Thr	Ser	Leu	Asp	Ala	Glu	Thr	Arg
1595						1600					1605			
Ser	Arg	Asn	Glu	Val	Leu	Arg	Val	Lys	Lys	Lys	Met	Glu	Gly	Asp
1610						1615					1620			
Leu	Asn	Glu	Met	Glu	Ile	Gln	Leu	Ser	His	Ala	Asn	Arg	Met	Ala
1625						1630					1635			
Ala	Glu	Ala	Gln	Lys	Gln	Val	Lys	Ser	Leu	Gln	Ser	Leu	Leu	Lys
1640						1645					1650			
Asp	Thr	Gln	Ile	Gln	Leu	Asp	Asp	Ala	Val	Arg	Ala	Asn	Asp	Asp
1655						1660					1665			
Leu	Lys	Glu	Asn	Ile	Ala	Ile	Val	Glu	Arg	Arg	Asn	Asn	Leu	Leu
1670						1675					1680			
Gln	Ala	Glu	Leu	Glu	Glu	Leu	Arg	Ala	Val	Val	Glu	Gln	Thr	Glu
1685						1690					1695			
Arg	Ser	Arg	Lys	Leu	Ala	Glu	Gln	Glu	Leu	Ile	Glu	Thr	Ser	Glu
1700						1705					1710			
Arg	Val	Gln	Leu	Leu	His	Ser	Gln	Asn	Thr	Ser	Leu	Ile	Asn	Gln
1715						1720					1725			
Lys	Lys	Lys	Met	Glu	Ser	Asp	Leu	Thr	Gln	Leu	Gln	Ser	Glu	Val
1730						1735					1740			
Glu	Glu	Ala	Val	Gln	Glu	Cys	Arg	Asn	Ala	Glu	Glu	Lys	Ala	Lys
1745						1750					1755			
Lys	Ala	Ile	Thr	Asp	Ala	Ala	Met	Met	Ala	Glu	Glu	Leu	Lys	Lys
1760						1765					1770			
Glu	Gln	Asp	Thr	Ser	Ala	His	Leu	Glu	Arg	Met	Lys	Lys	Asn	Met
1775						1780					1785			
Glu	Gln	Thr	Ile	Lys	Asp	Leu	Gln	His	Arg	Leu	Asp	Glu	Ala	Glu
1790						1795					1800			
Gln	Ile	Ala	Leu	Lys	Gly	Gly	Lys	Lys	Gln	Leu	Gln	Lys	Leu	Glu
1805						1810					1815			
Ala	Arg	Val	Arg	Glu	Leu	Glu	Gly	Glu	Leu	Glu	Ala	Glu	Gln	Lys
1820						1825					1830			
Arg	Asn	Ala	Glu	Ser	Val	Lys	Gly	Met	Arg	Lys	Ser	Glu	Arg	Arg
1835						1840					1845			

# N3027PCT\_sequ.list.txt

I l e Lys G u L e u T h r T y r G n T h r G u G u A s p Lys Lys A s n L e u  
 1850 1855 1860

L e u A r g L e u G n A s p L e u V a l A s p Lys L e u G n L e u Lys V a l Lys  
 1865 1870 1875

A l a T y r Lys A r g G n A l a G u G u A l a G u G u G n A l a A s n T h r  
 1880 1885 1890

A s n L e u S e r Lys P h e A r g Lys V a l G n H i s G u L e u A s p G u A l a  
 1895 1900 1905

G u G u A r g A l a A s p I l e A l a G u S e r G n V a l A s n Lys L e u A r g  
 1910 1915 1920

A l a Lys S e r A r g A s p I l e G y A l a Lys G n Lys M e t H i s A s p G u  
 1925 1930 1935

G u

<210> 65  
 <211> 6044  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> (1)..(6044)  
 <223> myosin, heavy chain 7, cardiac muscle, beta (MYH7)

<400> 65  
 cacagctctgtctctgtctgtctttccc tgcctgctctc aggtcccctg caggccttgg 60  
 ccccttttctt catctgtaga cacacttgag tagccaggc acagccatgg gagat t cggg 120  
 gatggcagtc tttggggctg ccgcccccta cctgcgcaag tcagagaagg agcggctaga 180  
 agcgcagacc aggccttttg acctcaagaa ggatgtcttc gtgcctgatg acaaacagga 240  
 gtttgtcaag gccaatatcg tgcctcgaga ggggtggcaa gt cactgccg agaccgagt a 300  
 tggcaagaca gtgaccgtga aggaggacca ggtgatgcag cagaaccac ccaagt t cga 360  
 caaaatcgag gacatggcca tgcctgacctt cctgcatgag cccgcgggtgc tctacaacct 420  
 caaggatcgc tacggctcct ggatgatcta cacctactcg ggcctcttct gtgtcaccgt 480  
 caacccttac aagtggctgc cgggtgtacac tctgaggtg gtggctgcct accgggggcaa 540  
 gaagaggagc gaggccccgc cccacatctt ctccatctcc gacaacgcct atcagtacat 600  
 gctgacagac agagaaaacc agtccatcct gatcaccgga gaatccggag cagggaagac 660  
 agtcaacacc aagagggtca tccagtactt tgcctgttat tgcagccattg gggaccgcag 720  
 caagaaggac cagagccccg gcaagggcac cctggaggac cagatcatcc aggccaaccc 780  
 tgcctctggag gcctttggca atgccaagac cgtccggaac gacaactcct cccgcttcgg 840  
 gaaattcatt cgaattcatt ttggggcaac aggaaagt tgcctctgcag acatagagac 900

N3027PCT\_sequ. list . . txt

ct at ct t ct g	gaaaaat cca	gagt t at t t t	ccagct gaaa	gcagagagag	at t at cacat	960
t t t ct accaa	at cct gt ct a	acaaaaagcc	t gagct gct g	gacat gct gc	t gat caccaa	1020
caaccct ac	gat t at gcat	t cat ct ccca	aggagagacc	accgt ggcct	ccat t gat ga	1080
cgct gaggag	ct cat ggcca	ct gat aacgc	t t t t gat gt g	ct gggct t ca	ct t cagagga	1140
gaaaaact cc	at gt at aagc	t gacaggcgc	cat cat gcac	t t t ggaaaca	t gaagt t caa	1200
gct gaagcag	cgggaggagc	aggcggagcc	agacggcact	gaagaggct g	acaagt ct gc	1260
ct acct cat g	gggct gaact	cagccgacct	gct caagggg	ct gt gccacc	ct cgggt gaa	1320
agt gggcaat	gagt acgt ca	ccaaggggca	gaat gt ccag	caggt gat at	at gccact gg	1380
ggcact ggcc	aaggcagt gt	at gagaggat	gt t caact gg	at ggt gacgc	gcat caat gc	1440
cacctt ggag	accaagcagc	cacgccagt a	ct t cat agga	gt cct ggaca	t cgct ggct t	1500
cgagat ct t c	gat t t caaca	gct t t gagca	gct ct gcat c	aact t cacca	acgagaagct	1560
gcagcagt t c	t t caaccacc	acat gt t t gt	gct ggagcag	gaggagt aca	agaaggaggg	1620
cat cgagt gg	acat t cat t g	act t t ggcat	ggacct gcag	gcct gcat t g	acct cat cga	1680
gaagcccat g	ggcat cat gt	ccat cct gga	agaggagt gc	at gt t ccca	aggccaccga	1740
cat gacct t c	aaggccaagc	t gt t t gacaa	ccacct gggc	aaat ccgcca	act t ccagaa	1800
gccacgcaat	at caagggga	agcct gaagc	ccact t ct cc	ct gat ccact	at gccggcat	1860
cgt ggact ac	aacat cat t g	gct ggct gca	gaagaacaag	gat cct ct ca	at gagact gt	1920
cgt gggct t g	t at cagaagt	ct t ccct caa	gct gct cagc	accct gt t t g	ccaact at gc	1980
t ggggct gat	gcgct at t g	agaaggggcaa	aggcaaggcc	aagaaaggct	cgt cct t t ca	2040
gact gt gt ca	gct ct gcaca	gggaaaat ct	gaacaagct g	at gaccaact	t gcgct ccac	2100
ccat ccccac	t t t gt acgt t	gt at cat ccc	t aat gagaca	aagt ct ccag	gggt gat gga	2160
caaccctt g	gt cat gcacc	agct gcgct g	caat ggt gt g	ct ggagggca	t ccgcat ct g	2220
caggaaaggc	t t cccaacc	gcat cct ct a	cggggact t c	cggcagaggt	at cgcat cct	2280
gaaccagcg	gccat cct g	agggacagt t	cat t gat agc	aggaaggggg	cagagaagct	2340
gct cagct cc	ct ggacat t g	at cacaacca	gt acaagt t t	ggccacacca	aggt gt t ct t	2400
caaggccggg	ct gct ggggc	t gct ggagga	aat gagggac	gagaggct ga	gccgcat cat	2460
cacgcgt at c	caggcccagt	cccaggt gt	gct cgccaga	at ggagt aca	aaaagct gct	2520
ggaacgt aga	gact ccct gc	t ggt aat cca	gt ggaacat t	cgggcct t ca	t ggggggt caa	2580
gaat t ggccc	t ggat gaagc	t ct act t caa	gat caagccg	ct gct gaaga	gt gcagaaag	2640
agagaaggag	at ggcct cca	t gaaggagga	gt t cacacgc	ct caaagagg	cgct agagaa	2700
gt ccgaggct	cgccgcaagg	agct ggagga	gaagat ggt g	t ccct gct gc	aggagaagaa	2760
t gacct gcag	ct ccaagt gc	aggcggaaca	agacaacct g	gcagat gct g	aggagcgct g	2820
t gat cagct g	at caaaaaca	agat t cagct	ggaggccaag	gt gaaggaga	t gaacgagag	2880
gct ggaggat	gaggaggaga	t gaat gct ga	gct cact gcc	aagaagcgca	agct ggaaga	2940

N3027PCT\_sequ. l i s t . . t x t

t gagt gct ca	gagct caaaa	gggacat cga	t gat ct ggag	ct gacact gg	ccaaagt gga	3000
gaaggagaaa	cacgcaacag	agaacaaggt	gaaaaacct g	acagaggaga	t ggct gggct	3060
ggat gagat c	at t gccaaagc	t gaccaagga	gaagaaagct	ct gcaagagg	cccaccaaca	3120
ggct ct ggat	gacct t cagg	ccgaggagga	caaggt caac	accct gact a	aggccaaagt	3180
caagct ggag	cagcaagt gg	at gat ct gga	aggat ccct g	gagcaagaga	agaaggt gcg	3240
cat ggacct g	gagcgagcga	agcggaagct	ggagggcgac	ct gaagct ga	cccaggagag	3300
cat cat ggac	ct ggagaat g	acaagcagca	gct ggat gag	cggct gaaaa	aaaaagact t	3360
t gagct gaat	gct ct caacg	caaggat t ga	ggat gaacag	gccct cggca	gccagct gca	3420
gaagaagct c	aaggagct t c	aggcacgcat	cgaggagct g	gaggaggagc	t ggaggccga	3480
gcgcaccgcc	agggt aagg	t ggagaagct	gcgct cagac	ct gt ct cggg	agct ggagga	3540
gat cagcgag	cggct ggaag	aggccggcgg	ggccacgt cc	gt gcagat cg	agat gaacaa	3600
gaagcgcgag	gccgagt t cc	agaagat gcg	gcgggacct g	gaggaggcca	cgct gcagca	3660
cgaggccact	gccgcggccc	t gcgcaagaa	gcacgccgac	agcgt ggccg	agct gggcga	3720
gcagat cgac	aacct gcagc	gggt gaagca	gaagct ggag	aaggagaaga	gcgagt t caa	3780
gct ggagct g	gat gacgt ca	cct ccaacat	ggagcagat c	at caaggcca	aggct aacct	3840
ggagaagat g	t gccggacct	t ggaagacca	gat gaat gag	caccggagca	aggcggagga	3900
gaccagcgt	t ct gt caacg	acct caccag	ccagcgggcc	aagt t gcaaa	ccgagaat gg	3960
t gagct gt cc	cggcagct gg	at gagaagga	ggcact gat c	t cccagct ga	cccgaggcaa	4020
gct cacct ac	accagcagc	t ggaggacct	caagaggcag	ct ggaggagg	aggt t aaggc	4080
gaagaacgcc	ct ggcccacg	cact gcagt c	ggcccggcat	gact gcgacc	t gct gcggga	4140
gcagt acgag	gaggagacgg	aggccaaggc	cgagct gcag	cgcgt cct t t	ccaaggccaa	4200
ct cggaggt g	gcccagt gga	ggaccaagt a	t gagacggac	gccat t cagc	ggact gagga	4260
gct cgaggag	gccaagaaga	agct ggccca	gcggct gcag	gaagct gagg	aggccgt gga	4320
ggct gt t aat	gccaagt gct	cct cgct gga	gaagaccaag	caccggct ac	agaat gagat	4380
cgaggact t g	at ggt ggacg	t agagcgct c	caat gct gct	gct gcagccc	t ggacaagaa	4440
gcagaggaac	t t cgacaaga	t cct ggccga	gt ggaagcag	aagt at gagg	agt cgcagt c	4500
ggagct ggag	t cct cgcaga	aggaggct cg	ct ccct cagc	acagagct ct	t caaact caa	4560
gaacgcct at	gaggagt ccc	t ggaacat ct	ggagacct t c	aagcgggaga	acaaaaacct	4620
gcaggaggag	at ct ccgact	t gact gagca	gt t ggggt t cc	agcggaaaga	ct at ccat ga	4680
gct ggagaag	gt ccgaaagc	agct ggaggc	cgagaagat g	gagct gcagt	cagccct gga	4740
ggaggccgag	gcct ccct gg	agcacgagga	gggcaagat c	ct ccgggccc	agct ggagt t	4800
caaccagat c	aaggcagaga	t cgagcgga	gct ggcagag	aaggacgagg	agat ggaaca	4860
ggccaagcgc	aaccacct gc	gggt ggt gga	ct cgct gcag	acct ccct gg	acgcagagac	4920
acgcagccgc	aacgaggccc	t gagggt gaa	gaagaagat g	gaaggagacc	t caat gagat	4980
ggagat ccag	ct cagccacg	ccaaccgcat	ggccgcccag	gcccagaagc	aagt caagag	5040

N3027PCT\_sequ.list.txt

```

cct ccagagc ttgttgaagg acaccagat t cagct ggac gat gcagt cc gt gccaacga 5100
cgacct gaag gagaacat cg ccat cgt gga gcggcgcaac aacct gct gc aggct gagct 5160
ggaggagt t g cgt gccgt gg t ggagcagac agagcggg cc cggaagct gg cggagcagga 5220
gct gat t gag act agt gagc gggg gcagct gct gcat t cc cagaacacca gcct cat caa 5280
ccagaagaag aagat ggat g ct gacct gt c ccagct ccag act gaagt gg aggaggcagt 5340
gcaggagt gc aggaat gct g aggagaaggc caagaaggcc at cacggat g ccgccat gat 5400
ggcagaggag ct gaagaagg agcaggacac cagcgcccac ct ggagcgca t gaagaagaa 5460
cat ggaacag accat t aagg acct gcagca ccggct ggac gaagccgagc agat cgccct 5520
caagggcggc aagaagcagc t gcagaagct ggaagcgcgg gt gcgggagc t ggagaat ga 5580
gct ggaggcc gagcagaagc gcaacgcaga gt cggt gaag ggcat gagga agagcgagcg 5640
gcgcat caag gagct cacct accagacgga ggaggacagg aaaaacct gc t gcggct gca 5700
ggacct ggt a gacaagct gc agct aaaggt caaggcct ac aagcgccagg ccgaggaggc 5760
ggaggagcaa gccaacacca acct gt ccaa gt t ccgcaag gt gcagcacg agct ggat ga 5820
ggcagaggag cgggcggaca t cgccgagt c ccaggt caac aagct gcggg ccaagagccg 5880
tgacat t ggc acgaagggt t gaat gagga gt agct t t gc cacat ct t ga t ct gct cagc 5940
cct ggaggt g ccagcaaagc cccat gct gg agcct gt gt a acagct cct t gggaggaagc 6000
agaat aaagc aat t t t cct t gaagccgaga aaaaaaaaaa aaaa 6044

```

<210> 66  
 <211> 1935  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1935)  
 <223> myosin, heavy chain 7, cardiac muscle, beta (MYH7)  
 <400> 66

Met Gly Asp Ser Glu Met Ala Val Phe Gly Ala Ala Ala Pro Tyr Leu  
1 5 10 15

Arg Lys Ser Glu Lys Glu Arg Leu Glu Ala Glu Thr Arg Pro Phe Asp  
20 25 30

Leu Lys Lys Asp Val Phe Val Pro Asp Asp Lys Glu Glu Phe Val Lys  
35 40 45

Ala Lys Ile Val Ser Arg Glu Gly Gly Lys Val Thr Ala Glu Thr Glu  
50 55 60

Tyr Gly Lys Thr Val Thr Val Lys Glu Asp Glu Val Met Glu Glu Asn  
65 70 75 80

Pro Pro Lys Phe Asp<sub>85</sub> Lys Ile Glu Asp<sub>90</sub> Met<sub>90</sub> Ala Met<sub>90</sub> Leu Thr Phe<sub>95</sub> Leu  
 His Glu Pro Ala<sub>100</sub> Val Leu Tyr Asn<sub>105</sub> Leu<sub>105</sub> Lys Asp Arg Tyr Gly<sub>110</sub> Ser Trp  
 Met<sub>115</sub> Ile Tyr<sub>115</sub> Thr Tyr Ser Gly<sub>120</sub> Leu<sub>120</sub> Phe Cys Val Thr Val<sub>125</sub> Asn Pro Tyr  
 Lys Trp<sub>130</sub> Leu Pro Val Tyr Thr<sub>135</sub> Pro Glu Val Val Ala<sub>140</sub> Ala Tyr Arg Gly  
 Lys<sub>145</sub> Lys Arg Ser Glu Ala<sub>150</sub> Pro Pro His Ile Phe<sub>155</sub> Ser Ile Ser Asp Asn<sub>160</sub>  
 Ala Tyr Gln Tyr Met<sub>165</sub> Leu Thr Asp Arg Glu<sub>170</sub> Asn Gln Ser Ile Leu<sub>175</sub> Ile  
 Thr Gly Glu Ser<sub>180</sub> Gly Ala Gly Lys Thr<sub>185</sub> Val Asn Thr Lys Arg<sub>190</sub> Val Ile  
 Gln Tyr Phe<sub>195</sub> Ala Val Ile Ala Ala<sub>200</sub> Ile Gly Asp Arg Ser<sub>205</sub> Lys Lys Asp  
 Gln Ser<sub>210</sub> Pro Gly Lys Gly Thr<sub>215</sub> Leu Glu Asp Gln Ile<sub>220</sub> Ile Gln Ala Asn  
 Pro<sub>225</sub> Ala Leu Glu Ala Phe<sub>230</sub> Gly Asn Ala Lys Thr<sub>235</sub> Val Arg Asn Asp Asn<sub>240</sub>  
 Ser Ser Arg Phe Gly<sub>245</sub> Lys Phe Ile Arg Ile<sub>250</sub> His Phe Gly Ala Thr<sub>255</sub> Gly  
 Lys Leu Ala Ser<sub>260</sub> Ala Asp Ile Glu Thr<sub>265</sub> Tyr Leu Leu Glu Lys<sub>270</sub> Ser Arg  
 Val Ile Phe<sub>275</sub> Gln Leu Lys Ala Glu Arg Asp Tyr His Ile<sub>285</sub> Phe Tyr Gln  
 Ile Leu Ser Asn Lys Lys Pro Glu Leu Leu Asp Met<sub>300</sub> Leu Leu Ile Thr  
 Asn<sub>305</sub> Asn Pro Tyr Asp Tyr<sub>310</sub> Ala Phe Ile Ser Gln<sub>315</sub> Gly Glu Thr Thr Val<sub>320</sub>  
 Ala Ser Ile Asp Asp<sub>325</sub> Ala Glu Glu Leu Met<sub>330</sub> Ala Thr Asp Asn Ala<sub>335</sub> Phe  
 Asp Val Leu Gly<sub>340</sub> Phe Thr Ser Glu Glu<sub>345</sub> Lys Asn Ser Met Tyr<sub>350</sub> Lys Leu  
 Thr Gly Ala Ile Met His Phe Gly Asn Met Lys Phe Lys Leu Lys Gln

355

Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Glu Ala Asp Lys Ser  
370 375 380

Ala Tyr Leu Met Gly Leu Asn Ser Ala Asp Leu Leu Lys Gly Leu Cys  
385 390 395 400

His Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly Gln Asn  
405 410 415

Val Gln Gln Val Ile Tyr Ala Thr Gly Ala Leu Ala Lys Ala Val Tyr  
420 425 430

Glu Arg Met Phe Asn Trp Met Val Thr Arg Ile Asn Ala Thr Leu Glu  
435 440 445

Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile Ala Gly  
450 455 460

Phe Glu Ile Phe Asp Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe  
465 470 475 480

Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe Val Leu  
485 490 495

Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr Phe Ile Asp  
500 505 510

Phe Gly Met Asp Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met  
515 520 525

Gly Ile Met Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr  
530 535 540

Asp Met Thr Phe Lys Ala Lys Leu Phe Asp Asn His Leu Gly Lys Ser  
545 550 555 560

Ala Asn Phe Gln Lys Pro Arg Asn Ile Lys Gly Lys Pro Glu Ala His  
565 570 575

Phe Ser Leu Ile His Tyr Ala Gly Ile Val Asp Tyr Asn Ile Ile Gly  
580 585 590

Trp Leu Gln Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val Gly Leu  
595 600 605

Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Thr Leu Phe Ala Asn Tyr  
610 615 620

Ala Gly Ala Asp Ala Pro Ile Glu Lys Gly Lys Gly Lys Ala Lys Lys  
625 630 635 640

N3027PCT\_sequ.list.txt

Gly Ser Ser Phe Gln Thr Val Ser Ala Leu His Arg Glu Asn Leu Asn  
 645 650 655  
 Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His Phe Val Arg Cys  
 660 665 670  
 Ile Ile Pro Asn Glu Thr Lys Ser Pro Gly Val Met Asp Asn Pro Leu  
 675 680 685  
 Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile  
 690 695 700  
 Cys Arg Lys Gly Phe Pro Asn Arg Ile Leu Tyr Gly Asp Phe Arg Gln  
 705 710 715 720  
 Arg Tyr Arg Ile Leu Asn Pro Ala Ala Ile Pro Glu Gly Gln Phe Ile  
 725 730 735  
 Asp Ser Arg Lys Gly Ala Glu Lys Leu Leu Ser Ser Leu Asp Ile Asp  
 740 745 750  
 His Asn Gln Tyr Lys Phe Gly His Thr Lys Val Phe Phe Lys Ala Gly  
 755 760 765  
 Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Arg Leu Ser Arg Ile  
 770 775 780  
 Ile Thr Arg Ile Gln Ala Gln Ser Arg Gly Val Leu Ala Arg Met Glu  
 785 790 795 800  
 Tyr Lys Lys Leu Leu Glu Arg Arg Asp Ser Leu Leu Val Ile Gln Trp  
 805 810 815  
 Asn Ile Arg Ala Phe Met Gly Val Lys Asn Trp Pro Trp Met Lys Leu  
 820 825 830  
 Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu Arg Glu Lys Glu  
 835 840 845  
 Met Ala Ser Met Lys Glu Glu Phe Thr Arg Leu Lys Glu Ala Leu Glu  
 850 855 860  
 Lys Ser Glu Ala Arg Arg Lys Glu Leu Glu Glu Lys Met Val Ser Leu  
 865 870 875 880  
 Leu Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln Ala Glu Gln Asp  
 885 890 895  
 Asn Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu Ile Lys Asn Lys  
 900 905 910

N3027PCT\_sequ.list.txt

I l e G n L e u G u A l a L y s V a l L y s G u M e t A s n G u A r g L e u G u A s p  
915 920 925

G u G u G u M e t A s n A l a G u L e u T h r A l a L y s L y s A r g L y s L e u G u  
930 935 940

A s p G u C y s S e r G u L e u L y s A r g A s p I l e A s p A s p L e u G u L e u T h r  
945 950 955 960

L e u A l a L y s V a l G u L y s G u L y s H i s A l a T h r G u A s n L y s V a l L y s  
965 970 975

A s n L e u T h r G u G u M e t A l a G y L e u A s p G u I l e I l e A l a L y s L e u  
980 985 990

T h r L y s G u L y s L y s A l a L e u G n G u A l a H i s G n G n A l a L e u A s p  
995 1000 1005

A s p L e u G n A l a G u G u A s p L y s V a l A s n T h r L e u T h r L y s A l a  
1010 1015 1020

L y s V a l L y s L e u G u G n G n V a l A s p A s p L e u G u G y S e r L e u  
1025 1030 1035

G u G n G u L y s L y s V a l A r g M e t A s p L e u G u A r g A l a L y s A r g  
1040 1045 1050

L y s L e u G u G y A s p L e u L y s L e u T h r G n G u S e r I l e M e t A s p  
1055 1060 1065

L e u G u A s n A s p L y s G n G n L e u A s p G u A r g L e u L y s L y s L y s  
1070 1075 1080

A s p P h e G u L e u A s n A l a L e u A s n A l a A r g I l e G u A s p G u G n  
1085 1090 1095

A l a L e u G y S e r G n L e u G n L y s L y s L e u L y s G u L e u G n A l a  
1100 1105 1110

A r g I l e G u G u L e u G u G u G u L e u G u A l a G u A r g T h r A l a  
1115 1120 1125

A r g A l a L y s V a l G u L y s L e u A r g S e r A s p L e u S e r A r g G u L e u  
1130 1135 1140

G u G u I l e S e r G u A r g L e u G u G u A l a G y G y A l a T h r S e r  
1145 1150 1155

V a l G n I l e G u M e t A s n L y s L y s A r g G u A l a G u P h e G n L y s  
1160 1165 1170

Met Arg Arg Asp Leu Glu Glu Ala Thr Leu Gln His Glu Ala Thr  
 1175 1180 1185  
 Ala Ala Ala Leu Arg Lys Lys His Ala Asp Ser Val Ala Glu Leu  
 1190 1200  
 Gly Glu Gln Ile Asp Asn Leu Gln Arg Val Lys Gln Lys Leu Glu  
 1205 1210 1215  
 Lys Glu Lys Ser Glu Phe Lys Leu Glu Leu Asp Asp Val Thr Ser  
 1220 1225 1230  
 Asn Met Glu Gln Ile Ile Lys Ala Lys Ala Asn Leu Glu Lys Met  
 1235 1240 1245  
 Cys Arg Thr Leu Glu Asp Gln Met Asn Glu His Arg Ser Lys Ala  
 1250 1255 1260  
 Glu Glu Thr Gln Arg Ser Val Asn Asp Leu Thr Ser Gln Arg Ala  
 1265 1270 1275  
 Lys Leu Gln Thr Glu Asn Gly Glu Leu Ser Arg Gln Leu Asp Glu  
 1280 1285 1290  
 Lys Glu Ala Leu Ile Ser Gln Leu Thr Arg Gly Lys Leu Thr Tyr  
 1295 1300 1305  
 Thr Gln Gln Leu Glu Asp Leu Lys Arg Gln Leu Glu Glu Glu Val  
 1310 1315 1320  
 Lys Ala Lys Asn Ala Leu Ala His Ala Leu Gln Ser Ala Arg His  
 1325 1330 1335  
 Asp Cys Asp Leu Leu Arg Glu Gln Tyr Glu Glu Glu Thr Glu Ala  
 1340 1345 1350  
 Lys Ala Glu Leu Gln Arg Val Leu Ser Lys Ala Asn Ser Glu Val  
 1355 1360 1365  
 Ala Gln Trp Arg Thr Lys Tyr Glu Thr Asp Ala Ile Gln Arg Thr  
 1370 1375 1380  
 Glu Glu Leu Glu Glu Ala Lys Lys Lys Leu Ala Gln Arg Leu Gln  
 1385 1390 1395  
 Glu Ala Glu Glu Ala Val Glu Ala Val Asn Ala Lys Cys Ser Ser  
 1400 1405 1410  
 Leu Glu Lys Thr Lys His Arg Leu Gln Asn Glu Ile Glu Asp Leu  
 1415 1420 1425  
 Met Val Asp Val Glu Arg Ser Asn Ala Ala Ala Ala Ala Ala Leu Asp

1430														
Lys	Lys	Gln	Arg	Asn	Phe	Asp	Lys	Ile	Leu	Ala	Glu	Trp	Lys	Gln
1445	1445					1450					1455			
Lys	Tyr	Glu	Glu	Ser	Gln	Ser	Glu	Leu	Glu	Ser	Ser	Gln	Lys	Glu
1460	1460					1465					1470			
Ala	Arg	Ser	Leu	Ser	Thr	Glu	Leu	Phe	Lys	Leu	Lys	Asn	Ala	Tyr
1475	1475					1480					1485			
Glu	Glu	Ser	Leu	Glu	His	Leu	Glu	Thr	Phe	Lys	Arg	Glu	Asn	Lys
1490	1490					1495					1500			
Asn	Leu	Gln	Glu	Glu	Ile	Ser	Asp	Leu	Thr	Glu	Gln	Leu	Gly	Ser
1505	1505					1510					1515			
Ser	Gly	Lys	Thr	Ile	His	Glu	Leu	Glu	Lys	Val	Arg	Lys	Gln	Leu
1520	1520					1525					1530			
Glu	Ala	Glu	Lys	Met	Glu	Leu	Gln	Ser	Ala	Leu	Glu	Glu	Ala	Glu
1535	1535					1540					1545			
Ala	Ser	Leu	Glu	His	Glu	Glu	Gly	Lys	Ile	Leu	Arg	Ala	Gln	Leu
1550	1550					1555					1560			
Glu	Phe	Asn	Gln	Ile	Lys	Ala	Glu	Ile	Glu	Arg	Lys	Leu	Ala	Glu
1565	1565					1570					1575			
Lys	Asp	Glu	Glu	Met	Glu	Gln	Ala	Lys	Arg	Asn	His	Leu	Arg	Val
1580	1580					1585					1590			
Val	Asp	Ser	Leu	Gln	Thr	Ser	Leu	Asp	Ala	Glu	Thr	Arg	Ser	Arg
1595	1595					1600					1605			
Asn	Glu	Ala	Leu	Arg	Val	Lys	Lys	Lys	Met	Glu	Gly	Asp	Leu	Asn
1610	1610					1615					1620			
Glu	Met	Glu	Ile	Gln	Leu	Ser	His	Ala	Asn	Arg	Met	Ala	Ala	Glu
1625	1625					1630					1635			
Ala	Gln	Lys	Gln	Val	Lys	Ser	Leu	Gln	Ser	Leu	Leu	Lys	Asp	Thr
1640	1640					1645					1650			
Gln	Ile	Gln	Leu	Asp	Asp	Ala	Val	Arg	Ala	Asn	Asp	Asp	Leu	Lys
1655	1655					1660					1665			
Glu	Asn	Ile	Ala	Ile	Val	Glu	Arg	Arg	Asn	Asn	Leu	Leu	Gln	Ala
1670	1670					1675					1680			
Glu	Leu	Glu	Glu	Leu	Arg	Ala	Val	Val	Glu	Gln	Thr	Glu	Arg	Ser
1685	1685					1690					1695			

N3027PCT\_sequ.list.txt

Arg Lys Leu Ala Gu Gn Gu Leu Ile Gu Thr Ser Gu Arg Val  
1700 1705 1710

Gn Leu Leu His Ser Gn Asn Thr Ser Leu Ile Asn Gn Lys Lys  
1715 1720 1725

Lys Met Asp Ala Asp Leu Ser Gn Leu Gn Thr Gu Val Gu Gu  
1730 1735 1740

Ala Val Gn Gu Cys Arg Asn Ala Gu Gu Lys Ala Lys Lys Ala  
1745 1750 1755

Ile Thr Asp Ala Ala Met Met Ala Gu Gu Leu Lys Lys Gu Gn  
1760 1765 1770

Asp Thr Ser Ala His Leu Gu Arg Met Lys Lys Asn Met Gu Gn  
1775 1780 1785

Thr Ile Lys Asp Leu Gn His Arg Leu Asp Gu Ala Gu Gn Ile  
1790 1795 1800

Ala Leu Lys Gly Gly Lys Lys Gn Leu Gn Lys Leu Gu Ala Arg  
1805 1810 1815

Val Arg Gu Leu Gu Asn Gu Leu Gu Ala Gu Gn Lys Arg Asn  
1820 1825 1830

Ala Gu Ser Val Lys Gly Met Arg Lys Ser Gu Arg Arg Ile Lys  
1835 1840 1845

Gu Leu Thr Tyr Gn Thr Gu Gu Asp Arg Lys Asn Leu Leu Arg  
1850 1855 1860

Leu Gn Asp Leu Val Asp Lys Leu Gn Leu Lys Val Lys Ala Tyr  
1865 1870 1875

Lys Arg Gn Ala Gu Gu Ala Gu Gu Gn Ala Asn Thr Asn Leu  
1880 1885 1890

Ser Lys Phe Arg Lys Val Gn His Gu Leu Asp Gu Ala Gu Gu  
1895 1900 1905

Arg Ala Asp Ile Ala Gu Ser Gn Val Asn Lys Leu Arg Ala Lys  
1910 1915 1920

Ser Arg Asp Ile Gly Thr Lys Gly Leu Asn Gu Gu  
1925 1930 1935

<210> 67  
<211> 6289  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6289)

&lt;223&gt; myosin, heavy chain 7B, cardiac muscle, beta (MYH7B)

&lt;400&gt; 67

```

tggggttttg atgtgttgcc caggctggtc ttgaactcct gagcttaagt gatgtgtccg      60
cctgggcctc ccaaagt gct ggaattacag acatgagtgg caataaaagg ggt agcagag      120
cttcctgccc tcaccgt ggt gccgagt gcc t gctgccttg ggccgccttg aacctccagg      180
gtttccagct cctcctcctt caccctcagt g ccactgccat gatggatgtg agtgaacttg      240
gggagtctgc ccgctacctc cgccagggct accaggagat gacgaagggtg cacactatcc      300
catgggacgg gaagaagcga gtctgggtgc ctgatgaaca ggacgcctac gtggaggccg      360
aggtcaagtc ggaggctacc gggggcagag tcaccgtgga gaccaaagac cagaagggtgc      420
tgatggtgcg tgaagccgag ctgcagccca tgaaccgcct tgccttcgac ttactggagg      480
acatggccat gatgacgcac ctgaacgagg cctctgtgct gcacaacctg cgccagcgct      540
atgcccgctg gatgatctat acctactcag gcctcttctg tgtcaccatc aaccctaca      600
aatggctccc agtctatacg gcctccgtag tggctgctta caagggaaag cgccgctcag      660
attccccgcc ccatatatat gcgggtggcg acaacgcctc caacgacatg ctgcgcaacc      720
gagacaacca gtccatgctg atcaccggag agtcgggggc cggtaagacg gttaacacca      780
agcgggtcat tcagtacttt gccatcgtcg ctgccctggg agacggggccg ggcaagaagg      840
cccaatttct ggcaacaaag acgggggggca cccttgagga tcaaatcatc gaggccaacc      900
ctgccatgga ggcctttggc aacgccaaga ccctgaggaa tgataactcc tcccgctttg      960
gcaagttcat ccgcatcac tttgggtccct ctgggaagct ggcatccgcg gatattgaca      1020
gctatctcct ggagaagtgc cgggtgatct tccagttgcc tgggtgagcgc agctaccatg      1080
tctactacca gatcctctca gggaggaagc cagagctgca ggacatgctg ctctgtctta      1140
tgaaccctta tgactaccac ttctgcagcc agggcgctcat caccgtggac aacatgaatg      1200
atggggagga gctcatcgcc accgaccatg ccatggacat cctaggcttc agcgtggtg      1260
agaaatgtgc ctgctataag atcgtggcg ccctcctgca ctttggcaac atgaagtca      1320
agcagaagca gcgggaggag caggcggagg ccgatggcac tgagagtgt gacaaggctg      1380
cctacctgat gggggtcagc agtggggacc tcctcaaagg ccttttgcac ccccggtgc      1440
gtgtagggaa cgagtacgtg accaagggcc agagtgtgga gcaggtggtg tttgctgtgg      1500
gggctctggc caaggccacc tatgaccggc tgttcaggtg gctggtgtct cggatcaacc      1560
agaccctgga cacaagctg ccccggcagt tcttcatcgg ggttctggac atcgctgggt      1620
ttgagatctt tgagtcaac agcttcgaac agctgtgcat caacttcacc aatgagaaat      1680
tgcagcagtt cttaaccag cacatgtttg tgctggagca ggaggagtac aagcgggagg      1740
gcatcgactg ggtcttcatc gacttcggcc ttgacctgca gccttgcac c gacctcatcg      1800

```

N3027PCT\_sequ. list.txt

agaagccact	gggcat cct g	t ccat cct gg	aggaggaat g	cat gt t cccc	aaggcct cag	1860
acgccagct t	ccgggccaag	ct ct acgaca	accacgcggg	gaagt ccccc	aat t t ccagc	1920
agcct cggcc	t gacaagaag	cgcaagt acc	aggccact t	cgaggt ggt c	cact acgcag	1980
gcgt ggt gcc	t t acagcat t	gt gggct ggc	t ggagaaaaa	caaggat ccc	ct gaat gaga	2040
ccgt ggt ccc	cat ct t ccag	aagt cacaga	at aggct cct	ggcgact ct c	t at gagaat t	2100
at gcgggct c	ct gct ccact	gagcccccca	agt ct ggggt	gaaagagaag	cgt aagaagg	2160
cagcat cgt t	ccagacggg t	t cccagct gc	acaaggagaa	cct caacaag	ct gat gacca	2220
acct gcgggc	cacacagccc	cact t cgt cc	gct gcat t gt	ccccaacgag	aacaaaaccc	2280
caggggt cat	ggat gcct t c	t t ggt gct ac	accagct gcg	ct gcaat ggg	gt cct ggagg	2340
ggat ccggat	ct gccgcca	gggt t ccca	acaggt t gct	ct acaccgac	t t ccggcagc	2400
ggg accgt at	cct gaacccc	agt gccat cc	cggat gacac	ct t cat ggac	agcaggaagg	2460
ccacagagaa	act gct gggc	t cgct ggact	t ggat cacac	ccagt accag	t t t ggccaca	2520
ccaaggt gt t	ct t caaggct	gggct t ct ag	gcgt cct gga	agagct ccgt	gaccagcgcc	2580
t ggccaaggt	gct gacgct g	ct gcaggcgc	ggagccgt gg	ccgcct cat g	cgct t gagt	2640
accagcgct	gct gggaggc	agggat gcgc	t gt t caccat	ccagt ggaac	at ccgt gcct	2700
t caat gccgt	caagaact gg	t cat ggat ga	agct ct t t t t	caagat gaag	ccgct gct gc	2760
gct cggcgca	ggct gaggag	gagct ggccg	ccct gcgggc	agagct gcgg	gggt t gcgag	2820
gggcgct ggc	t gcggccgag	gccaagcgcc	aggaact gga	ggagacgcac	gt cagcat ca	2880
cccaggagaa	gaat gacct g	gccct gcagc	t gcaggct ga	gcaggacaac	ct ggcagat g	2940
ccgaggagcg	ct gccact t g	ct gat caagt	ccaaggt gca	gct ggagggg	aaggt gaagg	3000
agct gagt ga	gcggct ggag	gat gaggagg	aggt gaacgc	t gacct ggcc	gcccgcgggc	3060
gcaagct gga	ggacgagt gc	acggagct ca	agaaggacat	t gat gacct g	aagct gacac	3120
t ggccaaagc	t gagaaggag	aagcaagcca	ct gagaacaa	ggg gaagaac	ct gacggaag	3180
agat ggct gc	gct ggacgag	t cagt ggccc	ggct gaccaa	ggagaagaag	gcgt t gcagg	3240
aggccacca	acaggccct g	ggg gacct gc	aggccgagga	ggaccgt gt g	agcgcgct ga	3300
ccaaggccaa	gct ccggct g	gagcaacagg	t ggaggacct	ggaat gct cc	ct ggagcagg	3360
agaagaagct	gcgcat ggac	acggagcggg	ccaagcgcaa	gct ggagggg	gacct gaagc	3420
t gacgcagga	gt cggt ggct	gat gct gct c	aagacaagca	gcagct ggag	gagaagct ca	3480
agaagaagga	ct ccgagct g	agccagct ga	gcct gcgggt	ggaagacgag	cagct ct t gg	3540
gggcccagat	gcagaagaag	at caaggagc	t gcaggct cg	ggcgaggagg	ct ggaagagg	3600
agct ggaggc	agagcgggca	gcccggggccc	gcgt ggagaa	gcagcgt gca	gaggcggcgc	3660
gggagct gga	ggagct gagc	gagcggct gg	aggaggcagg	cggcgcat cc	gcggggcagc	3720
gcgagggct g	ccgcaagcgg	gaggcggagc	t ggggaggct	gcggcgaggag	ct ggaggagg	3780
cggcgct gcg	gcacgaggcc	acagt ggccg	cact gcggcg	caagcaggcg	gagggcgcg	3840
cggagct ggg	ggagcaggt g	gacagcct gc	agcgggt gcg	gcagaagct g	gagaaggaga	3900

N3027PCT\_sequ. list . . txt

agagt gagct gcgcat ggag gt ggacgacc t ggct gccaa cgt ggagact ct gacccgcg	3960
ccaaggccag t gcagagaag ct gt gccgga cct at gagga t cagct aagc gaggccaaga	4020
t caaggt gga ggagct gcag cggcagct gg cggacgcaag cacgcagcgt gggcgact ac	4080
agacggaaag cggggagct g agt cgcct gc t agaggagaa ggagt gt ct g at cagt cagc	4140
t gagccgt gg aaaggccct g gccgccccaa gcct ggaaga gt t gcggcgc cagct agagg	4200
aggaaagcaa ggccaagagt gccct ggccc acgccgt gca ggct ct gcgg cagcact gt g	4260
acct cct gcg ggagcaacac gaggaggagg ct gaggccca ggct gagct g cagcggct gc	4320
t gt ccaaggc caat gccgag gt ggcccagt ggaggagcaa gt acgaagca gat gccat cc	4380
agaggaccga ggagct ggag gaggccaaaa aaaagct ggc act gcggct g caggaggcag	4440
aggagggcgt ggaggct gcc aacgccaagt gct cat cgt t ggagaaggcc aagct gcggc	4500
t acagacaga gt cagaggat gt aaccct gg agct ggagcg ggcgacct ca gcagct gct g	4560
cgct ggacaa gaagcagcgg cact t ggaac gggcact gga ggaacggcgg cggcaggagg	4620
aggagat gca gcgggagct g gaggcggcac agagggagt c ccgt ggcct g ggcaccgagc	4680
t ct t ccggct gcggcacggc cacgaggagg cact t gaagc cct ggagacg ct caagcggg	4740
agaacaagaa cct gcaggag gagat cagcg acct cacaga ccaggt gagt ct cagt ggga	4800
agagcat cca ggaact ggag aaaaccaaga aggcgct gga aggcgagaag agt gagat cc	4860
aggct gcact ggaggaggca gggggggccc t ggagct gga ggagaccaag acgct gcgga	4920
t ccagct gga gct ct cccag gt caaagcag aagt ggaccg gaagct ggca gaaaaagacg	4980
aggagt gcgc t aacct gagg cgcaaccacc agcgagct gt ggagt ccct g caggcct ccc	5040
t ggat gcaga gacacgggcc cgcaat gagg cgct gcggct caagaagaag at ggagggt g	5100
acct caacga cct ggagct g cagct gggcc at gccaccg t caggccaca gaggcccagg	5160
ct gccacgcg gct gat gcag gcacagct ca aggaggagca ggcagggcgg gacgaggagc	5220
agcggct ggc agct gagct c cacgagcagg cgcaggct ct ggagcgccgg gcct cgct gc	5280
t ggct gcgga gct ggaggag ct gcgggct g ccct ggagca gggcgagcgc agccggcgac	5340
t ggcagagca ggagct t t t g gaggccaccg agcgcct caa cct t ct gcat t cgcagaaca	5400
caggcct cct aaaccagaag aagaagct gg aggcggact t ggcccagct g agcggggagg	5460
t ggaggaggc t gcacaggag aggcgggagg ct gaggagaa ggccaaaaag gccat cact g	5520
at gcggccat gat ggccgag gagct gaaga aggagcagga cacaagt gca cacct ggaac	5580
ggat gaagaa gacgct ggag cagacggt gc gcgagct cca ggcccgcct t gaggaggcag	5640
aacaggccgc cct ccgt ggc gggaagaagc aggt gcagaa gct ggaggcc aaggt acggg	5700
agct ggaggc t gagct t gat gcagagcaga agaagcacgc cgaggccct t aagggcgt gc	5760
gcaagcat ga gcgccgt gt c aaggagct cg cat accaggc cgaggaggac aggaagaacc	5820
t ggct cgcat gcaggacct g gt ggacaagc t gcagagcaa ggt caagagc t acaagcgcc	5880
agt t t gagga ggcggagcag caggccaaca ccaacct ggc caagt at cgc aaggcccagc	5940

N3027PCT\_sequ.list.txt

```

acgagctgga t gatgcggag gagcgggcag acatggcgga aaccaggcc aacaagctgc 6000
gggcacggac ccgggacgcc ctgggccccca agcacaagga gtgacggcct gacccctgg 6060
gctctaaaga ggaatgtctg ctgttgaca tctggctgag gccacctgcc ccgatcctgc 6120
catctctgca tgcggccctg ctgccttcag ccttcctgg gccctgaata aacaccacag 6180
ccagtttctt tctcattctt tttttgggg ttgaggagga aaaacacagt cctagggaca 6240
aaagccaggt ccacagcagt catttttaa ataaagttaa ttaatagtc 6289

```

<210> 68  
 <211> 1983  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1983)  
 <223> myosin, heavy chain 7B, cardiac muscle, beta (MYH7B)

<400> 68

Met Ser Gly Asn Lys Arg Gly Ser Arg Ala Ser Cys Pro His Arg Gly  
1 5 10 15

Ala Glu Cys Leu Leu Pro Trp Ala Ala Leu Asn Leu Gln Gly Phe Gln  
20 25 30

Leu Leu Leu Leu His Pro Ser Ala Thr Ala Met Met Asp Val Ser Glu  
35 40 45

Leu Gly Glu Ser Ala Arg Tyr Leu Arg Gln Gly Tyr Gln Glu Met Thr  
50 55 60

Lys Val His Thr Ile Pro Trp Asp Gly Lys Lys Arg Val Trp Val Pro  
65 70 75 80

Asp Glu Gln Asp Ala Tyr Val Glu Ala Glu Val Lys Ser Glu Ala Thr  
85 90 95

Gly Gly Arg Val Thr Val Glu Thr Lys Asp Gln Lys Val Leu Met Val  
100 105 110

Arg Glu Ala Glu Leu Gln Pro Met Asn Pro Pro Arg Phe Asp Leu Leu  
115 120 125

Glu Asp Met Ala Met Met Thr His Leu Asn Glu Ala Ser Val Leu His  
130 135 140

Asn Leu Arg Gln Arg Tyr Ala Arg Trp Met Ile Tyr Thr Tyr Ser Gly  
145 150 155 160

Leu Phe Cys Val Thr Ile Asn Pro Tyr Lys Trp Leu Pro Val Tyr Thr  
165 170 175

N3027PCT\_sequ.list.txt

Ala Ser Val Val 180 Ala Ala Tyr Lys Gly 185 Lys Arg Arg Ser Asp 190 Ser Pro

Pro His Ile 195 Tyr Ala Val Ala Asp 200 Asn Ala Tyr Asn Asp 205 Met Leu Arg

Asn Arg 210 Asp Asn Gln Ser Met 215 Leu Ile Thr Gly Glu 220 Ser Gly Ala Gly

Lys 225 Thr Val Asn Thr Lys 230 Arg Val Ile Gln Tyr 235 Phe Ala Ile Val Ala 240

Ala Leu Gly Asp Gly 245 Pro Gly Lys Lys Ala 250 Gln Phe Leu Ala Thr 255 Lys

Thr Gly Gly Thr 260 Leu Glu Asp Gln Ile 265 Ile Glu Ala Asn Pro 270 Ala Met

Glu Ala Phe 275 Gly Asn Ala Lys Thr 280 Leu Arg Asn Asp Asn 285 Ser Ser Arg

Phe Gly 290 Lys Phe Ile Arg Ile 295 His Phe Gly Pro Ser 300 Gly Lys Leu Ala

Ser 305 Ala Asp Ile Asp Ser 310 Tyr Leu Leu Glu Lys 315 Ser Arg Val Ile Phe 320

Gln Leu Pro Gly Glu 325 Arg Ser Tyr His Val 330 Tyr Tyr Gln Ile Leu 335 Ser

Gly Arg Lys Pro 340 Glu Leu Gln Asp Met 345 Leu Leu Leu Ser Met 350 Asn Pro

Tyr Asp Tyr 355 His Phe Cys Ser Gln 360 Gly Val Ile Thr Val 365 Asp Asn Met

Asn Asp 370 Gly Glu Glu Leu Ile 375 Ala Thr Asp His Ala 380 Met Asp Ile Leu

Gly 385 Phe Ser Val Asp Glu 390 Lys Cys Ala Cys Tyr 395 Lys Ile Val Gly Ala 400

Leu Leu His Phe Gly 405 Asn Met Lys Phe Lys 410 Gln Lys Gln Arg Glu 415 Glu

Gln Ala Glu Ala 420 Asp Gly Thr Glu Ser 425 Ala Asp Lys Ala 430 Ala Tyr Leu

Met Gly Val 435 Ser Ser Gly Asp Leu 440 Leu Lys Gly Leu Leu 445 His Pro Arg

Val Arg Val Gly Asn Glu Tyr Val Thr Lys Gly Gln Ser Val Glu Gln  
 450 455 460  
 Val Val Phe Ala Val Gly Ala Leu Ala Lys Ala Thr Tyr Asp Arg Leu  
 465 470 475 480  
 Phe Arg Trp Leu Val Ser Arg Ile Asn Gln Thr Leu Asp Thr Lys Leu  
 485 490 495  
 Pro Arg Gln Phe Phe Ile Gly Val Leu Asp Ile Ala Gly Phe Glu Ile  
 500 505 510  
 Phe Glu Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe Thr Asn Glu  
 515 520 525  
 Lys Leu Gln Gln Phe Phe Asn Gln His Met Phe Val Leu Glu Gln Glu  
 530 535 540  
 Glu Tyr Lys Arg Glu Gly Ile Asp Trp Val Phe Ile Asp Phe Gly Leu  
 545 550 555 560  
 Asp Leu Gln Pro Cys Ile Asp Leu Ile Glu Lys Pro Leu Gly Ile Leu  
 565 570 575  
 Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Ser Asp Ala Ser  
 580 585 590  
 Phe Arg Ala Lys Leu Tyr Asp Asn His Ala Gly Lys Ser Pro Asn Phe  
 595 600 605  
 Gln Gln Pro Arg Pro Asp Lys Lys Arg Lys Tyr Gln Ala His Phe Glu  
 610 615 620  
 Val Val His Tyr Ala Gly Val Val Pro Tyr Ser Ile Val Gly Trp Leu  
 625 630 635 640  
 Glu Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val Pro Ile Phe Gln  
 645 650 655  
 Lys Ser Gln Asn Arg Leu Leu Ala Thr Leu Tyr Glu Asn Tyr Ala Gly  
 660 665 670  
 Ser Cys Ser Thr Glu Pro Pro Lys Ser Gly Val Lys Glu Lys Arg Lys  
 675 680 685  
 Lys Ala Ala Ser Phe Gln Thr Val Ser Gln Leu His Lys Glu Asn Leu  
 690 695 700  
 Asn Lys Leu Met Thr Asn Leu Arg Ala Thr Gln Pro His Phe Val Arg  
 705 710 715 720  
 Cys Ile Val Pro Asn Glu Asn Lys Thr Pro Gly Val Met Asp Ala Phe  
 Page 319

725

730

735

Leu Val Leu His Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg  
 740 745 750  
 Ile Cys Arg Gln Gly Phe Pro Asn Arg Leu Leu Tyr Thr Asp Phe Arg  
 755 760  
 Gln Arg Tyr Arg Ile Leu Asn Pro Ser Ala Ile Pro Asp Asp Thr Phe  
 770 775 780  
 Met Asp Ser Arg Lys Ala Thr Glu Lys Leu Leu Gly Ser Leu Asp Leu  
 785 790 795 800  
 Asp His Thr Gln Tyr Gln Phe Gly His Thr Lys Val Phe Phe Lys Ala  
 805 810 815  
 Gly Leu Leu Gly Val Leu Glu Glu Leu Arg Asp Gln Arg Leu Ala Lys  
 820 825 830  
 Val Leu Thr Leu Leu Gln Ala Arg Ser Arg Gly Arg Leu Met Arg Leu  
 835 840 845  
 Glu Tyr Gln Arg Leu Leu Gly Gly Arg Asp Ala Leu Phe Thr Ile Gln  
 850 855 860  
 Trp Asn Ile Arg Ala Phe Asn Ala Val Lys Asn Trp Ser Trp Met Lys  
 865 870 875 880  
 Leu Phe Phe Lys Met Lys Pro Leu Leu Arg Ser Ala Gln Ala Glu Glu  
 885 890 895  
 Glu Leu Ala Ala Leu Arg Ala Glu Leu Arg Gly Leu Arg Gly Ala Leu  
 900 905 910  
 Ala Ala Ala Glu Ala Lys Arg Gln Glu Leu Glu Glu Thr His Val Ser  
 915 920 925  
 Ile Thr Gln Glu Lys Asn Asp Leu Ala Leu Gln Leu Gln Ala Glu Gln  
 930 935 940  
 Asp Asn Leu Ala Asp Ala Glu Glu Arg Cys His Leu Leu Ile Lys Ser  
 945 950 955 960  
 Lys Val Gln Leu Glu Gly Lys Val Lys Glu Leu Ser Glu Arg Leu Glu  
 965 970 975  
 Asp Glu Glu Glu Val Asn Ala Asp Leu Ala Ala Arg Arg Arg Lys Leu  
 980 985 990  
 Glu Asp Glu Cys Thr Glu Leu Lys Lys Asp Ile Asp Asp Leu Lys Leu  
 995 1000 1005

N3027PCT\_sequ.list.txt

Thr	Leu	Ala	Lys	Ala	Glu	Lys	Glu	Lys	Gln	Ala	Thr	Glu	Asn	Lys
	1010					1015					1020			
Val	Lys	Asn	Leu	Thr	Glu	Glu	Met	Ala	Ala	Leu	Asp	Glu	Ser	Val
	1025					1030					1035			
Ala	Arg	Leu	Thr	Lys	Glu	Lys	Lys	Ala	Leu	Gln	Glu	Ala	His	Gln
	1040					1045					1050			
Gln	Ala	Leu	Gly	Asp	Leu	Gln	Ala	Glu	Glu	Asp	Arg	Val	Ser	Ala
	1055					1060					1065			
Leu	Thr	Lys	Ala	Lys	Leu	Arg	Leu	Glu	Gln	Gln	Val	Glu	Asp	Leu
	1070					1075					1080			
Glu	Cys	Ser	Leu	Glu	Gln	Glu	Lys	Lys	Leu	Arg	Met	Asp	Thr	Glu
	1085					1090					1095			
Arg	Ala	Lys	Arg	Lys	Leu	Glu	Gly	Asp	Leu	Lys	Leu	Thr	Gln	Glu
	1100					1105					1110			
Ser	Val	Ala	Asp	Ala	Ala	Gln	Asp	Lys	Gln	Gln	Leu	Glu	Glu	Lys
	1115					1120					1125			
Leu	Lys	Lys	Lys	Asp	Ser	Glu	Leu	Ser	Gln	Leu	Ser	Leu	Arg	Val
	1130					1135					1140			
Glu	Asp	Glu	Gln	Leu	Leu	Gly	Ala	Gln	Met	Gln	Lys	Lys	Ile	Lys
	1145					1150					1155			
Glu	Leu	Gln	Ala	Arg	Ala	Glu	Glu	Leu	Glu	Glu	Glu	Leu	Glu	Ala
	1160					1165					1170			
Glu	Arg	Ala	Ala	Arg	Ala	Arg	Val	Glu	Lys	Gln	Arg	Ala	Glu	Ala
	1175					1180					1185			
Ala	Arg	Glu	Leu	Glu	Glu	Leu	Ser	Glu	Arg	Leu	Glu	Glu	Ala	Gly
	1190					1195					1200			
Gly	Ala	Ser	Ala	Gly	Gln	Arg	Glu	Gly	Cys	Arg	Lys	Arg	Glu	Ala
	1205					1210					1215			
Glu	Leu	Gly	Arg	Leu	Arg	Arg	Glu	Leu	Glu	Glu	Ala	Ala	Leu	Arg
	1220					1225					1230			
His	Glu	Ala	Thr	Val	Ala	Ala	Leu	Arg	Arg	Lys	Gln	Ala	Glu	Gly
	1235					1240					1245			
Ala	Ala	Glu	Leu	Gly	Glu	Gln	Val	Asp	Ser	Leu	Gln	Arg	Val	Arg
	1250					1255					1260			

N3027PCT\_sequ.list.txt

Gln	Lys	Leu	Glu	Lys	Glu	Lys	Ser	Glu	Leu	Arg	Met	Glu	Val	Asp
	1265					1270					1275			
Asp	Leu	Ala	Ala	Asn	Val	Glu	Thr	Leu	Thr	Arg	Ala	Lys	Ala	Ser
	1280					1285					1290			
Ala	Glu	Lys	Leu	Cys	Arg	Thr	Tyr	Glu	Asp	Gln	Leu	Ser	Glu	Ala
	1295					1300					1305			
Lys	Ile	Lys	Val	Glu	Glu	Leu	Gln	Arg	Gln	Leu	Ala	Asp	Ala	Ser
	1310					1315					1320			
Thr	Gln	Arg	Gly	Arg	Leu	Gln	Thr	Glu	Ser	Gly	Glu	Leu	Ser	Arg
	1325					1330					1335			
Leu	Leu	Glu	Glu	Lys	Glu	Cys	Leu	Ile	Ser	Gln	Leu	Ser	Arg	Gly
	1340					1345					1350			
Lys	Ala	Leu	Ala	Ala	Gln	Ser	Leu	Glu	Glu	Leu	Arg	Arg	Gln	Leu
	1355					1360					1365			
Glu	Glu	Glu	Ser	Lys	Ala	Lys	Ser	Ala	Leu	Ala	His	Ala	Val	Gln
	1370					1375					1380			
Ala	Leu	Arg	His	Asp	Cys	Asp	Leu	Leu	Arg	Glu	Gln	His	Glu	Glu
	1385					1390					1395			
Glu	Ala	Glu	Ala	Gln	Ala	Glu	Leu	Gln	Arg	Leu	Leu	Ser	Lys	Ala
	1400					1405					1410			
Asn	Ala	Glu	Val	Ala	Gln	Trp	Arg	Ser	Lys	Tyr	Glu	Ala	Asp	Ala
	1415					1420					1425			
Ile	Gln	Arg	Thr	Glu	Glu	Leu	Glu	Glu	Ala	Lys	Lys	Lys	Leu	Ala
	1430					1435					1440			
Leu	Arg	Leu	Gln	Glu	Ala	Glu	Glu	Gly	Val	Glu	Ala	Ala	Asn	Ala
	1445					1450					1455			
Lys	Cys	Ser	Ser	Leu	Glu	Lys	Ala	Lys	Leu	Arg	Leu	Gln	Thr	Glu
	1460					1465					1470			
Ser	Glu	Asp	Val	Thr	Leu	Glu	Leu	Glu	Arg	Ala	Thr	Ser	Ala	Ala
	1475					1480					1485			
Ala	Ala	Leu	Asp	Lys	Lys	Gln	Arg	His	Leu	Glu	Arg	Ala	Leu	Glu
	1490					1495					1500			
Glu	Arg	Arg	Arg	Gln	Glu	Glu	Glu	Met	Gln	Arg	Glu	Leu	Glu	Ala
	1505					1510					1515			

Ala Gln Arg Gu Ser Arg Gly Leu Gly Thr Gu Leu Phe Arg Leu  
 1520 1525 1530  
 Arg His Gly His Gu Gu Ala Leu Gu Ala Leu Gu Thr Leu Lys  
 1535 1540 1545  
 Arg Gu Asn Lys Asn Leu Gln Gu Gu Ile Ser Asp Leu Thr Asp  
 1550 1555 1560  
 Gln Val Ser Leu Ser Gly Lys Ser Ile Gln Gu Leu Gu Lys Thr  
 1565 1570 1575  
 Lys Lys Ala Leu Gu Gly Gu Lys Ser Gu Ile Gln Ala Ala Leu  
 1580 1585 1590  
 Gu Gu Ala Gu Gly Ala Leu Gu Leu Gu Gu Thr Lys Thr Leu  
 1595 1600 1605  
 Arg Ile Gln Leu Gu Leu Ser Gln Val Lys Ala Gu Val Asp Arg  
 1610 1615 1620  
 Lys Leu Ala Gu Lys Asp Gu Gu Cys Ala Asn Leu Arg Arg Asn  
 1625 1630 1635  
 His Gln Arg Ala Val Gu Ser Leu Gln Ala Ser Leu Asp Ala Gu  
 1640 1645 1650  
 Thr Arg Ala Arg Asn Gu Ala Leu Arg Leu Lys Lys Lys Met Gu  
 1655 1660 1665  
 Gly Asp Leu Asn Asp Leu Gu Leu Gln Leu Gly His Ala Thr Arg  
 1670 1675 1680  
 Gln Ala Thr Gu Ala Gln Ala Ala Thr Arg Leu Met Gln Ala Gln  
 1685 1690 1695  
 Leu Lys Gu Gu Gln Ala Gly Arg Asp Gu Gu Gln Arg Leu Ala  
 1700 1705 1710  
 Ala Gu Leu His Gu Gln Ala Gln Ala Leu Gu Arg Arg Ala Ser  
 1715 1720 1725  
 Leu Leu Ala Ala Gu Leu Gu Gu Leu Arg Ala Ala Leu Gu Gln  
 1730 1735 1740  
 Gly Gu Arg Ser Arg Arg Leu Ala Gu Gln Gu Leu Leu Gu Ala  
 1745 1750 1755  
 Thr Gu Arg Leu Asn Leu Leu His Ser Gln Asn Thr Gly Leu Leu  
 1760 1765 1770  
 Asn Gln Lys Lys Lys Leu Gu Ala Asp Leu Ala Gln Leu Ser Gly

1775

1780

1785

G u Val 1790   G u G u A l a A l a G n 1795   G u A r g A r g G u A l a 1800   G u G u L y s  
 A l a L y s 1805   L y s A l a I l e T h r A s p 1810   A l a A l a M e t M e t A l a 1815   G u G u L e u  
 L y s L y s 1820   G u G n A s p T h r S e r 1825   A l a H i s L e u G u A r g 1830   M e t L y s L y s  
 T h r L e u 1835   G u G n T h r V a l A r g 1840   G u L e u G n A l a A r g 1845   L e u G u G u  
 A l a G u 1850   G n A l a A l a L e u A r g 1855   G y G y L y s L y s G n 1860   V a l G n L y s  
 L e u G u 1865   A l a L y s V a l A r g G u 1870   L e u G u A l a G u L e u 1875   A s p A l a G u  
 G n L y s 1880   L y s H i s A l a G u A l a 1885   L e u L y s G y V a l A r g 1890   L y s H i s G u  
 A r g A r g 1895   V a l L y s G u L e u A l a 1900   T y r G n A l a G u G u 1905   A s p A r g L y s  
 A s n L e u 1910   A l a A r g M e t G n A s p 1915   L e u V a l A s p L y s L e u 1920   G n S e r L y s  
 V a l L y s 1925   S e r T y r L y s A r g G n 1930   P h e G u G u A l a G u 1935   G n G n A l a  
 A s n T h r 1940   A s n L e u A l a L y s T y r 1945   A r g L y s A l a G n H i s 1950   G u L e u A s p  
 A s p A l a 1955   G u G u A r g A l a A s p 1960   M e t A l a G u T h r G n 1965   A l a A s n L y s  
 L e u A r g 1970   A l a A r g T h r A r g A s p 1975   A l a L e u G y P r o L y s 1980   H i s L y s G u

<210> 69  
 <211> 7474  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> (1) . . (7474)  
 <223> myosin, heavy chain 9, non-muscle (MYH9)

<400> 69  
 at acgact ca ct at agggcg at caggt gct ggaaagaagg ct aagcaagg ct gacct gct

60

N3027PCT\_sequ. list . . txt

gcagct cccg cct cgt gcgc t cgccccacc cggccgcccgc ccgagcgct c gagaaagt cc	120
t ct cgggaga agcagcgccct gt t cccgggg cagat ccagg t t caggt cct ggct at aagt	180
caccat ggca cagcaagct g ccgat aagt a t ct ct at gt g gat aaaaact t cat caacaa	240
t ccgct ggcc caggccgact gggct gccaa gaagct ggt a t gggg gcct t ccgacaagag	300
t ggct t t gag ccagccagcc t caaggagga ggt gggcgaa gaggccat cg t ggagct ggt	360
ggagaat ggg aagaaggt ga aggt gaacaa ggat gacat c cagaagat ga acccgcccaa	420
gt t ct ccaag gt ggaggaca t ggcagagct cacgt gcct c aacgaagcct cggg gct gca	480
caacct caag gagcgt t act act cagggct cat ct acacc t at t caggcc t gt t ct gt gt	540
ggg cat caat cct t acaaga acct gcccat ct act ct gaa gagat t gt gg aaat gt acaa	600
gggcaagaag aggcacgaga t gccccct ca cat ct at gcc at cacagaca ccgcct acag	660
gagt at gat g caagaccgag aagat caat c cat ct t gt gc act ggt gaat ct ggagct gg	720
caagacggag aacaccaaga aggt cat cca gt at ct ggcg t acgt ggcgt cct cgcacaa	780
gagcaagaag gaccagggcg agct ggagcg gcagct gct g caggccaacc ccat cct gga	840
ggcct t cggg aacgccaaga ccgt gaagaa t gacaact cc t cccgct t cg gcaaat t cat	900
t cgcat caac t t t gat gt ca at ggct acat t gt t ggagcc aacat t gaga ct t at ct t t t	960
ggagaaat ct cgt gct at cc gccaagccaa ggaagaacgg acct t ccaca t ct t ct at t a	1020
t ct cct gt ct ggggct ggag agcacct gaa gaccgat ct c ct gt t ggagc cgt acaacaa	1080
at accgct t c ct gt ccaat g gacacgt cac cat ccccggg cagcaggaca aggacat gt t	1140
ccaggagacc at ggaggcca t gaggat t at gggcat ccca gaagaggagc aaat gggcct	1200
gct gcgggt c at ct cagggg t t ct t cagct cggcaacat c gt ct t caaga aggagcggaa	1260
cact gaccag gcgt ccat gc ccgacaacac agct gcccaa aaggt gt ccc at ct ct t ggg	1320
t at caat gt g accgat t t ca ccagaggaat cct caccgccg cgcat caagg t gggacggga	1380
t t acgt ccag aaggcgcaga ct aaagagca ggct gact t t gccat cgagg cct t ggccaa	1440
ggcgacct at gagcggat gt t ccgct ggct ggt gct gcgc at caacaagg ct ct ggacaa	1500
gaccaagagg cagggcgccct cct t cat cgg gat cct ggac at t gccggct t cgagat ct t	1560
t gat ct gaac t cgt t t gagc agct gt gcat caat t acacc aat gagaagc t gcagcagct	1620
ct t caaccac accat gt t ca t cct ggagca ggaggagt ac cagcgcgagg gcat cgagt g	1680
gaact t cat c gact t t ggcc t cgacct gca gccct gcat c gacct cat t g agaagccagc	1740
aggccccccg ggcat t ct gg ccct gct gga cgaggagt gc t ggt t ccca aagccaccga	1800
caagagct t c gt ggagaagg t gat gcagga gcagggcacc caccccaagt t ccagaagcc	1860
caagcagct g aaggacaaag ct gat t t ct g cat t at ccac t at gccggca aggt ggat t a	1920
caaagct gac gagt ggct ga t gaagaacat ggat cccct g aat gacaaca t cgccacact	1980
gct ccaccag t cct ct gaca agt t t gt ct c ggagct gt gg aaggat gt gg accgcat cat	2040
cggcct ggac caggt ggccg gcat gt cgga gaccgcact g cccggggcct t caagacgcg	2100
gaagggcat g t t ccgcact g t ggggcagct t t acaaggag cagct ggcca agct gat ggc	2160

N3027PCT\_sequ. list . . txt

t acgct gagg aacacgaacc ccaact t t gt ccgct gcat c at ccccaacc acgagaagaa	2220
ggccggcaag ct ggacccgc at ct cgt gct ggaccagct g cgct gcaacg gt gt t ct cga	2280
gggcat ccgt at ct gccgcc agggct t ccc caacagggt g gt ct t ccagg agt t t cggca	2340
gagat at gag at cct gact c caaact ccat t cccaagggt t t cat ggacg ggaagcaggc	2400
gt gcgt gct c at gat aaaag ccct ggagct cgacagcaat ct gt accgca t t ggccagag	2460
caaagt ct t c t t ccgt gccg gt gt gct ggc ccacct ggag gaggagcgag acct gaagat	2520
caccgacgt c at cat aggggt t ccaggcct g ct gcaggggc t acct ggcca ggaaagcat t	2580
t gccaaagcgg cagcagcagc t t accgccat gaaggt cct c cagcggaact gcgct gcct a	2640
cct gaagct g cggaact ggc agt ggt ggcg gct ct t cacc aaggt caagc cgct gct gca	2700
ggt gagccgg caggaggagg agat gat ggc caaggaggag gagct ggt ga aggt cagaga	2760
gaagcagct g gct gcggaga acaggct cac ggagat ggag acgct gcagt ct cagct cat	2820
ggcagagaaa t t gcagct gc aggagcagct ccaggcagaa accgagct gt gt gccgaggc	2880
t gaggagct c cgggccccgc t gaccgccaa gaagcaggaa t t agaagaga t ct gccat ga	2940
cct agaggcc aggggt ggagg aggaggagga gcgct gccag cacct gcagg cggagaagaa	3000
gaagat gcag cagaacat cc aggagct t ga ggagcagct g gaggaggagg agagcgccccg	3060
gcagaagct g cagct ggaga aggt gaccac cgaggcgaag ct gaaaaagc t ggaggagga	3120
gcagat cat c ct ggaggacc agaact gcaa gct ggccaag gaaaagaaac t gct ggaaga	3180
cagaat agct gagt t cacca ccaacct cac agaagaggag gagaaat ct a agagcct cgc	3240
caagct caag aacaagcat g aggcaat gat cact gact t g gaagagcgcc t ccgcaggga	3300
ggagaagcag cgacaggagc t ggagaagac ccgccggaag ct ggagggag act ccacaga	3360
cct cagcgac cagat cgccg agct ccaggc ccagat cgcg gagct caaga t gcagct ggc	3420
caagaaagag gaggagct cc aggccgccct ggccagagt g gaagaggaag ct gccagaa	3480
gaacat ggcc ct caagaaga t ccgggagct ggaat ct cag at ct ct gaac t ccaggaaga	3540
cct ggagt ct gagcgt gct t ccaggaat aa agct gagaag cagaaacggg acct t gggga	3600
agagct agag gcgct gaaaa cagagt t gga ggacacgct g gat t ccacag ct gccagca	3660
ggagct cagg t caaaacgt g agcaggaggt gaacat cct g aagaagacc t ggaggagga	3720
ggccaagacc cagcaggccc agat ccagga gat gaggcag aagcact cac aggccgt gga	3780
ggagct ggcg gagcagct gg agcagacgaa gcgggt gaaa gcaaacct cg agaaggcaaa	3840
gcagact ct g gagaacgagc ggggggagct ggccaacgag gt gaaggt gc t gct gcaggg	3900
caaagggggac t cggagcaca agcgcaagaa agt ggaggcg cagct gcagg agct gcaggt	3960
caagt t caac gagggagagc gcgt gcgcac agagct ggcc gacaaggt ca ccaagct gca	4020
ggt ggagct g gacaacgt ga ccgggct t ct cagccagt cc gacagcaagt ccagcaagct	4080
caccaaggac t t ct ccgcgc t ggagt ccca gct gcaggac act caggagc t gct gcagga	4140
ggagaaccgg cagaagct ga gcct gagcac caagct caag caggt ggagg acgagaagaa	4200

N3027PCT\_sequ. l i s t . . t x t

t t c c t t c c g g	g a g c a g c t g g	a g g a g g a g g a	g g a g g c c a a g	c a c a a c c t g g	a g a a g c a g a t	4260
c g c c a c c c t c	c a t g c c c a g g	t g g c c g a c a t	g a a a a a g a a g	a t g g a g g a c a	g t g t g g g g t g	4320
c c t g g a a a c t	g c t g a g g a g g	t g a a g a g g a a	g c t c c a g a a g	g a c c t g g a g g	g c c t g a g c c a	4380
g c g g c a c g a g	g a g a a g g t g g	c c g c c t a c g a	c a a g c t g g a g	a a g a c c a a g a	c g c g g c t g c a	4440
g c a g g a g c t g	g a c g a c c t g c	t g g t g g a c c t	g g a c c a c c a g	c g c c a g a g c g	c g t g c a a c c t	4500
g g a g a a g a a g	c a g a a g a a g t	t t g a c c a g c t	c c t g g c g g a g	g a g a a g a c c a	t c t c t g c c a a	4560
g t a t g c a g a g	g a g c g c g a c c	g g g c t g a g g c	g g a g g c c c g a	g a g a a g g a g a	c c a a g g c t c t	4620
g t c g c t g g c c	c g g g c c c t g g	a g g a a g c c a t	g g a g c a g a a g	g c g g a g c t g g	a g c g g c t c a a	4680
c a a g c a g t t c	c g c a c g g a g a	t g g a g g a c c t	t a t g a g c t c c	a a g g a t g a t g	t g g g c a a g a g	4740
t g t c c a c g a g	c t g g a g a a g t	c c a a g c g g g c	c c t a g a g c a g	c a g g t g g a g g	a g a t g a a g a c	4800
g c a g c t g g a a	g a g c t g g a g g	a c g a g c t g c a	g g c c a c c g a a	g a t g c c a a g c	t g c g g t t g g a	4860
g g t c a a c c t g	c a g g c c a t g a	a g g c c c a g t t	c g a g c g g g a c	c t g c a g g g c c	g g g a c g a g c a	4920
g a g c g a g g a g	a a g a a g a a g c	a g c t g g t c a g	a c a g g t g c g g	g a g a t g g a g g	c a g a g c t g g a	4980
g g a c g a g a g g	a a g c a g c g c t	c g a t g g c a g t	g g c c g c c c g g	a a g a a g c t g g	a g a t g g a c c t	5040
g a a g g a c c t g	g a g g c g c a c a	t c g a c t c g g c	c a a c a a g a a c	c g g g a c g a a g	c c a t c a a a c a	5100
g c t g c g g a a g	c t g c a g g c c c	a g a t g a a g g a	c t g c a t g c g c	g a g c t g g a t g	a c a c c c g c g c	5160
c t c t c g t g a g	g a g a t c c t g g	c c c a g g c c a a	a g a g a a c g a g	a a g a a g c t g a	a g a g c a t g g a	5220
g g c c g a g a t g	a t c c a g t t g c	a g g a g g a a c t	g g c a g c c g c g	g a g c g t g c c a	a g c g c c a g g c	5280
c c a g c a g g a g	c g g g a t g a g c	t g g c t g a c g a	g a t c g c c a a c	a g c a g c g g c a	a a g g a g c c c t	5340
g g c g t t a g a g	g a g a a g c g g c	g t c t g g a g g c	c c g c a t c g c c	c a g c t g g a g g	a g g a g c t g g a	5400
g g a g g a g c a g	g g c a a c a c g g	a g c t g a t c a a	c g a c c g g c t g	a a g a a g g c c a	a c c t g c a g a t	5460
c g a c c a g a t c	a a c a c c g a c c	t g a a c c t g g a	g c g c a g c c a c	g c c c a g a a g a	a c g a g a a t g c	5520
t c g g c a g c a g	c t g g a a c g c c	a g a a c a a g g a	g c t t a a g g t c	a a g c t g c a g g	a g a t g g a g g g	5580
c a c t g t c a a g	t c c a a g t a c a	a g g c c t c c a t	c a c c g c c c t c	g a g g c c a a g a	t t g c a c a g c t	5640
g g a g g a g c a g	c t g g a c a a c g	a g a c c a a g g a	g c g c c a g g c a	g c c t g c a a a c	a g g t g c g t c g	5700
g a c c g a g a a g	a a g c t g a a g g	a t g t g c t g c t	g c a g g t g g a t	g a c g a g c g g a	g g a a c g c c g a	5760
g c a g t a c a a g	g a c c a g g c c g	a c a a g g c a t c	t a c c c g c c t g	a a g c a g c t c a	a g c g g c a g c t	5820
g g a g g a g g c c	g a a g a g g a g g	c c c a g c g g g c	c a a c g c c t c c	c g c c g g a a a c	t g c a g c g c g a	5880
g c t g g a g g a c	g c c a c t g a g a	c g g c c g a t g c	c a t g a a c c g c	g a a g t c a g c t	c c c t a a a g a a	5940
c a a g c t c a g g	c g c g g g g a c c	t g c c g t t t g t	c g t g c c c c g c	c g a a t g g c c c	g g a a a g g c g c	6000
c g g g g a t g g c	t c c g a c g a a g	a g g t a g a t g g	c a a a g c g g a t	g g g g c t g a g g	c c a a a c c t g c	6060
c g a a t a a g c c	t c t t c t c c t g	c a g c c t g a g a	t g g a t g g a c a	g a c a g a c a c c	a c a g c c t c c c	6120
c t t c c c a g a c	c c c g c a g c a c	g c c t c t c c c c	a c c t t c t t g g	g a c t g c t g t g	a a c a t g c c t c	6180
c t c c t g c c c t	c c g c c c c g t c	c c c c c a t c c c	g t t t c c c t c c	a g g t g t t g t t	g a g g g c a t t t	6240
g g c t t c c t c t	g c t g c a t c c c	c t t c c a g c t c	c c t c c c c t g c	t c a g a a t c t g	a t a c c a a a g a	6300

N3027PCT\_sequ.list.txt

gacagggccc gggcccaggc agagagcgac cagcaggctc ct cagccctc tcttgccaaa 6360  
aagcacaaga tgttgaggcg agcagggcag gcccccgagg agggggccaga gt t t t c t a t g 6420  
aatctat t t t t c t t c a g a c t g a g g c c t t t t g g t a g t c g g a g c c c c c g c a g t c g t c a g c c t 6480  
ccctgacgtc tggcaccagc gccccactc ct cct cct t t c t t t g c t g t t t g c a a t c a c a 6540  
cgt ggt gacc t c a c a c a c c t c t g c c c c t t g g g c c t c c c a c t c c c a t g g c t c t g g g c g g t c 6600  
cagaaggagc agggcctggg cctccacctc tgtgcagggc acagaaggct ggggtggggg 6660  
gaggagt gga t t c c t c c c c a c c c t g t c c c a g g c a g c g c c a c t g t c c g c t g t c t c c c t c c t 6720  
gat t c t a a a a t g t c t c a a g t g c a a t g c c c c c t c c c t t t a c c g a g g a c a g c c t g c c t 6780  
ctgccacagc aaggctgtcg ggggtcaagct ggaaaggcca gcagccttcc agtggcttct 6840  
cccaacactc ttggggacca aat at a t t t a a t g g t t a a g g g a c t t g t c c c a a g t c t g a c a 6900  
gccagagcgt tagagggggc agcggccctc ccaggcgatc ttgtgtctac tctaggactg 6960  
ggcccgagggtgggtttacct gcaccgttga ct c a g t a t a g t t t a a a a a t c t g c c a c c t g c 7020  
acaggtat t t t g a a a g c a a a a t a a g g t t t t c t t t t t t c c c c t t t c t t g t a a t a a t g a t 7080  
aaaat t c c g a g t c t t t c t c a c t g c c t t t g t t t a g a a g a g a g t a g c t c g t c c t c a c t g g t c 7140  
t a c a c t g g t t g c c g a a t t t a c t t g t a t t c c t a a c t g t t t t g t a t a t g c t g c a t t g a g a c t 7200  
t a c g g c a a g a a g g c a t t t t t t t t t t a a a g g a a c a a a c t c t c a a a t c a t g a a g t g a t a 7260  
t a a a a g c t g c a t a t g c c t a c a a g c t c t g a a t t c a g g t c c c a g t t g c t g t c a c a a a g g a g 7320  
t g a g t g a a a c t c c c a c c c t a c c c c t t t t t t a t a t a a t a a a a g t g c c t t a g c a t g t g t t g 7380  
c a g c t g t c a c c a c t a c a g t a a g c t g g t t t a c a g a t g t t t t c c a c t g a g c a t c a c a a t a a a 7440  
g a g a a c c a t g t g c t a a a a a a a a a a a a a a a a a a a 7474

<210> 70  
<211> 1960  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1960)  
<223> myosin, heavy chain 9, non-muscle (MYH9)

<400> 70

Met Ala Gln Gln Ala Ala Asp Lys Tyr Leu Tyr Val Asp Lys Asn Phe  
1 5 10 15

Ile Asn Asn Pro Leu Ala Gln Ala Asp Trp Ala Ala Lys Lys Leu Val  
20 25 30

Trp Val Pro Ser Asp Lys Ser Gly Phe Glu Pro Ala Ser Leu Lys Glu  
35 40 45

Glu Val Gly Glu Glu Ala Ile Val Glu Leu Val Glu Asn Gly Lys Lys  
50 55 60

N3027PCT\_sequ.list.txt

Val 65	Lys	Val	Asn	Lys	Asp 70	Asp	Ile	Gln	Lys	Met 75	Asn	Pro	Pro	Lys	Phe 80
Ser	Lys	Val	Glu 85	Asp	Met	Ala	Glu	Leu	Thr 90	Cys	Leu	Asn	Glu	Ala	Ser 95
Val	Leu	His	Asn 100	Leu	Lys	Glu	Arg	Tyr 105	Tyr	Ser	Gly	Leu	Ile	Tyr	Thr 110
Tyr	Ser	Gly 115	Leu	Phe	Cys	Val	Val 120	Ile	Asn	Pro	Tyr	Lys 125	Asn	Leu	Pro
Ile	Tyr 130	Ser	Glu	Glu	Ile	Val 135	Glu	Met	Tyr	Lys	Gly 140	Lys	Lys	Arg	His
Glu 145	Met	Pro	Pro	His	Ile 150	Tyr	Ala	Ile	Thr	Asp 155	Thr	Ala	Tyr	Arg	Ser 160
Met	Met	Gln	Asp	Arg 165	Glu	Asp	Gln	Ser	Ile 170	Leu	Cys	Thr	Gly	Glu 175	Ser
Gly	Ala	Gly	Lys 180	Thr	Glu	Asn	Thr	Lys 185	Lys	Val	Ile	Gln	Tyr 190	Leu	Ala
Tyr	Val	Ala 195	Ser	Ser	His	Lys	Ser 200	Lys	Lys	Asp	Gln	Gly 205	Glu	Leu	Glu
Arg	Gln 210	Leu	Leu	Gln	Ala	Asn 215	Pro	Ile	Leu	Glu	Ala 220	Phe	Gly	Asn	Ala
Lys 225	Thr	Val	Lys	Asn	Asp 230	Asn	Ser	Ser	Arg	Phe 235	Gly	Lys	Phe	Ile	Arg 240
Ile	Asn	Phe	Asp	Val 245	Asn	Gly	Tyr	Ile	Val 250	Gly	Ala	Asn	Ile	Glu 255	Thr
Tyr	Leu	Leu	Glu 260	Lys	Ser	Arg	Ala	Ile 265	Arg	Gln	Ala	Lys	Glu 270	Glu	Arg
Thr	Phe	His 275	Ile	Phe	Tyr	Tyr	Leu 280	Leu	Ser	Gly	Ala	Gly 285	Glu	His	Leu
Lys	Thr 290	Asp	Leu	Leu	Leu	Glu 295	Pro	Tyr	Asn	Lys	Tyr 300	Arg	Phe	Leu	Ser
Asn 305	Gly	His	Val	Thr	Ile 310	Pro	Gly	Gln	Gln	Asp 315	Lys	Asp	Met	Phe	Gln 320
Glu	Thr	Met	Glu	Ala 325	Met	Arg	Ile	Met	Gly 330	Ile	Pro	Glu	Glu	Glu 335	Gln

N3027PCT\_sequ.list.txt

Met Gly Leu Leu Arg Val Ile Ser Gly Val Leu Gln Leu Gly Asn Ile  
340 345 350

Val Phe Lys Lys Gu Arg Asn Thr Asp Gln Ala Ser Met Pro Asp Asn  
355 360 365

Thr Ala Ala Gln Lys Val Ser His Leu Leu Gly Ile Asn Val Thr Asp  
370 375 380

Phe Thr Arg Gly Ile Leu Thr Pro Arg Ile Lys Val Gly Arg Asp Tyr  
385 390 395 400

Val Gln Lys Ala Gln Thr Lys Gu Gln Ala Asp Phe Ala Ile Gu Ala  
405 410 415

Leu Ala Lys Ala Thr Tyr Gu Arg Met Phe Arg Trp Leu Val Leu Arg  
420 425 430

Ile Asn Lys Ala Leu Asp Lys Thr Lys Arg Gln Gly Ala Ser Phe Ile  
435 440 445

Gly Ile Leu Asp Ile Ala Gly Phe Gu Ile Phe Asp Leu Asn Ser Phe  
450 455 460

Gu Gln Leu Cys Ile Asn Tyr Thr Asn Gu Lys Leu Gln Gln Leu Phe  
465 470 475 480

Asn His Thr Met Phe Ile Leu Gu Gln Gu Gu Tyr Gln Arg Gu Gly  
485 490 495

Ile Gu Trp Asn Phe Ile Asp Phe Gly Leu Asp Leu Gln Pro Cys Ile  
500 505 510

Asp Leu Ile Gu Lys Pro Ala Gly Pro Pro Gly Ile Leu Ala Leu Leu  
515 520 525

Asp Gu Gu Cys Trp Phe Pro Lys Ala Thr Asp Lys Ser Phe Val Gu  
530 535 540

Lys Val Met Gln Gu Gln Gly Thr His Pro Lys Phe Gln Lys Pro Lys  
545 550 555 560

Gln Leu Lys Asp Lys Ala Asp Phe Cys Ile Ile His Tyr Ala Gly Lys  
565 570 575

Val Asp Tyr Lys Ala Asp Gu Trp Leu Met Lys Asn Met Asp Pro Leu  
580 585 590

Asn Asp Asn Ile Ala Thr Leu Leu His Gln Ser Ser Asp Lys Phe Val  
595 600 605

Ser 610 Glu Leu Trp Lys Asp Val 615 Asp Arg Ile Ile Gly 620 Leu Asp Gln Val

Ala 625 Gly Met Ser Glu Thr 630 Ala Leu Pro Gly 635 Ala Phe Lys Thr Arg Lys 640

Gly 645 Met Phe Arg Thr 645 Val Gly Gln Leu Tyr 650 Lys Glu Gln Leu Ala Lys 655

Leu 660 Met Ala Thr 660 Leu Arg Asn Thr 665 Asn Pro Asn Phe Val 670 Arg Cys Ile

Ile 675 Pro Asn 675 His Glu Lys Lys Ala 680 Gly Lys Leu Asp 685 Pro His Leu Val

Leu 690 Asp 690 Gln Leu Arg Cys Asn 695 Gly Val Leu Glu Gly 700 Ile Arg Ile Cys

Arg 705 Gln Gly Phe Pro Asn 710 Arg Val Val Phe 715 Gln Glu Phe Arg Gln Arg 720

Tyr 725 Glu Ile Leu Thr 725 Pro Asn Ser Ile 730 Pro Lys Gly Phe Met 735 Asp Gly

Lys 740 Gln Ala Cys 740 Val Leu Met Ile 745 Lys Ala Leu Glu Leu 750 Asp Ser Asn

Leu 755 Tyr Arg 755 Ile Gly Gln Ser 760 Lys Val Phe Phe Arg 765 Ala Gly Val Leu

Ala 770 His 770 Leu Glu Glu Glu Arg 775 Asp Leu Lys Ile Thr 780 Asp Val Ile Ile

Gly 785 Phe Gln Ala Cys 790 Cys Arg Gly Tyr Leu 795 Ala Arg Lys Ala Phe Ala 800

Lys 805 Arg Gln Gln Gln Leu Thr Ala 810 Met Lys Val Leu Gln Arg 815 Asn Cys

Ala 820 Ala Tyr 820 Leu Lys Leu Arg Asn Trp 825 Gln Trp Trp Arg 830 Leu Phe Thr

Lys 835 Val 835 Lys Pro Leu Leu Gln 840 Val Ser Arg Gln Glu 845 Glu Glu Met Met

Ala 850 Lys 850 Glu Glu Glu Leu Val 855 Lys Val Arg Glu 860 Lys Gln Leu Ala Ala

Glu 865 Asn Arg Leu Thr 870 Glu Met Glu Thr Leu 875 Gln Ser Gln Leu Met Ala 880

Glu 885 Lys Leu Gln Leu Gln Glu Gln Leu Gln Ala Glu Thr Glu Leu Cys

885

890

895

Ala Glu Ala Glu Glu Leu Arg Ala Arg Leu Thr Ala Lys Lys Gln Glu  
 900 905 910  
 Leu Glu Glu Ile Cys His Asp Leu Glu Ala Arg Val Glu Glu Glu Glu  
 915 920 925  
 Glu Arg Cys Gln His Leu Gln Ala Glu Lys Lys Lys Met Gln Gln Asn  
 930 935 940  
 Ile Gln Glu Leu Glu Glu Gln Leu Glu Glu Glu Glu Ser Ala Arg Gln  
 945 950 955 960  
 Lys Leu Gln Leu Glu Lys Val Thr Thr Glu Ala Lys Leu Lys Lys Leu  
 965 970 975  
 Glu Glu Glu Gln Ile Ile Leu Glu Asp Gln Asn Cys Lys Leu Ala Lys  
 980 985 990  
 Glu Lys Lys Leu Leu Glu Asp Arg Ile Ala Glu Phe Thr Thr Asn Leu  
 995 1000 1005  
 Thr Glu Glu Glu Glu Lys Ser Lys Ser Leu Ala Lys Leu Lys Asn  
 1010 1015 1020  
 Lys His Glu Ala Met Ile Thr Asp Leu Glu Glu Arg Leu Arg Arg  
 1025 1030 1035  
 Glu Glu Lys Gln Arg Gln Glu Leu Glu Lys Thr Arg Arg Lys Leu  
 1040 1045 1050  
 Glu Gly Asp Ser Thr Asp Leu Ser Asp Gln Ile Ala Glu Leu Gln  
 1055 1060 1065  
 Ala Gln Ile Ala Glu Leu Lys Met Gln Leu Ala Lys Lys Glu Glu  
 1070 1075 1080  
 Glu Leu Gln Ala Ala Leu Ala Arg Val Glu Glu Glu Ala Ala Gln  
 1085 1090 1095  
 Lys Asn Met Ala Leu Lys Lys Ile Arg Glu Leu Glu Ser Gln Ile  
 1100 1105 1110  
 Ser Glu Leu Gln Glu Asp Leu Glu Ser Glu Arg Ala Ser Arg Asn  
 1115 1120 1125  
 Lys Ala Glu Lys Gln Lys Arg Asp Leu Gly Glu Glu Leu Glu Ala  
 1130 1135 1140  
 Leu Lys Thr Glu Leu Glu Asp Thr Leu Asp Ser Thr Ala Ala Gln  
 1145 1150 1155

N3027PCT\_sequ.list.txt

G n	G u	Leu	Arg	Ser	Lys	Arg	G u	G n	G u	Val	Asn	I l e	Leu	Lys
	1160					1165					1170			
Lys	Thr	Leu	G u	G u	G u	Al a	Lys	Thr	Hi s	G u	Al a	G n	I l e	G n
	1175					1180					1185			
G u	Met	Arg	G n	Lys	Hi s	Ser	G n	Al a	Val	G u	G u	Leu	Al a	G u
	1190					1195					1200			
G n	Leu	G u	G n	Thr	Lys	Arg	Val	Lys	Al a	Asn	Leu	G u	Lys	Al a
	1205					1210					1215			
Lys	G n	Thr	Leu	G u	Asn	G u	Arg	G y	G u	Leu	Al a	Asn	G u	Val
	1220					1225					1230			
Lys	Val	Leu	Leu	G n	G y	Lys	G y	Asp	Ser	G u	Hi s	Lys	Arg	Lys
	1235					1240					1245			
Lys	Val	G u	Al a	G n	Leu	G n	G u	Leu	G n	Val	Lys	Phe	Asn	G u
	1250					1255					1260			
G y	G u	Arg	Val	Arg	Thr	G u	Leu	Al a	Asp	Lys	Val	Thr	Lys	Leu
	1265					1270					1275			
G n	Val	G u	Leu	Asp	Asn	Val	Thr	G y	Leu	Leu	Ser	G n	Ser	Asp
	1280					1285					1290			
Ser	Lys	Ser	Ser	Lys	Leu	Thr	Lys	Asp	Phe	Ser	Al a	Leu	G u	Ser
	1295					1300					1305			
G n	Leu	G n	Asp	Thr	G n	G u	Leu	Leu	G n	G u	G u	Asn	Arg	G n
	1310					1315					1320			
Lys	Leu	Ser	Leu	Ser	Thr	Lys	Leu	Lys	G n	Val	G u	Asp	G u	Lys
	1325					1330					1335			
Asn	Ser	Phe	Arg	G u	G n	Leu	G u	G u	G u	G u	G u	Al a	Lys	Hi s
	1340					1345					1350			
Asn	Leu	G u	Lys	G n	I l e	Al a	Thr	Leu	Hi s	Al a	G n	Val	Al a	Asp
	1355					1360					1365			
Met	Lys	Lys	Lys	Met	G u	Asp	Ser	Val	G y	Cys	Leu	G u	Thr	Al a
	1370					1375					1380			
G u	G u	Val	Lys	Arg	Lys	Leu	G n	Lys	Asp	Leu	G u	G y	Leu	Ser
	1385					1390					1395			
G n	Arg	Hi s	G u	G u	Lys	Val	Al a	Al a	Tyr	Asp	Lys	Leu	G u	Lys
	1400					1405					1410			

N3027PCT\_sequ.list.txt

Thr	Lys	Thr	Arg	Leu	Gln	Gln	Glu	Leu	Asp	Asp	Leu	Leu	Val	Asp
	1415					1420					1425			
Leu	Asp	His	Gln	Arg	Gln	Ser	Ala	Cys	Asn	Leu	Glu	Lys	Lys	Gln
	1430					1435					1440			
Lys	Lys	Phe	Asp	Gln	Leu	Leu	Ala	Glu	Glu	Lys	Thr	Ile	Ser	Ala
	1445					1450					1455			
Lys	Tyr	Ala	Glu	Glu	Arg	Asp	Arg	Ala	Glu	Ala	Glu	Ala	Arg	Glu
	1460					1465					1470			
Lys	Glu	Thr	Lys	Ala	Leu	Ser	Leu	Ala	Arg	Ala	Leu	Glu	Glu	Ala
	1475					1480					1485			
Met	Glu	Gln	Lys	Ala	Glu	Leu	Glu	Arg	Leu	Asn	Lys	Gln	Phe	Arg
	1490					1495					1500			
Thr	Glu	Met	Glu	Asp	Leu	Met	Ser	Ser	Lys	Asp	Asp	Val	Gly	Lys
	1505					1510					1515			
Ser	Val	His	Glu	Leu	Glu	Lys	Ser	Lys	Arg	Ala	Leu	Glu	Gln	Gln
	1520					1525					1530			
Val	Glu	Glu	Met	Lys	Thr	Gln	Leu	Glu	Glu	Leu	Glu	Asp	Glu	Leu
	1535					1540					1545			
Gln	Ala	Thr	Glu	Asp	Ala	Lys	Leu	Arg	Leu	Glu	Val	Asn	Leu	Gln
	1550					1555					1560			
Ala	Met	Lys	Ala	Gln	Phe	Glu	Arg	Asp	Leu	Gln	Gly	Arg	Asp	Glu
	1565					1570					1575			
Gln	Ser	Glu	Glu	Lys	Lys	Lys	Gln	Leu	Val	Arg	Gln	Val	Arg	Glu
	1580					1585					1590			
Met	Glu	Ala	Glu	Leu	Glu	Asp	Glu	Arg	Lys	Gln	Arg	Ser	Met	Ala
	1595					1600					1605			
Val	Ala	Ala	Arg	Lys	Lys	Leu	Glu	Met	Asp	Leu	Lys	Asp	Leu	Glu
	1610					1615					1620			
Ala	His	Ile	Asp	Ser	Ala	Asn	Lys	Asn	Arg	Asp	Glu	Ala	Ile	Lys
	1625					1630					1635			
Gln	Leu	Arg	Lys	Leu	Gln	Ala	Gln	Met	Lys	Asp	Cys	Met	Arg	Glu
	1640					1645					1650			
Leu	Asp	Asp	Thr	Arg	Ala	Ser	Arg	Glu	Glu	Ile	Leu	Ala	Gln	Ala
	1655					1660					1665			

Lys Glu Asn Glu Lys Lys Leu Lys Ser Met Glu Ala Glu Met Ile  
 1670 1675 1680  
 Gln Leu Gln Glu Glu Leu Ala Ala Ala Glu Arg Ala Lys Arg Gln  
 1685 1690 1695  
 Ala Gln Gln Glu Arg Asp Glu Leu Ala Asp Glu Ile Ala Asn Ser  
 1700 1705 1710  
 Ser Gly Lys Gly Ala Leu Ala Leu Glu Glu Lys Arg Arg Leu Glu  
 1715 1720 1725  
 Ala Arg Ile Ala Gln Leu Glu Glu Glu Leu Glu Glu Gln Gly  
 1730 1735 1740  
 Asn Thr Glu Leu Ile Asn Asp Arg Leu Lys Lys Ala Asn Leu Gln  
 1745 1750 1755  
 Ile Asp Gln Ile Asn Thr Asp Leu Asn Leu Glu Arg Ser His Ala  
 1760 1765 1770  
 Gln Lys Asn Glu Asn Ala Arg Gln Gln Leu Glu Arg Gln Asn Lys  
 1775 1780 1785  
 Glu Leu Lys Val Lys Leu Gln Glu Met Glu Gly Thr Val Lys Ser  
 1790 1795 1800  
 Lys Tyr Lys Ala Ser Ile Thr Ala Leu Glu Ala Lys Ile Ala Gln  
 1805 1810 1815  
 Leu Glu Glu Gln Leu Asp Asn Glu Thr Lys Glu Arg Gln Ala Ala  
 1820 1825 1830  
 Cys Lys Gln Val Arg Arg Thr Glu Lys Lys Leu Lys Asp Val Leu  
 1835 1840 1845  
 Leu Gln Val Asp Asp Glu Arg Arg Asn Ala Glu Gln Tyr Lys Asp  
 1850 1855 1860  
 Gln Ala Asp Lys Ala Ser Thr Arg Leu Lys Gln Leu Lys Arg Gln  
 1865 1870 1875  
 Leu Glu Glu Ala Glu Glu Glu Ala Gln Arg Ala Asn Ala Ser Arg  
 1880 1885 1890  
 Arg Lys Leu Gln Arg Glu Leu Glu Asp Ala Thr Glu Thr Ala Asp  
 1895 1900 1905  
 Ala Met Asn Arg Glu Val Ser Ser Leu Lys Asn Lys Leu Arg Arg  
 1910 1915 1920  
 Gly Asp Leu Pro Phe Val Val Pro Arg Arg Met Ala Arg Lys Gly

1925

Ala Gly Asp Gly Ser Asp Glu Glu Val Asp Gly Lys Ala Asp Gly  
1940 1945 1950

Ala Glu Ala Lys Pro Ala Glu  
1955 1960

<210> 71  
<211> 7619  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_ feat ure  
<222> (1) . . (7619)  
<223> myosin, heavy chain 10, non-muscle (MYH10)

```
<400> 71
actgaggcgc tggatctgtg gtcgcggtg gggacgtgcg cccgcgccac catcttcggc 60
tgaagaggca attgcttttg gatcggtcca tttacaatgg cgcagagAAC tggactcgag 120
gatccagaga ggtatctctt tgtggacagg gctgtcatct acaaccctgc cactcaagct 180
gattggacag ctaaaagct agtgtggtat ccatcagaac gccatggttt tgggacagct 240
agtatcaaag aagaacgggg agatgaagt atgggtggagt tggcagagaa tggaaagaaa 300
gcaatggtca acaaagatga tatcagaag atgaaccac ctAAGTtttc caaggtggag 360
gatatggcag aattgacatg ctitgaatgaa gcttccgttt tacaataatct gaaggatcgc 420
tactattcag gactaatcta tacttattct ggactcttct gtgtagttat aaacccttac 480
aagaatcttc caatttactc tgagaatat attgaaatgt acagagggaa gaagcgtcat 540
gagatgcctc cacacatcta tgctatatct gaatctgctt acagatgcat gcttcaagat 600
cgtgaggacc agtcaattct ttgcacgggt gaggcaggtg ctgggaagac agaaaataca 660
aagaaagtta ttcagtacct tgcccatgtt gcttcttcac ataaaggaag aaaggacat 720
aatattcctg gggaacttga acggcagctt ttgcaagcaa atccaattct ggaatcattt 780
ggaaatgcga agactgtgaa aaatgatAAC tcatctcgtt ttggcaaat tattcggatc 840
aactttgatg taactggcta tatcgttggg gccaacattg aaacatact tctggaaaag 900
tctcgtgctg ttctgcaagc aaaagatgaa cgtacttttc atatctttta ccagttgtta 960
tctggagcag gagaacacct aaagtctgat ttgcttcttg aaggatttaa taactacagg 1020
tttctctcca atggctatat tcctattccg ggacagcaag acaaagataa tttccaggag 1080
accatggaag caatgcacat aatgggcttc tcccatgaag agattctgtc aatgcttaa 1140
gtagtatctt cagtgtaca gtttggaaat atttctttca aaaaggagag aaatactgat 1200
caagcttcca tggcagaaaa tacagttgcg cagaagctct gccatcttct tgggatgaat 1260
gtgatggagt ttactcgggc catcctgact ccccgatca aggtcggccg agactatgtg 1320
caaaaagccc agaccaaaga acaggcagat tttgcagt ag aagcattggc aaaagctacc 1380
```

N3027PCT\_sequ. list.txt

t at gagcggc t c t t t c g c t g g c t c g t t c a t c g c a t c a a t a a a g c t c t g g a t a g g a c c a a a	1440
c g t c a g g g a g c a t c t t t c a t t g g a a t c c t g g a t a t t g c t g g a t t t g a a a t t t t t g a g c t g	1500
a a c t c c t t t g a a c a a c t t t g c a t c a a c t a c a c c a a t g a g a g c t g c a g c a g c t g t t c a a c	1560
c a c a c c a t g t t t a t c c t a g a a c a a g a g g a a t a c c a g c g c g a a g g c a t c g a g t g g a a c t t c	1620
a t c g a t t t c g g g c t g g a t c t g c a g c c a t g c a t c g a c c t a a t a g a g a g a c c t g c g a a c c c t	1680
c c t g g t g t a c t g g c c c t t t t g g a t g a a g a a t g c t g g t t c c c t a a a g c c a c a g a t a a a a c c	1740
t t t g t t g a a a a a c t g g t t c a a g a g c a a g g t t c c c a c t c c a a g t t t c a g a a a c c t c g a c a a	1800
t t a a a a g a c a a a g c t g a t t t t t g c a t t a t a c a t t a t g c a g g g a a g g t g g a c t a t a a g g c a	1860
g a t g a g t g g c t g a t g a a g a a t a t g g a c c c c c t g a a t g a c a a c g t g g c c a c c c t t t t g c a c	1920
c a g t c a t c a g a c a g a t t t g t g g c a g a g c t t t g g a a a g a t g t g g a c c g t a t c g t g g g t c t g	1980
g a t c a a g t c a c t g g t a t g a c t g a g a c a g c t t t t g g c t c c g c a t a t a a a a c c a a g a a g g g c	2040
a t g t t t c g t a c c g t t g g g c a a c t c t a c a a a g a a t c t c t c a c c a a g c t g a t g g c a a c t c t c	2100
c g a a a c a c c a a c c c t a a c t t t g t t c g t t g t a t c a t t c c a a a t c a c g a g a a g a g g g c t g g a	2160
a a a t t g g a t c c a c a c c t a g t c c t a g a t c a g c t t c g c t g t a a t g g t g t c c t g g a a g g g a t c	2220
c g a a t c t g t c g c c a g g g c t t c c c t a a c c g a a t a g t t t t c c a g g a a t t c a g a c a g a g a t a t	2280
g a g a t c c t a a c t c c a a a t g c t a t t c c t a a a g g t t t t a t g g a t g g t a a a c a g g c c t g t g a a	2340
c g a a t g a t c c g g g c t t t a g a a t t g g a c c c a a a c t t g t a c a g a a t t g g a c a g a g a a t a	2400
t t t t t c a g a g c t g g a g t t c t g g c a c a c t t a g a g g a a g a a a g a g a t t t a a a a a t c a c c g a t	2460
a t c a t t a t c t t c t t c c a g g c c g t t t g c a g a g g t t a c c t g g c c a g a a a g g c c t t t g c c a a g	2520
a a g c a g c a g c a a c t a a g t g c c t t a a a g g t c t t g c a g c g g a a c t g t g c c g c g t a c c t g a a a	2580
t t a c g g c a c t g g c a g t g g t g g c g a g t c t t c a c a a a g g t g a a g c c g c t t c t a c a a g t g a c t	2640
c g c c a g g a g g a a g a a c t t c a g g c c a a a g a t g a a g a g c t g t t g a a g g t g a a g g a g a a g c a g	2700
a c g a a g g t g g a a g g a g a g c t g g a g g a g a t g g a g c g g a a g c a c c a g c a g c t t t t a g a a g a g	2760
a a g a a t a t c c t t g c a g a a c a a c t a c a a g c a g a g a c t g a g c t c t t t g c t g a a g c a g a a g a g	2820
a t g a g g g c a a g a c t t g c t g c t a a a a a g c a g g a a t t a g a a g a g a t t c t a c a t g a c t t g g a g	2880
t c t a g g g t t g a a g a a g a a g a a a a g a a a c c a a t c c t c c a a a t g a a a a g a a a a a a a a t g	2940
c a a g c a c a t a t t c a g g a c c t g g a a g a a c a g c t a g a c g a g g a g g a a g g g g c t c g g c a a a a g	3000
c t g c a g c t g g a a a a g g t g a c a g c a g a g g c c a a g a t c a a g a g a t g g a a g a g g a g a t t c t g	3060
c t t c t c g a g g a c c a a a a t t c c a a g t t c a t c a a a g a a a a g a a a c t c a t g g a a g a t c g c a t t	3120
g c t g a g t g t t c c t c t c a g c t g g c t g a a g a g a a g a a g a a a a a g c g a a a a a c t t g g c c a a a a t c	3180
a g g a a t a a g c a a g a a g t g a t g a t c t c a g a t t t a g a a g a a c g c t t a a a g a a g g a a g a a a a g	3240
a c t c g t c a g g a a c t g g a a a a g g c c a a a a g a a a a c t c g a c g g g g a g a c g a c c g a c c t g c a g	3300
g a c c a g a t c g c a g a g c t g c a g g c g c a g a t t g a t g a g c t c a a g c t g c a g c t g g c c a a g a a g	3360
g a g g a g g a g c t g c a g g g c g c a c t g g c c a g a g g t g a t g a t g a a a c a c t c c a t a a g a a c a a t	3420
g c c c t t a a a g t t g t g c g a g a g c t a c a a g c c c a a a t t g c t g a a c t t c a g g a a g a c t t t g a a	3480

N3027PCT\_sequ. list . . txt

t ccgagaagg	ct t cacggaa	caaggccgaa	aagcagaaaa	gggact t gag	t gaggaact g	3540
gaagct ct ga	aaacagagct	ggaggacacg	ct ggacacca	cggcagccca	gcaggaact a	3600
cgt acaaaac	gt gaacaaga	agt ggcagag	ct gaagaaag	ct ct t gagga	ggaaact aag	3660
aacat gaag	ct caaat cca	ggacat gaga	caaagacacg	caacagccct	ggaggagct c	3720
t cagagcagc	t ggaacaggc	caagcgggt t c	aaagcaaat c	t agagaagaa	caagcagggc	3780
ct ggagacag	at aacaagga	gct ggcgt gt	gaggt gaagg	t cct gcagca	ggg caaggct	3840
gagt ct gagc	acaagaggaa	gaagct cgac	gcgcaggt cc	aggagct cca	t gccaaagg t c	3900
t ct gaaggcg	acaggct cag	ggg ggagct g	gcggagaaag	caagt aagct	gcagaat gag	3960
ct agat aat g	t ct ccaccct	t ct ggaagaa	gcagagaaga	agggt at t aa	at t t gct aag	4020
gat gcagct a	gt ct t gagt c	t caact acag	gat acacagg	agct t ct t ca	ggaggagaca	4080
cgccagaaac	t aaacct gag	cagt cggat c	cggcagct gg	aagaggagaa	gaacagt ct t	4140
caggagcagc	aggaggagga	ggaggaggcc	aggaagaacc	t ggagaagca	agt gct ggcc	4200
ct gcagt ccc	agt t ggct ga	t accaagaag	aaagt agat g	acgacct ggg	aacaat t gaa	4260
agt ct ggaag	aagccaagaa	gaagct t ct g	aaggacgcgg	aggccct gag	ccagcgcct g	4320
gaggagaagg	cact ggcgt a	t gacaaact g	gagaagacca	agaaccgcct	gcagcaggag	4380
ct ggacgacc	t cacgggt gga	cct ggaccac	cagcgccagg	t cgcct ccaa	ct t ggagaag	4440
aagcagaaga	agt t t gacca	gct gt t agca	gaagagaaga	gcat ct ct gc	t cgct at gcc	4500
gaagagcggg	accgggcca	agccgaggcc	agagagaaag	aaaccaaagc	cct gt cact g	4560
gcccgggccc	t cgaggaagc	cct ggaggcc	aaggaggagt	t t gagaggca	gaacaagcag	4620
ct ccgagcag	acat ggaaga	cct cat gagc	t ccaaagat g	at gt gggaaa	aaacgt t cac	4680
gaact t gaaa	aat ccaaagc	ggccct agag	cagcaggt gg	aggaaat gag	gacccagct g	4740
gaggagct gg	aagacgaact	ccaggccacg	gaagat gcca	agct t cgt ct	ggaggt caac	4800
at gcaggcca	t gaaggcgca	gt t cgagaga	gacct gcaaa	ccagggat ga	gcagaat gaa	4860
gagaagaagc	ggct gct gat	caaacaggt g	cgggagct cg	aggcggagct	ggaggat gag	4920
aggaaacagc	gggcgct t gc	t gt agct t ca	aagaaaaaga	t ggagat aga	cct gaaggac	4980
ct cgaagccc	aaat cgaggc	t gcgaacaaa	gct cgggat g	aggt gat t aa	gcagct ccgc	5040
aagct ccagg	ct cagat gaa	ggat t accaa	cgt gaat t ag	aagaagct cg	t gcat ccaga	5100
gat gagat t t	t t gct caat c	caaagagagt	gaaaagaaat	t gaagagt ct	ggaagcagaa	5160
at cct t caat	t gcaggagga	act t gcct ca	t ct gagcgag	cccgccgaca	cgccgagcag	5220
gagagagat g	agct ggcgga	cgagat cacc	aacagcgctt	ct ggcaagt c	cgcgct gct g	5280
gat gagaagc	ggcgt ct gga	agct cggat c	gcacagct gg	aggaggagct	ggaagaggag	5340
cagagcaaca	t ggagct gct	caacgaccgc	t t ccgcaaga	ccact ct aca	ggg ggacaca	5400
ct gaacgccg	agct agcagc	cgagcgagc	gccgccgaga	agagt gacaa	t gcacgccag	5460
caact ggagc	ggcagaacaa	ggagct gaag	gccaaagct gc	aggaact cga	gggt gct gt c	5520

N3027PCT\_sequ. list.txt

aagt ct aagt t caaggccac cat ct cagcc ct ggaggcca agat t gggca gct ggaggag	5580
cagct t gagc aggaagccaa ggaacgagca gccgccaaca aat t agt ccg t cgcact gag	5640
aagaagct ga aagaaat ct t cat gcaggt t gaggat gagc gt cgacacgc ggaccagt at	5700
aaagagcaga t ggagaaggc caacgct cgg at gaagcagc t t aaacgcca gct ggaggaa	5760
gcagaagaag aagcgacgcg t gccaacgca t ct cggcgt a aact ccagcg ggaact ggat	5820
gat gccaccg aggccaacga gggcct gagc cgcgaggt ca gcaccct gaa gaaccggct g	5880
aggcgggggt g gcccct cag ct t ct ct t cc agccgat ct g gccggcgcca gct gcacct t	5940
gaaggagct t ccct ggagct ct ccgacgat gacacagaaa gt aagaccag t gat gt caac	6000
gagacgcagc caccctcagt c agagt aaagt t gcaggaagc cagaggaggc aat acagt gg	6060
gacagt t agg aat gcaccgc gggcct cct g cagat t t cgg aaat t ggcaa gct acgggat	6120
t cct t cct ga aagat caact gt gt ct t aag gct ct ccagc ct at gcat ac t gt at cct gc	6180
t t cagact t a ggt acaat t g ct cccct t t t t at at at aga cacacacagg acacat at at	6240
t aaacagat t gt t t cat cat t gcat ct at t t t ccat at ag t cat caagag accat t t t at	6300
aaaacat ggt aagaccct t t t t aaaacaaa ct ccaggccc t t ggt t gcgg gt cgct gggt	6360
t at t ggggca gcgccgt ggt cgt cact cag t cgct ct gca t gct ct ct gt cat acagaca	6420
ggt aacct ag t t ct gt gt t c acgt ggcccc cgact cct ca gccacat caa gt ct cct aga	6480
ccact gt gga ct ct aaact g cact t gt ct c t ct cat t t cc t t caaat aat gat caat gct	6540
at t t cagt ga gcaaact gt g aaaggggct t t ggaaagagt aggaggggt g ggct ggat cg	6600
gaagcaacac ccat t t gggg t t accat gt c cat ccccca gggggggccct gccct cgag	6660
t cgat ggt gt cccgcat ct a ct cat gt gaa ct ggcct t gg cgaggggt gg t ct gt gcat a	6720
gaagggat ag t ggccacact gcagct gagg cccaggt gg cagccat gga t cat gt agac	6780
t t ccagat gg t ct cccgaac cgcct ggct c t gccggcgcc ct cct cacgt caggagcaag	6840
cagccgt gga cccct aagcc gagct ggt gg aaggccccct c cct gt cgcca gccggggccct	6900
cat gct gacc t t gcaaat t c agccgct gct t t gagcccaa aat gggaat a t t ggt t t t gt	6960
gt ccgaggct t gt t ccaagt t t gt caat ga ggt t t at gga gcct ccagaa cagat gccat	7020
ct t cct gaat gt t gacat gc cagt ggggt gt gact cct t ca t t t t t cct t c t cct t cct	7080
t t ggacagt g t t acagt gaa cact t agcat cct gt t t t t g gt t ggt agt t aagcaaact g	7140
acat t acgga aagt gcct t a gacact acag t act aagaca at gt t gaat a t at cat t cgc	7200
ct ct at aaca at t t aat gt a t t cagt t t t g act gt gct t c at at cat gt a cct ct ct agt	7260
caaagt ggt a t t acagacat t cagt gacaa t gaat cagt g t t aat t ct aa at cct t gat c	7320
ct ct gcaat g t gct t gaaaa cacaacct t t t ggggt t aaa agct t t aaca t ct at t agga	7380
agaat t t gt c ct gt ggggt t t ggaat ct t gg at t t t ccccc t t t at gaact gt act ggct g	7440
t t gaccacca gacacct gac cgcaaat at c t t t t ct t gt a t t cccat at t t ct agacaat	7500
gat t t t t gt a agacaat aaa t t t at t cat t at agat at t t gcgcct gct c t gt t t act t g	7560
aagaaaaaag caccctg gga gaat aaagag acct caat aa acaagaat aa t cat gt gaa	7619

<210> 72  
 <211> 1976  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1976)  
 <223> myosin, heavy chain 10, non-muscle (MYH10)

<400> 72

Met Ala Gln Arg Thr Gly Leu Glu Asp Pro Glu Arg Tyr Leu Phe Val  
 1 5 10 15

Asp Arg Ala Val Ile Tyr Asn Pro Ala Thr Gln Ala Asp Trp Thr Ala  
 20 25 30

Lys Lys Leu Val Trp Ile Pro Ser Glu Arg His Gly Phe Glu Ala Ala  
 35 40 45

Ser Ile Lys Glu Glu Arg Gly Asp Glu Val Met Val Glu Leu Ala Glu  
 50 55 60

Asn Gly Lys Lys Ala Met Val Asn Lys Asp Asp Ile Gln Lys Met Asn  
 65 70 75 80

Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu  
 85 90 95

Asn Glu Ala Ser Val Leu His Asn Leu Lys Asp Arg Tyr Tyr Ser Gly  
 100 105 110

Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Ile Asn Pro Tyr  
 115 120 125

Lys Asn Leu Pro Ile Tyr Ser Glu Asn Ile Ile Glu Met Tyr Arg Gly  
 130 135 140

Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ser Glu Ser  
 145 150 155 160

Ala Tyr Arg Cys Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys  
 165 170 175

Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile  
 180 185 190

Gln Tyr Leu Ala His Val Ala Ser Ser His Lys Gly Arg Lys Asp His  
 195 200 205

Asn Ile Pro Gly Glu Leu Glu Arg Gln Leu Leu Gln Ala Asn Pro Ile  
 210 215 220

N3027PCT\_sequ.list.txt

Leu 225 Glu Ser Phe Gly Asn 230 Ala Lys Thr Val Lys 235 Asn Asp Asn Ser Ser 240  
 Arg Phe Gly Lys Phe 245 Ile Arg Ile Asn Phe 250 Asp Val Thr Gly Tyr 255 Ile  
 Val Gly Ala Asn 260 Ile Glu Thr Tyr Leu 265 Leu Glu Lys Ser Arg 270 Ala Val  
 Arg Gln Ala 275 Lys Asp Glu Arg Thr 280 Phe His Ile Phe Tyr 285 Gln Leu Leu  
 Ser Gly 290 Ala Gly Glu His Leu 295 Lys Ser Asp Leu 300 Leu Glu Gly Phe  
 Asn 305 Asn Tyr Arg Phe Leu 310 Ser Asn Gly Tyr Ile 315 Pro Ile Pro Gly Gln 320  
 Gln Asp Lys Asp Asn 325 Phe Gln Glu Thr Met 330 Glu Ala Met His Ile 335 Met  
 Gly Phe Ser His 340 Glu Glu Ile Leu Ser 345 Met Leu Lys Val Val 350 Ser Ser  
 Val Leu Gln 355 Phe Gly Asn Ile Ser 360 Phe Lys Lys Glu Arg 365 Asn Thr Asp  
 Gln Ala 370 Ser Met Pro Glu Asn 375 Thr Val Ala Gln Lys 380 Leu Cys His Leu  
 Leu 385 Gly Met Asn Val Met 390 Glu Phe Thr Arg Ala 395 Ile Leu Thr Pro Arg 400  
 Ile Lys Val Gly Arg 405 Asp Tyr Val Gln Lys 410 Ala Gln Thr Lys Glu 415 Gln  
 Ala Asp Phe Ala 420 Val Glu Ala Leu Ala 425 Lys Ala Thr Tyr Glu 430 Arg Leu  
 Phe Arg Trp 435 Leu Val His Arg Ile 440 Asn Lys Ala Leu Asp 445 Arg Thr Lys  
 Arg Gln Gly Ala Ser Phe Ile 455 Gly Ile Leu Asp Ile 460 Ala Gly Phe Glu  
 Ile 465 Phe Glu Leu Asn Ser 470 Phe Glu Gln Leu Cys 475 Ile Asn Tyr Thr Asn 480  
 Glu Lys Leu Gln 485 Gln Leu Phe Asn His Thr 490 Met Phe Ile Leu Glu 495 Gln

N3027PCT\_sequ.list.txt

G u G u Tyr G n Arg G u G y I l e G u Trp Asn Phe I l e Asp Phe G y  
 500 505 510  
 Leu Asp Leu G n Pro Cys I l e Asp Leu I l e G u Arg Pro Al a Asn Pro  
 515 520 525  
 Pro G y Val Leu Al a Leu Leu Asp G u G u Cys Trp Phe Pro Lys Al a  
 530 535 540  
 Thr Asp Lys Thr Phe Val G u Lys Leu Val G n G u G n G y Ser Hi s  
 545 550 555 560  
 Ser Lys Phe G n Lys Pro Arg G n Leu Lys Asp Lys Al a Asp Phe Cys  
 565 570 575  
 I l e I l e Hi s Tyr Al a G y Lys Val Asp Tyr Lys Al a Asp G u Trp Leu  
 580 585 590  
 Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Al a Thr Leu Leu Hi s  
 595 600 605  
 G n Ser Ser Asp Arg Phe Val Al a G u Leu Trp Lys Asp Val Asp Arg  
 610 615 620  
 I l e Val G y Leu Asp G n Val Thr G y Met Thr G u Thr Al a Phe G y  
 625 630 635 640  
 Ser Al a Tyr Lys Thr Lys Lys G y Met Phe Arg Thr Val G y G n Leu  
 645 650 655  
 Tyr Lys G u Ser Leu Thr Lys Leu Met Al a Thr Leu Arg Asn Thr Asn  
 660 665 670  
 Pro Asn Phe Val Arg Cys I l e I l e Pro Asn Hi s G u Lys Arg Al a G y  
 675 680 685  
 Lys Leu Asp Pro Hi s Leu Val Leu Asp G n Leu Arg Cys Asn G y Val  
 690 695 700  
 Leu G u G y I l e Arg I l e Cys Arg G n G y Phe Pro Asn Arg I l e Val  
 705 710 715 720  
 Phe G n G u Phe Arg G n Arg Tyr G u I l e Leu Thr Pro Asn Al a I l e  
 725 730 735  
 Pro Lys G y Phe Met Asp G y Lys G n Al a Cys G u Arg Met I l e Arg  
 740 745 750  
 Al a Leu G u Leu Asp Pro Asn Leu Tyr Arg I l e G y G n Ser Lys I l e  
 755 760 765

N3027PCT\_sequ.list.txt

Phe Phe Arg Ala Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu  
770 775 780

Lys Ile Thr Asp Ile Ile Ile Phe Phe Gln Ala Val Cys Arg Gly Tyr  
785 790 795 800

Leu Ala Arg Lys Ala Phe Ala Lys Lys Gln Gln Gln Leu Ser Ala Leu  
805 810 815

Lys Val Leu Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg His Trp  
820 825 830

Gln Trp Trp Arg Val Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr  
835 840 845

Arg Gln Glu Glu Glu Leu Gln Ala Lys Asp Glu Glu Leu Leu Lys Val  
850 855 860

Lys Glu Lys Gln Thr Lys Val Glu Gly Glu Leu Glu Glu Met Glu Arg  
865 870 875 880

Lys His Gln Gln Leu Leu Glu Glu Lys Asn Ile Leu Ala Glu Gln Leu  
885 890 895

Gln Ala Glu Thr Glu Leu Phe Ala Glu Ala Glu Glu Met Arg Ala Arg  
900 905 910

Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Asp Leu Glu  
915 920 925

Ser Arg Val Glu Glu Glu Glu Glu Arg Asn Gln Ile Leu Gln Asn Glu  
930 935 940

Lys Lys Lys Met Gln Ala His Ile Gln Asp Leu Glu Glu Gln Leu Asp  
945 950 955 960

Glu Glu Glu Gly Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala  
965 970 975

Glu Ala Lys Ile Lys Lys Met Glu Glu Glu Ile Leu Leu Leu Glu Asp  
980 985 990

Gln Asn Ser Lys Phe Ile Lys Glu Lys Lys Leu Met Glu Asp Arg Ile  
995 1000 1005

Ala Glu Cys Ser Ser Gln Leu Ala Glu Glu Glu Glu Lys Ala Lys  
1010 1015 1020

Asn Leu Ala Lys Ile Arg Asn Lys Gln Glu Val Met Ile Ser Asp  
1025 1030 1035

Leu Glu Glu Arg Leu Lys Lys Glu Glu Lys Thr Arg Gln Glu Leu

Glu	Lys	Ala	Lys	Arg	Lys	Leu	Asp	Gly	Glu	Thr	Thr	Asp	Leu	Gln
Asp	Gln	Ile	Ala	Glu	Leu	Gln	Ala	Gln	Ile	Asp	Glu	Leu	Lys	Leu
Gln	Leu	Ala	Lys	Lys	Glu	Glu	Glu	Leu	Gln	Gly	Ala	Leu	Ala	Arg
Gly	Asp	Asp	Glu	Thr	Leu	His	Lys	Asn	Asn	Ala	Leu	Lys	Val	Val
Arg	Glu	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Gln	Glu	Asp	Phe	Glu
Ser	Glu	Lys	Ala	Ser	Arg	Asn	Lys	Ala	Glu	Lys	Gln	Lys	Arg	Asp
Leu	Ser	Glu	Glu	Leu	Glu	Ala	Leu	Lys	Thr	Glu	Leu	Glu	Asp	Thr
Leu	Asp	Thr	Thr	Ala	Ala	Gln	Gln	Glu	Leu	Arg	Thr	Lys	Arg	Glu
Gln	Glu	Val	Ala	Glu	Leu	Lys	Lys	Ala	Leu	Glu	Glu	Glu	Thr	Lys
Asn	His	Glu	Ala	Gln	Ile	Gln	Asp	Met	Arg	Gln	Arg	His	Ala	Thr
Ala	Leu	Glu	Glu	Leu	Ser	Glu	Gln	Leu	Glu	Gln	Ala	Lys	Arg	Phe
Lys	Ala	Asn	Leu	Glu	Lys	Asn	Lys	Gln	Gly	Leu	Glu	Thr	Asp	Asn
Lys	Glu	Leu	Ala	Cys	Glu	Val	Lys	Val	Leu	Gln	Gln	Val	Lys	Ala
Glu	Ser	Glu	His	Lys	Arg	Lys	Lys	Leu	Asp	Ala	Gln	Val	Gln	Glu
Leu	His	Ala	Lys	Val	Ser	Glu	Gly	Asp	Arg	Leu	Arg	Val	Glu	Leu
Ala	Glu	Lys	Ala	Ser	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Asn	Val	Ser
Thr	Leu	Leu	Glu	Glu	Ala	Glu	Lys	Lys	Gly	Ile	Lys	Phe	Ala	Lys

N3027PCT\_sequ.list.txt

Asp Ala Ala Ser Leu Gu Ser Gln Leu Gln Asp Thr Gln Gu Leu  
 1310 1315 1320  
 Leu Gln Gu Gu Thr Arg Gln Lys Leu Asn Leu Ser Ser Arg Ile  
 1325 1330 1335  
 Arg Gln Leu Gu Gu Gu Lys Asn Ser Leu Gln Gu Gln Gln Gu  
 1340 1345 1350  
 Gu Gu Gu Gu Ala Arg Lys Asn Leu Gu Lys Gln Val Leu Ala  
 1355 1360 1365  
 Leu Gln Ser Gln Leu Ala Asp Thr Lys Lys Lys Val Asp Asp Asp  
 1370 1375 1380  
 Leu Gly Thr Ile Gu Ser Leu Gu Gu Ala Lys Lys Lys Leu Leu  
 1385 1390 1395  
 Lys Asp Ala Gu Ala Leu Ser Gln Arg Leu Gu Gu Lys Ala Leu  
 1400 1405 1410  
 Ala Tyr Asp Lys Leu Gu Lys Thr Lys Asn Arg Leu Gln Gln Gu  
 1415 1420 1425  
 Leu Asp Asp Leu Thr Val Asp Leu Asp His Gln Arg Gln Val Ala  
 1430 1435 1440  
 Ser Asn Leu Gu Lys Lys Gln Lys Lys Phe Asp Gln Leu Leu Ala  
 1445 1450 1455  
 Gu Gu Lys Ser Ile Ser Ala Arg Tyr Ala Gu Gu Arg Asp Arg  
 1460 1465 1470  
 Ala Gu Ala Gu Ala Arg Gu Lys Gu Thr Lys Ala Leu Ser Leu  
 1475 1480 1485  
 Ala Arg Ala Leu Gu Gu Ala Leu Gu Ala Lys Gu Gu Phe Gu  
 1490 1495 1500  
 Arg Gln Asn Lys Gln Leu Arg Ala Asp Met Gu Asp Leu Met Ser  
 1505 1510 1515  
 Ser Lys Asp Asp Val Gly Lys Asn Val His Gu Leu Gu Lys Ser  
 1520 1525 1530  
 Lys Arg Ala Leu Gu Gln Gln Val Gu Gu Met Arg Thr Gln Leu  
 1535 1540 1545  
 Gu Gu Leu Gu Asp Gu Leu Gln Ala Thr Gu Asp Ala Lys Leu  
 1550 1555 1560

N3027PCT\_sequ.list.txt

Arg	Leu	Glu	Val	Asn	Met	Gln	Ala	Met	Lys	Ala	Gln	Phe	Glu	Arg
	1565					1570					1575			
Asp	Leu	Gln	Thr	Arg	Asp	Glu	Gln	Asn	Glu	Glu	Lys	Lys	Arg	Leu
	1580					1585					1590			
Leu	Ile	Lys	Gln	Val	Arg	Glu	Leu	Glu	Ala	Glu	Leu	Glu	Asp	Glu
	1595					1600					1605			
Arg	Lys	Gln	Arg	Ala	Leu	Ala	Val	Ala	Ser	Lys	Lys	Lys	Met	Glu
	1610					1615					1620			
Ile	Asp	Leu	Lys	Asp	Leu	Glu	Ala	Gln	Ile	Glu	Ala	Ala	Asn	Lys
	1625					1630					1635			
Ala	Arg	Asp	Glu	Val	Ile	Lys	Gln	Leu	Arg	Lys	Leu	Gln	Ala	Gln
	1640					1645					1650			
Met	Lys	Asp	Tyr	Gln	Arg	Glu	Leu	Glu	Glu	Ala	Arg	Ala	Ser	Arg
	1655					1660					1665			
Asp	Glu	Ile	Phe	Ala	Gln	Ser	Lys	Glu	Ser	Glu	Lys	Lys	Leu	Lys
	1670					1675					1680			
Ser	Leu	Glu	Ala	Glu	Ile	Leu	Gln	Leu	Gln	Glu	Glu	Leu	Ala	Ser
	1685					1690					1695			
Ser	Glu	Arg	Ala	Arg	Arg	His	Ala	Glu	Gln	Glu	Arg	Asp	Glu	Leu
	1700					1705					1710			
Ala	Asp	Glu	Ile	Thr	Asn	Ser	Ala	Ser	Gly	Lys	Ser	Ala	Leu	Leu
	1715					1720					1725			
Asp	Glu	Lys	Arg	Arg	Leu	Glu	Ala	Arg	Ile	Ala	Gln	Leu	Glu	Glu
	1730					1735					1740			
Glu	Leu	Glu	Glu	Glu	Gln	Ser	Asn	Met	Glu	Leu	Leu	Asn	Asp	Arg
	1745					1750					1755			
Phe	Arg	Lys	Thr	Thr	Leu	Gln	Val	Asp	Thr	Leu	Asn	Ala	Glu	Leu
	1760					1765					1770			
Ala	Ala	Glu	Arg	Ser	Ala	Ala	Gln	Lys	Ser	Asp	Asn	Ala	Arg	Gln
	1775					1780					1785			
Gln	Leu	Glu	Arg	Gln	Asn	Lys	Glu	Leu	Lys	Ala	Lys	Leu	Gln	Glu
	1790					1795					1800			
Leu	Glu	Gly	Ala	Val	Lys	Ser	Lys	Phe	Lys	Ala	Thr	Ile	Ser	Ala
	1805					1810					1815			

N3027PCT\_sequ.list.txt

Leu G u Ala Lys Ile Gly G n Leu G u G u G n Leu G u G n G u  
 1820 1825 1830

Ala Lys G u Arg Ala Ala Ala Asn Lys Leu Val Arg Arg Thr G u  
 1835 1840 1845

Lys Lys Leu Lys G u Ile Phe Met G n Val G u Asp G u Arg Arg  
 1850 1855 1860

His Ala Asp G n Tyr Lys G u G n Met G u Lys Ala Asn Ala Arg  
 1865 1870 1875

Met Lys G n Leu Lys Arg G n Leu G u G u Ala G u G u G u Ala  
 1880 1885 1890

Thr Arg Ala Asn Ala Ser Arg Arg Lys Leu G n Arg G u Leu Asp  
 1895 1900 1905

Asp Ala Thr G u Ala Asn G u Gly Leu Ser Arg G u Val Ser Thr  
 1910 1915 1920

Leu Lys Asn Arg Leu Arg Arg Gly Gly Pro Ile Ser Phe Ser Ser  
 1925 1930 1935

Ser Arg Ser Gly Arg Arg G n Leu His Leu G u Gly Ala Ser Leu  
 1940 1945 1950

G u Leu Ser Asp Asp Asp Thr G u Ser Lys Thr Ser Asp Val Asn  
 1955 1960 1965

G u Thr G n Pro Pro G n Ser G u  
 1970 1975

<210> 73  
 <211> 6882  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mi sc\_feat ure  
 <222> (1)..(6882)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant  
 SMI A

<400> 73  
 gggagatttg gacgctccgg cctgggaggt gcgtcagatc cgagctcgcc atccagtttc 60  
 ctctccacta gtccccccag ttggagatct gggaccaaca aggcaccatg gcgcagaagg 120  
 gccaaactcag tgacgatgag aagttcctct ttgtggacaa aaacttcatc aacagcccag 180  
 tggcccaggc tgactgggcc gccaaagagac tcgtctgggt cccctcggag aagcagggct 240  
 tcgaggcagc cagcat taag gaggagaagg gggatgaggt ggttgtggag ctggtggaga 300  
 atggcaagaa ggtcacggtt gggaaagatg acatccagaa gatgaacca cccaagttct 360

## N3027PCT\_sequ. list.txt

ccaaggt gga ggacat ggcg gagct gacgt gcct caacga agcct ccgt g ct acacaacc	420
t gagggagcg gt act t ct ca gggct aat at at acgt act c t ggcct ct t c t gcgt ggt gg	480
t caaccct a t aaacacct g cccat ct act cggagaagat cgt cgacat g t acaagggca	540
agaagaggca cgagat gccg cct cacat ct acgccat cgc agacacggcc t accggagca	600
t gct t caaga t cgggaggac cagt ccat t c t at gcacagg cgagt ct gga gccgggaaaa	660
ccgaaaacac caagaaggt c at t cagt acc t ggccgt ggt ggcct cct cc cacaagggca	720
agaaagacac aagt at cacg ggagagct gg aaaagcagct t ct acaagca aaccgat t c	780
t ggaggct t t cggcaacgcc aaaacagt ga agaacgacaa ct cct cacga t t cggcaaat	840
t cat ccgcat caact t cgac gt cacgggt t acat cgt ggg agccaacat t gagacct at c	900
t gct agaaaa at cacgggca at t cgccaag ccagagacga gaggacat t c cacat ct t t t	960
act acat gat t gct ggagcc aaggagaaga t gagaagt ga ct t gct t t t g gagggct t ca	1020
acaact acac ct t cct ct cc aat ggct t t g t gcccat ccc agcagcccag gat gat gaga	1080
t gt t ccagga aaccgt ggag gccat ggcaa t cat ggg t t cagcgaggag gagcagct at	1140
ccat at t gaa ggt ggt at ca t cgg t cct gc agct t ggaaa t at cgt ct t c aagaaggaaa	1200
gaaacacaga ccaggcgt cc at gccagat a acacagct gc t cagaaagt t t gccacct ca	1260
t gggaat t aa t gt gacagat t t caccagat ccat cct cac t cct cgt at c aaggt t gggc	1320
gagat gt ggt acagaaagct cagacaaaag aacaggct ga ct t t gct gt a gaggct t t gg	1380
ccaaggcaac at at gagcgc ct t t t ccgct ggat act cac ccgcgt gaac aaagccct gg	1440
acaagaccca t cggcaagg gct t cct t cc t ggggat cct ggat at agct ggat t t gaga	1500
t ct t t gaggt gaact cct t c gagcagct gt gcat caact a caccaacgag aagct gcagc	1560
agct ct t caa ccacaccat g t t cat cct gg agcaggagga gt accagcgc gagggcat cg	1620
agt ggaact t cat cgact t t gggct ggacc t acagccct g cat cgagct c at cgagcgac	1680
cgaacaaccc t ccaggt gt g ct ggccct gc t ggacgagga at gct ggt t c cccaaagcca	1740
cggacaagt c t t t cgt ggag aagct gt gca cggagcaggg cagccacccc aagt t ccaga	1800
agcccaagca gct caaggac aagact gagt t ct ccat cat ccat t at gct gggaaggt gg	1860
act at aat gc gagt gcct gg ct gaccaaga at at ggaccc gct gaat gac aacgt gact t	1920
ccct gct caa t gcct cct cc gacaagt t t g t ggccgacct gt ggaaggac gt ggaccgca	1980
t cgt gggcct ggaccagat g gccaagat ga cggagagct c gct gcccagc gcct ccaaga	2040
ccaagaaggg cat gt t ccgc acagt ggggc agct gt acaa ggagcagct g ggcaagct ga	2100
t gaccacgct acgcaacacc acgcccact t cgt gcgct g cat cat cccc aaccacgaga	2160
agaggt ccgg caagct ggat gcgt t cct gg t gct ggagca gct gcggt gc aat ggggt gc	2220
t ggaaggcat t cgcat ct gc cggcagggt t ccccaaccg gat cgt ct t c caggagt t cc	2280
gccaacgct a cgagat cct g gcggcgaat g ccat ccccaa aggct t cat g gacgggaagc	2340
aggcct gcat t ct cat gat c aaagccct gg aact t gaccc caact t at ac aggat agggc	2400
agagcaaaaat ct t ct t ccga act ggct cc t ggccacct agaggaggag cgagat t t ga	2460

N3027PCT\_sequ. list . . txt

agat caccga t gt cat cat g gcct t ccagg cgat gt gt cg t ggct act t g gccagaaagg	2520
ct t t t gccaa gaggcagcag cagct gaccg ccat gaaggt gat t cagagg aact gcgccc	2580
cct acct caa gct gcggaac t ggcagt ggt ggaggct t t t caccaaagt g aagccact gc	2640
t gcaggt gac acggcaggag gaggagat gc aggccaagga ggat gaact g cagaagacca	2700
aggagcggca gcagaaggca gagaat gaggc t t aaggagct ggaacagaag cact cgcagc	2760
t gaccgagga gaagaacct g ct acaggaac agct gcaggc agagacagag ct gt at gcag	2820
aggct gagga gat gcgggt g cggct ggagg ccaagaagca ggagct ggag gagat act gc	2880
at gagat gga ggcccgcct g gaggaggagg aagacagggg ccagcagct a caggct gaaa	2940
ggaagaagat ggcccagcag at gct ggacc t t gaagaaca gct ggaggag gaggaagct g	3000
ccaggcagaa gct gcaact t gagaaggt ca cggct gaggc caagat caag aaact ggagg	3060
at gagat cct ggt cat ggat gat cagaaca at aaact at c aaaagaacga aaact cct t g	3120
aggagaggat t agt gact t a acgacaaat c t t gcagaaga ggaagaaaag gccagaat c	3180
t t accaagct gaaaaacaag cat gaat ct a t gat t t caga act ggaagt g cggct aaaga	3240
aggaagagaa gagccgacag gagct ggaga agct gaaacg gaagct ggag ggt gat gcca	3300
gcgact t cca cgagcagat c gct gacct cc aggcgagat cgcagagct c aagat gcagc	3360
t ggccaagaa ggaggaggag ct gcaggcgg ccct ggccag gct t gacgat gaaat cgct c	3420
agaagaacaa t gccct gaag aagat ccggg agct ggaggg ccacat ct ca gacct ccagg	3480
aggacct gga ct cagagcgg gccgccagga acaaggct ga aaagcagaag cgagacct cg	3540
gcgaggagct ggaggccct a aagacagagc t ggaagacac act ggacagc acagccact c	3600
agcaggagct cagggccaag agggagcagg aggt gacggt gct gaagaag gccct ggat g	3660
aagagacgcg gt cccat gag gct caggt cc aggagat gag gcagaaacac gcacaggcgg	3720
t ggaggagct cacagagcag ct t gaggagt t caagagggc caaggcgaac ct agacaaga	3780
at aagcagac gct ggagaaa gagaacgcag acct ggccgg ggagct gcgg gt cct gggcc	3840
aggccaagca ggaggt ggaa cat aagaaga agaagct gga ggcgaggt g caggagct gc	3900
agt ccaagt g cagcgat ggg gagcggggccc gggcgagct caat gacaaa gt ccacaagc	3960
t gcagaat ga agt t gagagc gt cacaggga t gct t aacga ggccgagggg aaggccat t a	4020
agct ggccaa ggacgt ggcg t ccct cagt t cccagct cca ggacacccag gagct gct t c	4080
aagaagaaac ccggcagaag ct caacgt gt ct acgaagct gcgccagct g gaggaggagc	4140
ggaacagcct gcaagaccag ct ggacgagg agat ggaggc caagcagaac ct ggagcgcc	4200
acat ct ccac t ct caacat c cagct ct ccg act cgaagaa gaagct gcag gact t t gcc	4260
gcaccgt gga agct ct ggaa gaggggaaga agaggt t cca gaaggagat c gagaacct ca	4320
cccagcagt a cgaggagaag gcggccgct t at gat aaact ggaaaagacc aagaacaggc	4380
t t cagcagga gct ggacgac ct ggt t gt t g at t t ggacaa ccagcggcaa ct cgt gt cca	4440
acct ggaaaa gaagcagagg aaat t t gat c agt t gt t agc cgaggagaaa aacat ct ct t	4500

N3027PCT\_sequ. list .txt

ccaaat acgc	ggat gagagg	gacagagct g	aggcagaagc	cagggagaag	gaaaccaagg	4560
ccct gt ccct	ggct cgggcc	ct t gaagagg	cct t ggaagc	caaagaggaa	ct cgagcgga	4620
ccaacaaaat	gct caaagcc	gaaat ggaag	acct ggt cag	ct ccaaggat	gacgt gggca	4680
agaacgt cca	t gagct ggag	aagt ccaagc	gggccct gga	gaccagat g	gaggagat ga	4740
agacgcagct	ggaagagct g	gaggacgagc	t gcaagccac	ggaggacgcc	aaact gcggc	4800
t ggaagt caa	cat gcaggcg	ct caagggcc	agt t cgaaag	ggat ct ccaa	gcccgggacg	4860
agcagaat ga	ggagaagagg	aggcaact gc	agagacagct	t cacgagt at	gagacggaac	4920
t ggaagacga	gcgaaagcaa	cgt gccct gg	cagct gcagc	aaagaagaag	ct ggaagggg	4980
acct gaaaga	cct ggagct t	caggccgact	ct gccat caa	ggggagggag	gaagccat ca	5040
agcagct acg	caaact gcag	gct cagat ga	aggact t t ca	aagagagct g	gaagat gccc	5100
gt gcct ccag	agat gagat c	t t t gccacag	ccaaagagaa	t gagaagaaa	gccaagagct	5160
t ggaagcaga	cct cat gcag	ct acaagagg	acct cgccgc	cgct gagagg	gct cgcaaac	5220
aagcggacct	cgagaaggag	gaact ggcag	aggagct ggc	cagt agcct g	t cggaagga	5280
acgcact cca	ggacgagaag	cgccgcct gg	agggccggat	cgcccagct g	gaggaggagc	5340
t ggaggagga	gcagggcaac	at ggaggcca	t gagcgaccg	ggt ccgcaa	gccacacagc	5400
aggccgagca	gct cagcaac	gagct ggcca	cagagcgagc	cacggcccag	aagaat gaga	5460
gt gcccggca	gcagct cgag	cggcagaaca	aggagct ccg	gagcaagct c	cacgagat gg	5520
agggggccgt	caagt ccaag	t t caagt cca	ccat cgcggc	gct ggaggcc	aagat t gcac	5580
agct ggagga	gcaggt cgag	caggaggcca	gagagaaaca	ggcgccacc	aagt cgct ga	5640
agcagaaaaga	caagaagct g	aaggaaat ct	t gct gcaggt	ggaggacgag	cgcaagat gg	5700
ccgagcagt a	caaggagcag	gcagagaaag	gcaat gccag	ggt caagcag	ct caagaggc	5760
agct ggagga	ggcagaggag	gagt cccagc	gcat caacgc	caaccgcagg	aagct gcagc	5820
gggagct gga	t gaggccacg	gagagcaacg	aggccat ggg	ccgcgaggt g	aacgcact ca	5880
agagcaagct	caggcgagga	aacgagacct	ct t t cgt t cc	t t ct agaagg	t ct ggaggac	5940
gt agagt t at	t gaaaat gca	gat ggt t ct g	aggaggaaac	ggacact cga	gacgcagact	6000
t caat ggaac	caaggccagt	gaat aagcaa	ct t t ct acag	t t t t gcacca	cggcaagaaa	6060
acaaaaaac	aaaacaaaca	aacaaaaaaa	acccaacaac	aaccagaac	aaagcaaaac	6120
ccagcagact	gt act t agca	t t gt ct aaat	ccat t ct caa	at t ccaaat a	t cacagacac	6180
ccct cacaca	aggaat at aa	aaaccaccac	cct ccagcct	gggcaacgt a	gt aaaacct c	6240
at ct at acaa	gaat t t aaaa	at aagct ggg	cgt ggt ggt a	cacacct gt g	gt cccagct a	6300
ct agggaggc	t gagccagga	agaacgct cc	agcccaggac	t t cgaggct g	caat gagct a	6360
t aat t gcat c	at t gcact cc	agcct gggca	acagagaccc	t gt ct caacc	accaccacca	6420
ccaccacccc	t act acccct	gt at t caagg	t aaaaat t ga	agt t t gt at g	at gt aagaga	6480
t gagaaaaac	ccaacaggaa	acacagacac	at cct ccagt	t ct at caat g	gat t gt gcag	6540
acact gagt t	t t t agaaaaa	cat at ccacg	gt aaccggt c	cct ggcaat t	ct gt t t acat	6600

N3027PCT\_sequ.list.txt

```

gaaatgggga gaaagtcacc gaaatgggtg ccgccggccc ccactcccaa ttcattccct 6660
aacctgcaaa cctttccaac tttcacgtc aggcctttga gaattctttc cccctctcct 6720
ggtttccaca cctcagacac gcacagttca ccaagtgcct tctgtagtca catgaattga 6780
aaaggagacg ctgctccac ggaggggagc aggaatgctg cactgtttac accctgactg 6840
tgcttaaaaa cactttcact aataaatggt tataaatcac aa 6882

```

```

<210> 74
<211> 1972
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> MSC_FEATURE
<222> (1)..(1972)
<223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant
      SMIA

```

<400> 74

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
1      5      10
Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
20     25     30
Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
35     40     45
Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
50     55     60
Asn Gly Lys Lys Val Thr Val Gly Lys Asp Asp Ile Gln Lys Met Asn
65     70     75     80
Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu
85     90     95
Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg Tyr Phe Ser Gly
100    105    110
Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Val Asn Pro Tyr
115    120    125
Lys His Leu Pro Ile Tyr Ser Glu Lys Ile Val Asp Met Tyr Lys Gly
130    135    140
Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ala Asp Thr
145    150    155    160
Ala Tyr Arg Ser Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys
165    170    175

```

N3027PCT\_sequ.list.txt

Thr Gly Gu Ser Gly Ala Gly Lys Thr Gu Asn Thr Lys Lys Val Ile  
180 185 190

Gln Tyr Leu Ala Val Val Ala Ser Ser His Lys Gly Lys Lys Asp Thr  
195 200 205

Ser Ile Thr Gly Gu Leu Gu Lys Gln Leu Leu Gln Ala Asn Pro Ile  
210 215 220

Leu Gu Ala Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser  
225 230 235 240

Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile  
245 250 255

Val Gly Ala Asn Ile Gu Thr Tyr Leu Leu Gu Lys Ser Arg Ala Ile  
260 265 270

Arg Gln Ala Arg Asp Gu Arg Thr Phe His Ile Phe Tyr Tyr Met Ile  
275 280 285

Ala Gly Ala Lys Gu Lys Met Arg Ser Asp Leu Leu Leu Gu Gly Phe  
290 295 300

Asn Asn Tyr Thr Phe Leu Ser Asn Gly Phe Val Pro Ile Pro Ala Ala  
305 310 315 320

Gln Asp Asp Gu Met Phe Gln Gu Thr Val Gu Ala Met Ala Ile Met  
325 330 335

Gly Phe Ser Gu Gu Gu Gln Leu Ser Ile Leu Lys Val Val Ser Ser  
340 345 350

Val Leu Gln Leu Gly Asn Ile Val Phe Lys Lys Gu Arg Asn Thr Asp  
355 360 365

Gln Ala Ser Met Pro Asp Asn Thr Ala Ala Gln Lys Val Cys His Leu  
370 375 380

Met Gly Ile Asn Val Thr Asp Phe Thr Arg Ser Ile Leu Thr Pro Arg  
385 390 395 400

Ile Lys Val Gly Arg Asp Val Val Gln Lys Ala Gln Thr Lys Gu Gln  
405 410 415

Ala Asp Phe Ala Val Gu Ala Leu Ala Lys Ala Thr Tyr Gu Arg Leu  
420 425 430

Phe Arg Trp Ile Leu Thr Arg Val Asn Lys Ala Leu Asp Lys Thr His  
435 440 445

Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala Gly Phe Glu  
 450 455 460  
 Ile Phe Glu Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn  
 465 470 475 480  
 Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln  
 485 490 495  
 Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly  
 500 505 510  
 Leu Asp Leu Gln Pro Cys Ile Glu Leu Ile Glu Arg Pro Asn Asn Pro  
 515 520 525  
 Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala  
 530 535 540  
 Thr Asp Lys Ser Phe Val Glu Lys Leu Cys Thr Glu Gln Gly Ser His  
 545 550 555 560  
 Pro Lys Phe Gln Lys Pro Lys Gln Leu Lys Asp Lys Thr Glu Phe Ser  
 565 570 575  
 Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Asn Ala Ser Ala Trp Leu  
 580 585 590  
 Thr Lys Asn Met Asp Pro Leu Asn Asp Asn Val Thr Ser Leu Leu Asn  
 595 600 605  
 Ala Ser Ser Asp Lys Phe Val Ala Asp Leu Trp Lys Asp Val Asp Arg  
 610 615 620  
 Ile Val Gly Leu Asp Gln Met Ala Lys Met Thr Glu Ser Ser Leu Pro  
 625 630 635 640  
 Ser Ala Ser Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu  
 645 650 655  
 Tyr Lys Glu Gln Leu Gly Lys Leu Met Thr Thr Leu Arg Asn Thr Thr  
 660 665 670  
 Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ser Gly  
 675 680 685  
 Lys Leu Asp Ala Phe Leu Val Leu Glu Gln Leu Arg Cys Asn Gly Val  
 690 695 700  
 Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile Val  
 705 710 715 720  
 Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Ala Ala Asn Ala Ile

725

730

735

Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Ile Leu Met Ile Lys  
 740 745 750  
 Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Ile Gly Gln Ser Lys Ile  
 755 760 765  
 Phe Phe Arg Thr Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu  
 770 775 780  
 Lys Ile Thr Asp Val Ile Met Ala Phe Gln Ala Met Cys Arg Gly Tyr  
 785 790 795 800  
 Leu Ala Arg Lys Ala Phe Ala Lys Arg Gln Gln Gln Leu Thr Ala Met  
 805 810 815  
 Lys Val Ile Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg Asn Trp  
 820 825 830  
 Gln Trp Trp Arg Leu Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr  
 835 840 845  
 Arg Gln Glu Glu Glu Met Gln Ala Lys Glu Asp Glu Leu Gln Lys Thr  
 850 855 860  
 Lys Glu Arg Gln Gln Lys Ala Glu Asn Glu Leu Lys Glu Leu Glu Gln  
 865 870 875 880  
 Lys His Ser Gln Leu Thr Glu Glu Lys Asn Leu Leu Gln Glu Gln Leu  
 885 890 895  
 Gln Ala Glu Thr Glu Leu Tyr Ala Glu Ala Glu Glu Met Arg Val Arg  
 900 905 910  
 Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Glu Met Glu  
 915 920 925  
 Ala Arg Leu Glu Glu Glu Glu Asp Arg Gly Gln Gln Leu Gln Ala Glu  
 930 935 940  
 Arg Lys Lys Met Ala Gln Gln Met Leu Asp Leu Glu Glu Gln Leu Glu  
 945 950 955 960  
 Glu Glu Glu Ala Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala  
 965 970 975  
 Glu Ala Lys Ile Lys Lys Leu Glu Asp Glu Ile Leu Val Met Asp Asp  
 980 985 990  
 Gln Asn Asn Lys Leu Ser Lys Glu Arg Lys Leu Leu Glu Glu Arg Ile  
 995 1000 1005

N3027PCT\_sequ.list.txt

Ser	Asp	Leu	Thr	Thr	Asn	Leu	Ala	Glu	Glu	Glu	Glu	Lys	Ala	Lys
	1010					1015					1020			
Asn	Leu	Thr	Lys	Leu	Lys	Asn	Lys	His	Glu	Ser	Met	Ile	Ser	Glu
	1025					1030					1035			
Leu	Glu	Val	Arg	Leu	Lys	Lys	Glu	Glu	Lys	Ser	Arg	Gln	Glu	Leu
	1040					1045					1050			
Glu	Lys	Leu	Lys	Arg	Lys	Leu	Glu	Gly	Asp	Ala	Ser	Asp	Phe	His
	1055					1060					1065			
Glu	Gln	Ile	Ala	Asp	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Lys	Met
	1070					1075					1080			
Gln	Leu	Ala	Lys	Lys	Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	Ala	Arg
	1085					1090					1095			
Leu	Asp	Asp	Glu	Ile	Ala	Gln	Lys	Asn	Asn	Ala	Leu	Lys	Lys	Ile
	1100					1105					1110			
Arg	Glu	Leu	Glu	Gly	His	Ile	Ser	Asp	Leu	Gln	Glu	Asp	Leu	Asp
	1115					1120					1125			
Ser	Glu	Arg	Ala	Ala	Arg	Asn	Lys	Ala	Glu	Lys	Gln	Lys	Arg	Asp
	1130					1135					1140			
Leu	Gly	Glu	Glu	Leu	Glu	Ala	Leu	Lys	Thr	Glu	Leu	Glu	Asp	Thr
	1145					1150					1155			
Leu	Asp	Ser	Thr	Ala	Thr	Gln	Gln	Glu	Leu	Arg	Ala	Lys	Arg	Glu
	1160					1165					1170			
Gln	Glu	Val	Thr	Val	Leu	Lys	Lys	Ala	Leu	Asp	Glu	Glu	Thr	Arg
	1175					1180					1185			
Ser	His	Glu	Ala	Gln	Val	Gln	Glu	Met	Arg	Gln	Lys	His	Ala	Gln
	1190					1195					1200			
Ala	Val	Glu	Glu	Leu	Thr	Glu	Gln	Leu	Glu	Gln	Phe	Lys	Arg	Ala
	1205					1210					1215			
Lys	Ala	Asn	Leu	Asp	Lys	Asn	Lys	Gln	Thr	Leu	Glu	Lys	Glu	Asn
	1220					1225					1230			
Ala	Asp	Leu	Ala	Gly	Glu	Leu	Arg	Val	Leu	Gly	Gln	Ala	Lys	Gln
	1235					1240					1245			
Glu	Val	Glu	His	Lys	Lys	Lys	Lys	Leu	Glu	Ala	Gln	Val	Gln	Glu
	1250					1255					1260			

N3027PCT\_sequ.list.txt

Leu Gln Ser Lys Cys Ser Asp Gly Glu Arg Ala Arg Ala Glu Leu  
 1265 1270 1275  
 Asn Asp Lys Val His Lys Leu Gln Asn Glu Val Glu Ser Val Thr  
 1280 1285 1290  
 Gly Met Leu Asn Glu Ala Glu Gly Lys Ala Ile Lys Leu Ala Lys  
 1295 1300 1305  
 Asp Val Ala Ser Leu Ser Ser Gln Leu Gln Asp Thr Gln Glu Leu  
 1310 1315 1320  
 Leu Gln Glu Glu Thr Arg Gln Lys Leu Asn Val Ser Thr Lys Leu  
 1325 1330 1335  
 Arg Gln Leu Glu Glu Glu Arg Asn Ser Leu Gln Asp Gln Leu Asp  
 1340 1345 1350  
 Glu Glu Met Glu Ala Lys Gln Asn Leu Glu Arg His Ile Ser Thr  
 1355 1360 1365  
 Leu Asn Ile Gln Leu Ser Asp Ser Lys Lys Lys Leu Gln Asp Phe  
 1370 1375 1380  
 Ala Ser Thr Val Glu Ala Leu Glu Glu Gly Lys Lys Arg Phe Gln  
 1385 1390 1395  
 Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr Glu Glu Lys Ala Ala  
 1400 1405 1410  
 Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg Leu Gln Gln Glu  
 1415 1420 1425  
 Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg Gln Leu Val  
 1430 1435 1440  
 Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu Leu Ala  
 1445 1450 1455  
 Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp Arg  
 1460 1465 1470  
 Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu  
 1475 1480 1485  
 Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu  
 1490 1495 1500  
 Arg Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser  
 1505 1510 1515

Ser Lys Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser  
 1520 1525 1530  
 Lys Arg Ala Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu  
 1535 1540 1545  
 Glu Glu Leu Glu Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu  
 1550 1555 1560  
 Arg Leu Glu Val Asn Met Gln Ala Leu Lys Gly Gln Phe Glu Arg  
 1565 1570 1575  
 Asp Leu Gln Ala Arg Asp Glu Gln Asn Glu Glu Lys Arg Arg Gln  
 1580 1585 1590  
 Leu Gln Arg Gln Leu His Glu Tyr Glu Thr Glu Leu Glu Asp Glu  
 1595 1600 1605  
 Arg Lys Gln Arg Ala Leu Ala Ala Ala Ala Lys Lys Lys Leu Glu  
 1610 1615 1620  
 Gly Asp Leu Lys Asp Leu Glu Leu Gln Ala Asp Ser Ala Ile Lys  
 1625 1630 1635  
 Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg Lys Leu Gln Ala Gln  
 1640 1645 1650  
 Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala Arg Ala Ser Arg  
 1655 1660 1665  
 Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys Lys Ala Lys  
 1670 1675 1680  
 Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu Ala Ala  
 1685 1690 1695  
 Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu Leu  
 1700 1705 1710  
 Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln  
 1715 1720 1725  
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu  
 1730 1735 1740  
 Glu Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg  
 1745 1750 1755  
 Val Arg Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu  
 1760 1765 1770  
 Ala Thr Glu Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln  
 1775

1775

1780

1785

G n Leu G u Arg G n Asn Lys G u Leu Arg Ser Lys Leu H i s G u  
 1790 1795 1800  
 M e t G u G y A l a V a l L y s S e r L y s P h e L y s S e r T h r I l e A l a A l a  
 1805 1810 1815  
 L e u G u A l a L y s I l e A l a G n L e u G u G u G n V a l G u G n G u  
 1820 1825 1830  
 A l a Arg G u L y s G n A l a A l a T h r L y s S e r L e u L y s G n L y s A s p  
 1835 1840 1845  
 L y s L y s L e u L y s G u I l e L e u L e u G n V a l G u A s p G u Arg L y s  
 1850 1855 1860  
 M e t A l a G u G n T y r L y s G u G n A l a G u L y s G y A s n A l a Arg  
 1865 1870 1875  
 V a l L y s G n L e u L y s Arg G n L e u G u G u A l a G u G u G u S e r  
 1880 1885 1890  
 G n Arg I l e A s n A l a A s n Arg Arg L y s L e u G n Arg G u L e u A s p  
 1895 1900 1905  
 G u A l a T h r G u S e r A s n G u A l a M e t G y Arg G u V a l A s n A l a  
 1910 1915 1920  
 L e u L y s S e r L y s L e u Arg Arg G y A s n G u T h r S e r P h e V a l P r o  
 1925 1930 1935  
 S e r Arg Arg S e r G y G y Arg Arg V a l I l e G u A s n A l a A s p G y  
 1940 1945 1950  
 S e r G u G u G u T h r A s p T h r Arg A s p A l a A s p P h e A s n G y T h r  
 1955 1960 1965  
 L y s A l a S e r G u  
 1970

<210> 75  
 <211> 6903  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> (1)..(6903)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant  
 SM1B

<400> 75  
 gggagatttg gacgctccgg cctgggaggt gcgtcagatc cgagctcgcc atccagtttc

60

N3027PCT\_sequ. list . . txt

ct ct ccaact a gt cccccccag t t ggagat ct gggaccaaca aggcaccat g gcgcagaagg	120
gccaaact cag t gacgat gag aagt t cct ct t t gt ggacaa aaact t cat c aacagcccag	180
t ggcccaggc t gact gggcc gccaaagagac t cgt ct gggg cccct cggag aagcagggct	240
t cgaggcagc cagcat t aag gaggagaagg gggat gaggt ggt t gt ggag ct ggt ggaga	300
at ggcaagaa ggt cacgggt t gggaaagat g acat ccagaa gat gaacca cccaagt t ct	360
ccaaggt gga ggacat ggcg gagct gacgt gcct caacga agcct ccgt g ct acacaacc	420
t gagggagcg gt act t ct ca gggct aat at at acgt act c t ggcct ct t c t gcgt ggt gg	480
t caaccct a t aaacacct g cccat ct act cggagaagat cgt cgacat g t acaagggca	540
agaagaggca cgagat gccg cct cacat ct acgccat cgc agacacggcc t accggagca	600
t gct t caaga t cgggaggac cagt ccat t c t at gcacagg cgagt ct gga gccgggaaaa	660
ccgaaaacac caagaaggt c at t cagt acc t ggccgt ggt ggcct cct cc cacaagggca	720
agaaagacac aagt at cacg caaggcccat ct t t t gcct a cggagagct g gaaaagcagc	780
t t ct acaagc aaacccgat t ct ggaggct t t cggcaacgc caaaacagt g aagaacgaca	840
act cct cacg at t cggcaaa t t cat ccgca t caact t cga cgt cacgggt t acat cgt gg	900
gagccaacat t gagacct at ct gct agaaa aat cacgggc aat t cgccaa gccagagacg	960
agaggacat t ccacat ct t t t act acat ga t t gct ggagc caaggagaag at gagaagt g	1020
act t gct t t t ggagggct t c aacaact aca cct t cct ct c caat ggct t t gt gcccat cc	1080
cagcagccca ggat gat gag at gt t ccagg aaaccgt gga ggccat ggca at cat ggggt t	1140
t cagcgagga ggagcagct a t ccat at t ga aggt ggt at c at cgggt cct g cagct t ggaa	1200
at at cgt ct t caagaaggaa agaaacacag accaggcgt c cat gccagat aacacagct g	1260
ct cagaaaagt t t gccacct c at gggaat t a at gt gacaga t t t caccaga t ccat cct ca	1320
ct cct cgt at caaggt t ggg cgagat gt gg t acagaaagc t cagacaaaa gaacaggct g	1380
act t t gct gt agaggct t t g gccaaggcaa cat at gagcg cct t t t ccgc t ggat act ca	1440
cccgcgt gaa caaagccct g gacaagacc at cggcaagg ggct t cct t c ct ggggat cc	1500
t ggat at agc t ggat t t gag at ct t t gagg t gaact cct t cgagcagct g t gcat caact	1560
acaccaacga gaagct gcag cagct ct t ca accacacat gt t cat cct g gagcaggagg	1620
agt accagcg cgagggcac c gagt ggaact t cat cgact t t gggct ggac ct acagccct	1680
gcat cgagct cat cgagcga ccgaacaacc ct ccagggt gt gct ggccct g ct ggacgagg	1740
aat gct ggt t ccccaaagcc acggacaagt ct t t cgt gga gaagct gt gc acggagcagg	1800
gcagccaccc caagt t ccag aagcccaagc agct caagga caagact gag t t ct ccat ca	1860
t ccat t at gc t gggaaggt g gact at aat g cgagt gcct g gct gaccaag aat at ggacc	1920
cgct gaat ga caacgt gact t ccct gct ca at gcct cct c cgacaagt t t gt ggccgacc	1980
t gt ggaagga cgt ggaccgc at cgt gggcc t ggaccagat ggccaagat g acggagagct	2040
cgct gccag cgcct ccaag accaagaagg gcat gt t ccg cacagt gggg cagct gt aca	2100

N3027PCT\_sequ. list .txt

aggagcagct	gggcaagct g	at gaccacgc	t acgcaacac	cacgcccac	t t cgt gcgct	2160
gcat cat ccc	caaccacgag	aagaggt ccg	gcaagct gga	t gcgt t cct g	gt gct ggagc	2220
agct gcggt g	caat ggggt g	ct ggaaggca	t t cgcgt ct g	ccggcagggc	t t ccccaacc	2280
ggat cgt ct t	ccaggagt t c	cgccaacgct	acgagat cct	ggcggcgaat	gccat cccca	2340
aaggt t cat	ggacgggaag	caggcct gca	t t ct cat gat	caaagccct g	gaact t gacc	2400
ccaact t at a	caggat aggg	cagagcaaaa	t ct t ct t ccg	aact ggcgt c	ct ggcccacc	2460
t agaggagga	gcgagat t t g	aagat caccg	at gt cat cat	ggcct t ccag	gcgat gt gt c	2520
gt ggct act t	ggccagaaa	gct t t t gcca	agaggcagca	gcagct gacc	gccat gaagg	2580
t gat t cagag	gaact gcgcc	gcct acct ca	agct gcggaa	ct ggcagt gg	t ggaggct t t	2640
t caccaaagt	gaagccact g	ct gcaggt ga	cacggcagga	ggaggagat g	caggccaagg	2700
aggat gaact	gcagaagacc	aaggagcggc	agcagaaggc	agagaat gag	ct t aaggagc	2760
t ggaacagaa	gcact cgcag	ct gaccgagg	agaagaacct	gct acaggaa	cagct gcagg	2820
cagagacaga	gct gt at gca	gaggct gagg	agat gcgggt	gcggct ggcg	gccaagaagc	2880
aggagct gga	ggagat act g	cat gagat gg	aggcccgct	ggaggaggag	gaagacaggg	2940
gccagcagct	acaggct gaa	aggaagaaga	t ggcccagca	gat gct ggac	ct t gaagaac	3000
agct ggagga	ggaggaagct	gccaggcaga	agct gcaact	t gagaaggt c	acggct gagg	3060
ccaagat caa	gaaact ggag	gat gagat cc	t ggt cat gga	t gat cagaac	aat aaact at	3120
caaaagaacg	aaaact cct t	gaggagagga	t t agt gact t	aacgacaaat	ct t gcagaag	3180
aggaagaaaa	ggccaagaat	ct t accaagc	t gaaaaacaa	gcat gaat ct	at gat t t cag	3240
aact ggaagt	gcggct aaag	aaggaagaga	agagccgaca	ggagct ggag	aagct gaaac	3300
ggaagct gga	gggt gat gcc	agcgact t cc	acgagcagat	cgct gacct c	caggcgcaga	3360
t cgcagagct	caagat gcag	ct ggccaaga	aggaggagga	gct gcaggcg	gccct ggcca	3420
ggct t gacga	t gaaat cgct	cagaagaaca	at gccct gaa	gaagat ccgg	gagct ggagg	3480
gccacat ct c	agacct ccag	gaggacct gg	act cagagcg	ggccgccagg	aacaaggct g	3540
aaaagcagaa	gcgagacct c	ggcgaggagc	t ggaggccct	aaagacagag	ct ggaagaca	3600
cact ggacag	cacagccact	cagcaggagc	t cagggccaa	gagggagcag	gaggt gacgg	3660
t gct gaagaa	ggccct ggat	gaagagacgc	ggc ccat ga	ggct caggt c	caggagat ga	3720
ggcagaaaca	cgcacaggcg	gt ggaggagc	t cacagagca	gct t gagcag	t t caagaggg	3780
ccaaggcgaa	cct agacaag	aat aagcaga	cgct ggagaa	agagaacgca	gacct ggccg	3840
gggagct gcg	ggt cct gggc	caggccaagc	aggaggt gga	acat aagaag	aagaagct gg	3900
aggcgcaggt	gcaggagct g	cagt ccaagt	gcagcgat gg	ggagcgggcc	cgggcggagc	3960
t caat gacaa	agt ccacaag	ct gcagaat g	aagt t gagag	cgt cacaggg	at gct t aacg	4020
aggccgaggg	gaaggccat t	aagct ggcca	aggacgt ggc	gt ccct cagt	t cccagct cc	4080
aggacaccca	ggagct gct t	caagaagaaa	cccggcagaa	gct caacgt g	t ct acgaagc	4140
t gcgccagct	ggaggaggag	cggaacagcc	t gcaagacca	gct ggacgag	gagat ggagg	4200

N3027PCT\_sequ. list . . txt

ccaagcagaa	cctggagcgc	cacatctcca	ctctcaacat	ccagctctcc	gactcgaaga	4260
agaagctgca	ggactttgcc	agcaccgtgg	aagctctgga	agaggggaag	aagaggttcc	4320
agaaggagat	cgagaacctc	accagcagti	acgaggagaa	ggcgcccgct	t at gat aaac	4380
tggaaaagac	caagaacagg	cttcagcagg	agctggacga	cctggttgtt	gatttggaca	4440
accagcggca	actcgtgtcc	aacctggaaa	agaagcagag	gaaatttgat	cagttgttag	4500
ccgaggagaa	aaacatctct	tccaaat acg	cggatgagag	ggacagagct	gaggcagaag	4560
ccagggagaa	ggaaaccaag	gccctgtccc	tggctcgggc	ccttgaagag	gcctt ggaag	4620
ccaaagagga	actcgagcgg	accaacaaaa	tgctcaaagc	cgaaatggaa	gacctggtca	4680
gctccaagga	t gacgtgggc	aagaacgtcc	atgagctgga	gaagtccaag	cgggccctgg	4740
agaccagat	ggaggagatg	aagacgcagc	t ggaagagct	ggaggacgag	ct gcaagcca	4800
cggaggacgc	caaactgcgg	ctggaagtca	acatgcaggc	gctcaagggc	cagttcgaaa	4860
gggatctcca	agcccgggac	gagcagaatg	aggagaagag	gaggcaactg	cagagacagc	4920
ttcacgagta	t gagacggaa	ctggaagacg	agcgaaagca	acgtgccctg	gcagctgcag	4980
caaagaagaa	gctggaaggg	gacctgaaag	acctggagct	t caggccgac	tctgccatca	5040
aggggagggg	ggaagccatc	aagcagctac	gcaaactgca	ggctcagatg	aaggactttc	5100
aaagagagct	ggaagatgcc	cgtgcctcca	gagatgagat	ctttgccaca	gccaaagaga	5160
atgagaagaa	agccaagagc	ttggaagcag	acctcatgca	gctacaagag	gacctcgccg	5220
ccgctgagag	ggctcgcaaa	caagcggacc	t cgagaagga	ggaactggca	gaggagctgg	5280
ccagt agcct	gtcggggaagg	aacgcactcc	aggacgagaa	gcgccgcctg	gaggcccgga	5340
t cgcccagct	ggaggaggag	ctggaggagg	agcagggcaa	catggaggcc	atgagcgacc	5400
gggtccgcaa	agccacacag	caggccgagc	agctcagcaa	cgagctggcc	acagagcgca	5460
gcacggccca	gaagaatgag	agtccccggc	agcagctcga	gcggcagaac	aaggagctcc	5520
ggagcaagct	ccacgagatg	gagggggccg	t caagtccaa	gtt caagtcc	accatcgcgg	5580
cgctggaggc	caagattgca	cagctggagg	agcaggtcga	gcaggaggcc	agagagaaac	5640
aggcggccac	caagt cgctg	aagcagaaaag	acaagaagct	gaaggaaatc	tt gctgcagg	5700
tggaggacga	gcgcaagatg	gccgagcagti	acaaggagca	ggcagagaaa	ggcaatgcca	5760
gggtcaagca	gctcaagagg	cagctggagg	aggcagagga	ggagtcccag	cgcatcaacg	5820
ccaaccgcag	gaagctgcag	cgggagctgg	atgaggccac	ggagagcaac	gaggccatgg	5880
gccgcgaggt	gaacgcactc	aagagcaagc	t caggcgagg	aaacgagacc	tctttcgttc	5940
cttct agaag	gtctggagga	cgt agagtta	tt gaaaatgc	agatggttct	gaggaggaaa	6000
cggacactcg	agacgcagac	ttcaatggaa	ccaaggccag	tgaat aagca	actttctaca	6060
gttttgcacc	acggcaagaa	aaccaaaaaac	caaaacaaac	aaacaaaaaa	aaccacaaca	6120
caaccagaa	caaagcaaaa	cccagcagac	tgtacttagc	attgtctaaa	tccattctca	6180
aattccaaat	atcacagaca	cccctcacac	aaggaatat a	aaaaccacca	ccctccagcc	6240

N3027PCT\_sequ.list.txt

```

t g g g c a a c g t   a g t a a a c c t   c a t c t a t a c a   a g a a t t t a a a   a a t a a g c t g g   g c g t g g t g g t   6300
a c a c a c c t g t   g g t c c c a g c t   a c t a g g g a g g   c t g a g c c a g g   a a g a a c g c t c   c a g c c c a g g a   6360
c t t c g a g g c t   g c a a t g a g c t   a t a a t t g c a t   c a t t g c a c t c   c a g c c t g g g c   a a c a g a g a c c   6420
c t g t c t c a a c   c a c c a c c a c c   a c c a c c a c c c   c t a c t a c c c c   t g t a t t c a a g   g t a a a a t t g   6480
a a g t t t g t a t   g a t g t a a g a g   a t g a g a a a a a   c c c a a c a g g a   a a c a c a g a c a   c a t c c t c c a g   6540
t t c t a t c a a t   g g a t t g t g c a   g a c a c t g a g t   t t t t a g a a a a   a c a t a t c c a c   g g t a a c c g g t   6600
c c c t g g c a a t   t c t g t t t a c a   t g a a a t g g g g   a g a a a g t c a c   c g a a a t g g g t   g c c g c c g g c c   6660
c c c a c t c c c a   a t t c a t t c c c   t a a c c t g c a a   a c c t t t c c a a   c t t c t c a c g t   c a g g c c t t t g   6720
a g a a t t c t t t   c c c c t c t c c   t g g t t t c c a c   a c c t c a g a c a   c g c a c a g t t c   a c c a a g t g c c   6780
t t c t g t a g t c   a c a t g a a t t g   a a a a g g a g a c   g c t g c t c c c a   c g g a g g g g a g   c a g g a a t g c t   6840
g c a c t g t t t a   c a c c c t g a c t   g t g c t t a a a a   a c a c t t t c a c   t a a t a a a t g g   t t a t a a a t c a   6900
c a a   6903

```

<210> 76  
 <211> 1979  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1979)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SMI B

<400> 76

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
1      5      10      15

Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
20      25      30

Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
35      40      45

Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
50      55      60

Asn Gly Lys Lys Val Thr Val Gly Lys Asp Asp Ile Gln Lys Met Asn
65      70      75      80

Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu
85      90      95

Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg Tyr Phe Ser Gly
100     105     110

Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Val Asn Pro Tyr
115     120     125

```

N3027PCT\_sequ.list.txt

Lys	His	Leu	Pro	Ile	Tyr	Ser	Glu	Lys	Ile	Val	Asp	Met	Tyr	Lys	Gly
130						135					140				
Lys	Lys	Arg	His	Glu	Met	Pro	Pro	His	Ile	Tyr	Ala	Ile	Ala	Asp	Thr
145					150					155					160
Ala	Tyr	Arg	Ser	Met	Leu	Gln	Asp	Arg	Glu	Asp	Gln	Ser	Ile	Leu	Cys
				165					170					175	
Thr	Gly	Glu	Ser	Gly	Ala	Gly	Lys	Thr	Glu	Asn	Thr	Lys	Lys	Val	Ile
			180					185					190		
Gln	Tyr	Leu	Ala	Val	Val	Ala	Ser	Ser	His	Lys	Gly	Lys	Lys	Asp	Thr
		195					200					205			
Ser	Ile	Thr	Gln	Gly	Pro	Ser	Phe	Ala	Tyr	Gly	Glu	Leu	Glu	Lys	Gln
	210					215					220				
Leu	Leu	Gln	Ala	Asn	Pro	Ile	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr
225					230					235					240
Val	Lys	Asn	Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Phe	Ile	Arg	Ile	Asn
				245					250					255	
Phe	Asp	Val	Thr	Gly	Tyr	Ile	Val	Gly	Ala	Asn	Ile	Glu	Thr	Tyr	Leu
			260					265					270		
Leu	Glu	Lys	Ser	Arg	Ala	Ile	Arg	Gln	Ala	Arg	Asp	Glu	Arg	Thr	Phe
		275					280					285			
His	Ile	Phe	Tyr	Tyr	Met	Ile	Ala	Gly	Ala	Lys	Glu	Lys	Met	Arg	Ser
	290					295					300				
Asp	Leu	Leu	Leu	Glu	Gly	Phe	Asn	Asn	Tyr	Thr	Phe	Leu	Ser	Asn	Gly
305					310					315					320
Phe	Val	Pro	Ile	Pro	Ala	Ala	Gln	Asp	Asp	Glu	Met	Phe	Gln	Glu	Thr
				325					330					335	
Val	Glu	Ala	Met	Ala	Ile	Met	Gly	Phe	Ser	Glu	Glu	Glu	Gln	Leu	Ser
			340					345					350		
Ile	Leu	Lys	Val	Val	Ser	Ser	Val	Leu	Gln	Leu	Gly	Asn	Ile	Val	Phe
		355					360					365			
Lys	Lys	Glu	Arg	Asn	Thr	Asp	Gln	Ala	Ser	Met	Pro	Asp	Asn	Thr	Ala
	370					375					380				
Ala	Gln	Lys	Val	Cys	His	Leu	Met	Gly	Ile	Asn	Val	Thr	Asp	Phe	Thr
385					390					395					400

N3027PCT\_sequ.list.txt

Arg Ser Ile Leu Thr 405 Pro Arg Ile Lys Val 410 Gly Arg Asp Val Val 415 Gln

Lys Ala Gln Thr 420 Lys Glu Gln Ala Asp 425 Phe Ala Val Glu Ala 430 Leu Ala

Lys Ala Thr 435 Tyr Glu Arg Leu Phe 440 Arg Trp Ile Leu Thr 445 Arg Val Asn

Lys Ala 450 Leu Asp Lys Thr His 455 Arg Gln Gly Ala Ser 460 Phe Leu Gly Ile

Leu 465 Asp Ile Ala Gly Phe 470 Glu Ile Phe Glu Val 475 Asn Ser Phe Glu Gln 480

Leu Cys Ile Asn Tyr 485 Thr Asn Glu Lys Leu 490 Gln Gln Leu Phe Asn His 495

Thr Met Phe 500 Ile Leu Glu Gln Glu 505 Tyr Gln Arg Glu Gly 510 Ile Glu

Trp Asn Phe 515 Ile Asp Phe Gly Leu 520 Asp Leu Gln Pro Cys 525 Ile Glu Leu

Ile Glu 530 Arg Pro Asn Asn Pro 535 Pro Gly Val Leu Ala 540 Leu Leu Asp Glu

Glu 545 Cys Trp Phe Pro Lys 550 Ala Thr Asp Lys Ser 555 Phe Val Glu Lys Leu 560

Cys Thr Glu Gln Gly 565 Ser His Pro Lys Phe 570 Gln Lys Pro Lys Gln Leu 575

Lys Asp Lys Thr 580 Glu Phe Ser Ile Ile 585 His Tyr Ala Gly Lys 590 Val Asp

Tyr Asn Ala 595 Ser Ala Trp Leu Thr 600 Lys Asn Met Asp Pro 605 Leu Asn Asp

Asn Val 610 Thr Ser Leu Leu Asn 615 Ala Ser Ser Asp Lys 620 Phe Val Ala Asp

Leu 625 Trp Lys Asp Val Asp 630 Arg Ile Val Gly Leu 635 Asp Gln Met Ala Lys 640

Met Thr Glu Ser 645 Leu Pro Ser Ala Ser 650 Lys Thr Lys Lys Gly 655 Met

Phe Arg Thr Val 660 Gly Gln Leu Tyr Lys 665 Glu Gln Leu Gly Lys 670 Leu Met

Thr Thr Leu Arg Asn Thr Thr Pro Asn Phe Val Arg Cys Ile Ile Pro  
 675 680 685  
 Asn His Glu Lys Arg Ser Gly Lys Leu Asp Ala Phe Leu Val Leu Glu  
 690 695 700  
 Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile Cys Arg Gln  
 705 710 715 720  
 Gly Phe Pro Asn Arg Ile Val Phe Gln Glu Phe Arg Gln Arg Tyr Glu  
 725 730 735  
 Ile Leu Ala Ala Asn Ala Ile Pro Lys Gly Phe Met Asp Gly Lys Gln  
 740 745 750  
 Ala Cys Ile Leu Met Ile Lys Ala Leu Glu Leu Asp Pro Asn Leu Tyr  
 755 760 765  
 Arg Ile Gly Gln Ser Lys Ile Phe Phe Arg Thr Gly Val Leu Ala His  
 770 775 780  
 Leu Glu Glu Glu Arg Asp Leu Lys Ile Thr Asp Val Ile Met Ala Phe  
 785 790 795 800  
 Gln Ala Met Cys Arg Gly Tyr Leu Ala Arg Lys Ala Phe Ala Lys Arg  
 805 810 815  
 Gln Gln Gln Leu Thr Ala Met Lys Val Ile Gln Arg Asn Cys Ala Ala  
 820 825 830  
 Tyr Leu Lys Leu Arg Asn Trp Gln Trp Trp Arg Leu Phe Thr Lys Val  
 835 840 845  
 Lys Pro Leu Leu Gln Val Thr Arg Gln Glu Glu Glu Met Gln Ala Lys  
 850 855 860  
 Glu Asp Glu Leu Gln Lys Thr Lys Glu Arg Gln Gln Lys Ala Glu Asn  
 865 870 875 880  
 Glu Leu Lys Glu Leu Glu Gln Lys His Ser Gln Leu Thr Glu Glu Lys  
 885 890 895  
 Asn Leu Leu Gln Glu Gln Leu Gln Ala Glu Thr Glu Leu Tyr Ala Glu  
 900 905 910  
 Ala Glu Glu Met Arg Val Arg Leu Ala Ala Lys Lys Gln Glu Leu Glu  
 915 920 925  
 Glu Ile Leu His Glu Met Glu Ala Arg Leu Glu Glu Glu Glu Asp Arg  
 930 935 940  
 Gly Gln Gln Leu Gln Ala Glu Arg Lys Lys Met Ala Gln Gln Met Leu  
 Page 365

945                      950                      955                      960  
 Asp Leu Glu Glu Gln Leu Glu Glu Glu Glu Ala Ala Arg Gln Lys Leu  
                                  965                                   970                                   975  
 Gln Leu Glu Lys Val Thr Ala Glu Ala Lys Ile Lys Lys Leu Glu Asp  
                                  980                                   985                                   990  
 Glu Ile Leu Val Met Asp Asp Gln Asn Asn Lys Leu Ser Lys Glu Arg  
                                  995                                   1000                                   1005  
 Lys Leu Leu Glu Glu Arg Ile Ser Asp Leu Thr Thr Asn Leu Ala  
                                  1010                                   1015                                   1020  
 Glu Glu Glu Glu Lys Ala Lys Asn Leu Thr Lys Leu Lys Asn Lys  
                                  1025                                   1030                                   1035  
 His Glu Ser Met Ile Ser Glu Leu Glu Val Arg Leu Lys Lys Glu  
                                  1040                                   1045                                   1050  
 Glu Lys Ser Arg Gln Glu Leu Glu Lys Leu Lys Arg Lys Leu Glu  
                                  1055                                   1060                                   1065  
 Gly Asp Ala Ser Asp Phe His Glu Gln Ile Ala Asp Leu Gln Ala  
                                  1070                                   1075                                   1080  
 Gln Ile Ala Glu Leu Lys Met Gln Leu Ala Lys Lys Glu Glu Glu  
                                  1085                                   1090                                   1095  
 Leu Gln Ala Ala Leu Ala Arg Leu Asp Asp Glu Ile Ala Gln Lys  
                                  1100                                   1105                                   1110  
 Asn Asn Ala Leu Lys Lys Ile Arg Glu Leu Glu Gly His Ile Ser  
                                  1115                                   1120                                   1125  
 Asp Leu Gln Glu Asp Leu Asp Ser Glu Arg Ala Ala Arg Asn Lys  
                                  1130                                   1135                                   1140  
 Ala Glu Lys Gln Lys Arg Asp Leu Gly Glu Glu Leu Glu Ala Leu  
                                  1145                                   1150                                   1155  
 Lys Thr Glu Leu Glu Asp Thr Leu Asp Ser Thr Ala Thr Gln Gln  
                                  1160                                   1165                                   1170  
 Glu Leu Arg Ala Lys Arg Glu Gln Glu Val Thr Val Leu Lys Lys  
                                  1175                                   1180                                   1185  
 Ala Leu Asp Glu Glu Thr Arg Ser His Glu Ala Gln Val Gln Glu  
                                  1190                                   1195                                   1200  
 Met Arg Gln Lys His Ala Gln Ala Val Glu Glu Leu Thr Glu Gln  
                                  1205                                   1210                                   1215

N3027PCT\_sequ.list.txt

Leu	Glu	Gln	Phe	Lys	Arg	Ala	Lys	Ala	Asn	Leu	Asp	Lys	Asn	Lys
	1220					1225					1230			
Gln	Thr	Leu	Glu	Lys	Glu	Asn	Ala	Asp	Leu	Ala	Gly	Glu	Leu	Arg
	1235					1240					1245			
Val	Leu	Gly	Gln	Ala	Lys	Gln	Glu	Val	Glu	His	Lys	Lys	Lys	Lys
	1250					1255					1260			
Leu	Glu	Ala	Gln	Val	Gln	Glu	Leu	Gln	Ser	Lys	Cys	Ser	Asp	Gly
	1265					1270					1275			
Glu	Arg	Ala	Arg	Ala	Glu	Leu	Asn	Asp	Lys	Val	His	Lys	Leu	Gln
	1280					1285					1290			
Asn	Glu	Val	Glu	Ser	Val	Thr	Gly	Met	Leu	Asn	Glu	Ala	Glu	Gly
	1295					1300					1305			
Lys	Ala	Ile	Lys	Leu	Ala	Lys	Asp	Val	Ala	Ser	Leu	Ser	Ser	Gln
	1310					1315					1320			
Leu	Gln	Asp	Thr	Gln	Glu	Leu	Leu	Gln	Glu	Glu	Thr	Arg	Gln	Lys
	1325					1330					1335			
Leu	Asn	Val	Ser	Thr	Lys	Leu	Arg	Gln	Leu	Glu	Glu	Glu	Arg	Asn
	1340					1345					1350			
Ser	Leu	Gln	Asp	Gln	Leu	Asp	Glu	Glu	Met	Glu	Ala	Lys	Gln	Asn
	1355					1360					1365			
Leu	Glu	Arg	His	Ile	Ser	Thr	Leu	Asn	Ile	Gln	Leu	Ser	Asp	Ser
	1370					1375					1380			
Lys	Lys	Lys	Leu	Gln	Asp	Phe	Ala	Ser	Thr	Val	Glu	Ala	Leu	Glu
	1385					1390					1395			
Glu	Gly	Lys	Lys	Arg	Phe	Gln	Lys	Glu	Ile	Glu	Asn	Leu	Thr	Gln
	1400					1405					1410			
Gln	Tyr	Glu	Glu	Lys	Ala	Ala	Ala	Tyr	Asp	Lys	Leu	Glu	Lys	Thr
	1415					1420					1425			
Lys	Asn	Arg	Leu	Gln	Gln	Glu	Leu	Asp	Asp	Leu	Val	Val	Asp	Leu
	1430					1435					1440			
Asp	Asn	Gln	Arg	Gln	Leu	Val	Ser	Asn	Leu	Glu	Lys	Lys	Gln	Arg
	1445					1450					1455			
Lys	Phe	Asp	Gln	Leu	Leu	Ala	Glu	Glu	Lys	Asn	Ile	Ser	Ser	Lys
	1460					1465					1470			

N3027PCT\_sequ.list.txt

Tyr Ala Asp Glu Arg Asp Arg Ala Glu Ala Glu Ala Arg Glu Lys  
 1475 1480 1485  
 Glu Thr Lys Ala Leu Ser Leu Ala Arg Ala Leu Glu Glu Ala Leu  
 1490 1495 1500  
 Glu Ala Lys Glu Glu Leu Glu Arg Thr Asn Lys Met Leu Lys Ala  
 1505 1510 1515  
 Glu Met Glu Asp Leu Val Ser Ser Lys Asp Asp Val Gly Lys Asn  
 1520 1525 1530  
 Val His Glu Leu Glu Lys Ser Lys Arg Ala Leu Glu Thr Glu Met  
 1535 1540 1545  
 Glu Glu Met Lys Thr Glu Leu Glu Glu Leu Glu Asp Glu Leu Glu  
 1550 1555 1560  
 Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn Met Glu Ala  
 1565 1570 1575  
 Leu Lys Gly Glu Phe Glu Arg Asp Leu Glu Ala Arg Asp Glu Glu  
 1580 1585 1590  
 Asn Glu Glu Lys Arg Arg Glu Leu Glu Arg Glu Leu His Glu Tyr  
 1595 1600 1605  
 Glu Thr Glu Leu Glu Asp Glu Arg Lys Glu Arg Ala Leu Ala Ala  
 1610 1615 1620  
 Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu  
 1625 1630 1635  
 Glu Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Glu  
 1640 1645 1650  
 Leu Arg Lys Leu Glu Ala Glu Met Lys Asp Phe Glu Arg Glu Leu  
 1655 1660 1665  
 Glu Asp Ala Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys  
 1670 1675 1680  
 Glu Asn Glu Lys Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Glu  
 1685 1690 1695  
 Leu Glu Glu Asp Leu Ala Ala Ala Glu Arg Ala Arg Lys Glu Ala  
 1700 1705 1710  
 Asp Leu Glu Lys Glu Glu Leu Ala Glu Glu Leu Ala Ser Ser Leu  
 1715 1720 1725

Ser Gly Arg Asn Ala Leu Gln Asp Glu Lys Arg Arg Leu Glu Ala  
 1730 1735 1740  
 Arg Ile Ala Gln Leu Glu Glu Glu Leu Glu Glu Glu Gln Gly Asn  
 1745 1750 1755  
 Met Glu Ala Met Ser Asp Arg Val Arg Lys Ala Thr Gln Gln Ala  
 1760 1765 1770  
 Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu Arg Ser Thr Ala Gln  
 1775 1780 1785  
 Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg Gln Asn Lys Glu  
 1790 1795 1800  
 Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val Lys Ser Lys  
 1805 1810 1815  
 Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala Gln Leu  
 1820 1825 1830  
 Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala Thr  
 1835 1840 1845  
 Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu  
 1850 1855 1860  
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln  
 1865 1870 1875  
 Ala Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu  
 1880 1885 1890  
 Glu Glu Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg  
 1895 1900 1905  
 Lys Leu Gln Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala  
 1910 1915 1920  
 Met Gly Arg Glu Val Asn Ala Leu Lys Ser Lys Leu Arg Arg Gly  
 1925 1930 1935  
 Asn Glu Thr Ser Phe Val Pro Ser Arg Arg Ser Gly Gly Arg Arg  
 1940 1945 1950  
 Val Ile Glu Asn Ala Asp Gly Ser Glu Glu Glu Thr Asp Thr Arg  
 1955 1960 1965  
 Asp Ala Asp Phe Asn Gly Thr Lys Ala Ser Glu  
 1970 1975

<211> 6921  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(6921)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SM2A

```

<400> 77
gggagatttg gacgctccgg cctgggaggt gcgtcagatc cgagctcgcc atccagtttc      60
ctctccacta gtccccccag ttggagatct gggaccaaca aggcaccatg gcgcagaagg      120
gccaactcag tgacgatgag aagttcctct ttgtggacaa aaacttcatc aacagcccag      180
tggcccaggc tgactgggcc gccaagagac tcgtctgggt cccctcggag aagcagggct      240
tcgaggcagc cagcattaag gaggagaagg gggatgaggt ggttgtggag ctggtggaga      300
atggcaagaa ggtcacggtt gggaaagatg acatccagaa gatgaacca cccaagttct      360
ccaagggtgga ggacatggcg gagctgacgt gcctcaacga agcctccgtg ctacacaacc      420
tgagggagcg gtacttctca gggctaatat atacgtactc tggcctcttc tgcgtggtgg      480
tcaaccctat taaacacctg cccatctact cggagaagat cgtcgacatg tacaagggca      540
agaagaggca cgagatgccg cctcacatct acgccatcgc agacacggcc taccggagca      600
tgcttcaaga tcgggaggac cagtccattc tatgcacagg cgagtctgga gccgggaaaa      660
ccgaaaacac caagaaggtc attcagtacc tggccgtggt ggcctcctcc cacaagggca      720
agaaagacac aagtatcacg ggagagctgg aaaagcagct tctacaagca aaccgcattc      780
tggaggcttt cggcaacgcc aaaacagtga agaacgacaa ctctcacga ttcggcaaat      840
tcatccgcat caacttcgac gtcacgggtt acatcgtggg agccaacatt gagacctatc      900
tgctagaaaa atcacgggca attcgccaag ccagagacga gaggacattc cacatctttt      960
actacatgat tgctggagcc aaggagaaga tgagaagtga cttgcttttg gagggcttca     1020
acaactacac ctctctctcc aatggctttg tggccatccc agcagcccag gatgatgaga     1080
tgttccagga aaccgtggag gccatggcaa tcatgggttt cagcgaggag gagcagctat     1140
ccatattgaa ggtggtatca tcggtcctgc agcttggaaa tatcgtcttc aagaaggaaa     1200
gaaacacaga ccaggcgtcc atgccagatg acacagctgc tcagaaagt tggccacctca     1260
tgggaattaa tgtgacagat ttaccagat ccatcctcac tcctcgtatc aagggttgggc     1320
gagatgtggt acagaaagct cagacaaaag aacaggctga ctttgctgta gaggctttgg     1380
ccaaggcaac atatgagcgc cttttccgct ggatactcac ccgcgtgaac aaagccctgg     1440
acaagaccca tcggcaaggg gcttcttcc tggggatcct ggatatagct ggatttgaga     1500
tctttgaggt gaactccttc gagcagctgt gcatcaacta caccaacgag aagctgcagc     1560
agctcttcaa ccacaccatg ttcatcctgg agcaggagga gtaccagcgc gagggcatcg     1620
agtggaactt catcgacttt gggctggacc tacagccctg catcgagctc atcgagcgac     1680
cgaacaaccc tcagggtgtg ctggccctgc tggacgagga atgctggttc cccaaagcca     1740

```

N3027PCT\_sequ. list . . txt

cggacaagt c	t t t cgt ggag	aagct gt gca	cggagcaggg	cagccacccc	aagt t ccaga	1800
agcccaagca	gct caaggac	aagact gagt	t ct ccat cat	ccat t at gct	gggaaggt gg	1860
act at aat gc	gagt gcct gg	ct gaccaaga	at at ggaccc	gct gaat gac	aacgt gact t	1920
ccct gct caa	t gcct cct cc	gacaagt t t g	t ggccgacct	gt ggaaggac	gt ggaccgca	1980
t cgt gggcct	ggaccagat g	gccaagat ga	cggagagct c	gct gcccagc	gcct ccaaga	2040
ccaagaaggg	cat gt t ccgc	acagt ggggc	agct gt acaa	ggagcagct g	ggcaagct ga	2100
t gaccacgct	acgcaacacc	acgcccact	t cgt gcgct g	cat cat cccc	aaccacgaga	2160
agaggt ccgg	caagct ggat	gcgt t cct gg	t gct ggagca	gct gcggt gc	aat ggggt gc	2220
t ggaaggcat	t cgcct ct gc	cggcagggct	t ccccaaccg	gat cgt ct t c	caggagt t cc	2280
gccaacgct a	cgagat cct g	gcggcgaat g	ccat ccccaa	aggct t cat g	gacgggaagc	2340
aggcct gcat	t ct cat gat c	aaagccct gg	aact t gaccc	caact t at ac	aggat agggc	2400
agagcaaaat	ct t ct t ccga	act ggcgt cc	t ggcccacct	agaggaggag	cgagat t t ga	2460
agat caccga	t gt cat cat g	gcct t ccagg	cgat gt gt cg	t ggct act t g	gccagaaagg	2520
ct t t t gccaa	gaggcagcag	cagct gaccg	ccat gaaggt	gat t cagagg	aact gcgccg	2580
cct acct caa	gct gcggaac	t ggcagt ggt	ggaggct t t t	caccaaagt g	aagccact gc	2640
t gcaggt gac	acggcaggag	gaggagat gc	aggccaagga	ggat gaact g	cagaagacca	2700
aggagcggca	gcagaaggca	gagaat gagc	t t aaggagct	ggaacagaag	cact cgcagc	2760
t gaccgagga	gaagaacct g	ct acaggaac	agct gcaggc	agagacagag	ct gt at gcag	2820
aggct gagga	gat gcgggt g	cggct ggcg	ccaagaagca	ggagct ggag	gagat act gc	2880
at gagat gga	ggcccgct g	gaggaggagg	aagacagggg	ccagcagct a	caggct gaaa	2940
ggaagaagat	ggcccagcag	at gct ggacc	t t gaagaaca	gct ggaggag	gaggaagct g	3000
ccaggcagaa	gct gcaact t	gagaaggt ca	cggct gaggc	caagat caag	aaact ggagg	3060
at gagat cct	ggt cat ggat	gat cagaaca	at aaact at c	aaaagaacga	aaact cct t g	3120
aggagaggat	t agt gact t a	acgacaaat c	t t gcagaaga	ggaagaaaag	gccaagaat c	3180
t t accaagct	gaaaaacaag	cat gaat ct a	t gat t t caga	act ggaagt g	cggct aaaga	3240
aggaagagaa	gagccgacag	gagct ggaga	agct gaaacg	gaagct ggag	ggt gat gcca	3300
gcgact t cca	cgagcagat c	gct gacct cc	aggcgcagat	cgcagagct c	aagat gcagc	3360
t ggccaagaa	ggaggaggag	ct gcaggcg	ccct ggccag	gct t gacgat	gaaat cgct c	3420
agaagaacaa	t gccct gaag	aagat ccggg	agct ggaggg	ccacat ct ca	gacct ccagg	3480
aggacct gga	ct cagagcgg	gccgccagga	acaaggct ga	aaagcagaag	cgagacct cg	3540
gcgaggagct	ggaggccct a	aagacagagc	t ggaagacac	act ggacagc	acagccact c	3600
agcaggagct	cagggccaag	agggagcagg	aggt gacggt	gct gaagaag	gccct ggat g	3660
aagagacgcg	gt cccat gag	gct cagggt cc	aggagat gag	gcagaaacac	gcacaggcgg	3720
t ggaggagct	cacagagcag	ct t gagcagt	t caagagggc	caaggcgaac	ct agacaaga	3780

N3027PCT\_sequ. l i s t . . t x t

at aagcagac	gct ggagaaa	gagaacgcag	acct ggccgg	ggagct gcgg	gt cct gggcc	3840
aggccaagca	ggaggt ggaa	cat aagaaga	agaagct gga	ggcgcaggt g	caggagct gc	3900
agt ccaagt g	cagcgat ggg	gagcggggccc	gggcggagct	caat gacaaa	gt ccacaagc	3960
t gcagaat ga	agt t gagagc	gt cacagggga	t gct t aacga	ggccgagggg	aaggccat t a	4020
agct ggccaa	ggacgt ggcg	t ccct cagt t	cccagct cca	ggacacccag	gagct gct t c	4080
aagaagaaac	ccggcagaag	ct caacgt gt	ct acgaagct	gcgccagct g	gaggaggagc	4140
ggaacagcct	gcaagaccag	ct ggacgagg	agat ggaggc	caagcagaac	ct ggagcgcc	4200
acat ct ccac	t ct caacat c	cagct ct ccg	act cgaagaa	gaagct gcag	gact t t gcca	4260
gcaccgt gga	agct ct ggaa	gaggggaaga	agaggt t cca	gaaggagat c	gagaacct ca	4320
cccagcagt a	cgaggagaag	gcggccgct t	at gat aaact	ggaaaagacc	aagaacaggc	4380
t t cagcagga	gct ggacgac	ct ggt t gt t g	at t t ggacaa	ccagcggcaa	ct cgt gt cca	4440
acct ggaaaa	gaagcagagg	aaat t t gat c	agt t gt t agc	cgaggagaaa	aacat ct ct t	4500
ccaaat acgc	ggat gagagg	gacagagct g	aggcagaagc	cagggagaag	gaaaccaagg	4560
ccct gt ccct	ggct cgggcc	ct t gaagagg	cct t ggaagc	caaagaggaa	ct cgagcgga	4620
ccaacaaaat	gct caaagcc	gaaat ggaag	acct ggt cag	ct ccaaggat	gacgt gggca	4680
agaacgt cca	t gagct ggag	aagt ccaagc	gggccct gga	gaccagat g	gaggagat ga	4740
agacgcagct	ggaagagct g	gaggacgagc	t gcaagccac	ggaggacgcc	aaact gcggc	4800
t ggaagt caa	cat gcaggcg	ct caagggcc	agt t cgaaag	ggat ct ccaa	gcccgggacg	4860
agcagaat ga	ggagaagagg	aggcaact gc	agagacagct	t cacgagt at	gagacggaac	4920
t ggaagacga	gcgaaagcaa	cgt gccct gg	cagct gcagc	aaagaagaag	ct ggaagggg	4980
acct gaaaga	cct ggagct t	caggccgact	ct gccat caa	ggggagggag	gaagccat ca	5040
agcagct acg	caaact gcag	gct cagat ga	aggact t t ca	aagagagct g	gaagat gccc	5100
gt gcct ccag	agat gagat c	t t t gccacag	ccaaagagaa	t gagaagaaa	gccaaagact	5160
t ggaagcaga	cct cat gcag	ct acaagagg	acct cgccgc	cgct gagagg	gct cgcaaac	5220
aagcggacct	cgagaaggag	gaact ggcag	aggagct ggc	cagt agcct g	t cggaagga	5280
acgcact cca	ggacgagaag	cgccgcct gg	aggcccggat	cgcccagct g	gaggaggagc	5340
t ggaggagga	gcagggcaac	at ggaggcca	t gagcgaccg	ggt ccgcaaa	gccacacagc	5400
aggccgagca	gct cagcaac	gagct ggcca	cagagcgagc	cacggcccag	aagaat gaga	5460
gt gcccggca	gcagct cgag	cggcagaaca	aggagct ccg	gagcaagct c	cacgagat gg	5520
agggggccgt	caagt ccaag	t t caagt cca	ccat cgcggc	gct ggaggcc	aagat t gcac	5580
agct ggagga	gcaggt cgag	caggaggcca	gagagaaaca	ggcggccacc	aagt cgct ga	5640
agcagaaaga	caagaagct g	aaggaaat ct	t gct gcaggt	ggaggacgag	cgcaagat gg	5700
ccgagcagt a	caaggagcag	gcagagaaaag	gcaat gccag	ggt caagcag	ct caagaggc	5760
agct ggagga	ggcagaggag	gagt cccagc	gcat caacgc	caaccgcagg	aagct gcagc	5820
gggagct gga	t gaggccacg	gagagcaacg	aggccat ggg	ccgcgaggt g	aacgcact ca	5880

N3027PCT\_sequ.list.txt

```

agagcaagct cagagggccc ccccccacagg aaacttcgca gtgatgcacc aggcgaggaa 5940
acgagacctc ttctcgttcct tctagaaggt ctggaggacg tagagttatt gaaaatgcag 6000
atggttctga ggaggaaacg gacactcgag acgcagactt caatggaacc aaggccagt g 6060
aat aagcaac ttctctacagt ttctgcaccac ggcaagaaaa ccaaaaacca aaacaacaa 6120
acaaaaaaaaa cccaacaaca acccagaaca aagcaaaacc cagcagactg t acttagcat 6180
tgtctaaatc catctctcaa ttccaaat at cacagacacc cctcacacaa ggaat at aaa 6240
aaccaccacc ctccagcctg ggcaacgt ag taaaacct ca tct atacaag aat t taaaaa 6300
taagctgggc gtggtggt ac acacctgtgg tcccagct ac tagggaggct gagccaggaa 6360
gaacgctcca gcccaggact tcgaggctgc aatgagct at aat tgcac ca ttgcactcca 6420
gcctgggcaa cagagacctt gtctcaacca ccaccaccac caccaccct act acccct g 6480
tattcaaggt aaaaattgaa gt t t g t at ga t g t aagagat gagaaaaacc caacaggaaa 6540
cacagacaca tctctcagtt ctatcaatgg at t g t g c a g a c a c t g a g t t t t t a g a a a a c 6600
at at ccacgg taaccggtcc ctggcaattc t g t t t a c a t g a a a t g g g g a g a a a g t c a c c g 6660
aaatgggtgc cgccggcccc cactccaat tcat tccct a acctgcaaac ct t t c c a a c t 6720
tctcacgtca ggcct t t g a g a a t t c t t t c c c c t c t c t g g t t t c c a c a c c t c a g a c a c g 6780
cacagttcac caagtgcctt ctgtagtac atgaattgaa aaggagacgc t g c t c c c a c g 6840
gaggggagca ggaatgctgc actgtttaca ccctgactgt gct t a a a a a c a c t t t c a c t a 6900
at aaat ggt t at aaat c a c a a 6921

```

<210> 78  
 <211> 1938  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1938)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SM2A

<400> 78

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
1          5          10          15

Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
          20          25          30

Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
          35          40          45

Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
50          55          60

Asn Gly Lys Lys Val Thr Val Gly Lys Asp Asp Ile Gln Lys Met Asn

```

65		70		75		80									
Pro	Pro	Lys	Phe	Ser <sub>85</sub>	Lys	Val	Glu	Asp	Met <sub>90</sub>	Ala	Glu	Leu	Thr	Cys <sub>95</sub>	Leu
Asn	Glu	Ala	Ser <sub>100</sub>	Val	Leu	His	Asn	Leu <sub>105</sub>	Arg	Glu	Arg	Tyr	Phe	Ser	Gly
Leu	Ile	Tyr <sub>115</sub>	Thr	Tyr	Ser	Gly	Leu <sub>120</sub>	Phe	Cys	Val	Val	Val <sub>125</sub>	Asn	Pro	Tyr
Lys	His <sub>130</sub>	Leu	Pro	Ile	Tyr	Ser <sub>135</sub>	Glu	Lys	Ile	Val	Asp <sub>140</sub>	Met	Tyr	Lys	Gly
Lys <sub>145</sub>	Lys	Arg	His	Glu	Met <sub>150</sub>	Pro	Pro	His	Ile	Tyr <sub>155</sub>	Ala	Ile	Ala	Asp	Thr <sub>160</sub>
Ala	Tyr	Arg	Ser	Met <sub>165</sub>	Leu	Gln	Asp	Arg	Glu <sub>170</sub>	Asp	Gln	Ser	Ile	Leu <sub>175</sub>	Cys
Thr	Gly	Glu	Ser <sub>180</sub>	Gly	Ala	Gly	Lys	Thr <sub>185</sub>	Glu	Asn	Thr	Lys	Lys <sub>190</sub>	Val	Ile
Gln	Tyr	Leu <sub>195</sub>	Ala	Val	Val	Ala	Ser <sub>200</sub>	Ser	His	Lys	Gly	Lys <sub>205</sub>	Lys	Asp	Thr
Ser	Ile <sub>210</sub>	Thr	Gly	Glu	Leu	Glu <sub>215</sub>	Lys	Gln	Leu	Leu	Gln <sub>220</sub>	Ala	Asn	Pro	Ile
Leu <sub>225</sub>	Glu	Ala	Phe	Gly	Asn <sub>230</sub>	Ala	Lys	Thr	Val	Lys <sub>235</sub>	Asn	Asp	Asn	Ser	Ser <sub>240</sub>
Arg	Phe	Gly	Lys	Phe <sub>245</sub>	Ile	Arg	Ile	Asn	Phe <sub>250</sub>	Asp	Val	Thr	Gly	Tyr <sub>255</sub>	Ile
Val	Gly	Ala	Asn <sub>260</sub>	Ile	Glu	Thr	Tyr	Leu <sub>265</sub>	Leu	Glu	Lys	Ser	Arg <sub>270</sub>	Ala	Ile
Arg	Gln	Ala <sub>275</sub>	Arg	Asp	Glu	Arg	Thr <sub>280</sub>	Phe	His	Ile	Phe	Tyr <sub>285</sub>	Tyr	Met	Ile
Ala	Gly <sub>290</sub>	Ala	Lys	Glu	Lys	Met <sub>295</sub>	Arg	Ser	Asp	Leu	Leu <sub>300</sub>	Leu	Glu	Gly	Phe
Asn <sub>305</sub>	Asn	Tyr	Thr	Phe	Leu <sub>310</sub>	Ser	Asn	Gly	Phe	Val <sub>315</sub>	Pro	Ile	Pro	Ala	Ala <sub>320</sub>
Gln	Asp	Asp	Glu	Met <sub>325</sub>	Phe	Gln	Glu	Thr	Val <sub>330</sub>	Glu	Ala	Met	Ala	Ile	Met <sub>335</sub>
Gly	Phe	Ser	Glu <sub>340</sub>	Glu	Glu	Gln	Leu	Ser <sub>345</sub>	Ile	Leu	Lys	Val	Val <sub>350</sub>	Ser	Ser

N3027PCT\_sequ.list.txt

Val Leu Gln Leu Gly Asn Ile Val Phe Lys Lys Glu Arg Asn Thr Asp  
355 360 365

Gln Ala Ser Met Pro Asp Asn Thr Ala Ala Gln Lys Val Cys His Leu  
370 375 380

Met Gly Ile Asn Val Thr Asp Phe Thr Arg Ser Ile Leu Thr Pro Arg  
385 390 395 400

Ile Lys Val Gly Arg Asp Val Val Gln Lys Ala Gln Thr Lys Glu Gln  
405 410 415

Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu  
420 425 430

Phe Arg Trp Ile Leu Thr Arg Val Asn Lys Ala Leu Asp Lys Thr His  
435 440 445

Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala Gly Phe Glu  
450 455 460

Ile Phe Glu Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn  
465 470 475 480

Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln  
485 490 495

Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly  
500 505 510

Leu Asp Leu Gln Pro Cys Ile Glu Leu Ile Glu Arg Pro Asn Asn Pro  
515 520 525

Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala  
530 535 540

Thr Asp Lys Ser Phe Val Glu Lys Leu Cys Thr Glu Gln Gly Ser His  
545 550 555 560

Pro Lys Phe Gln Lys Pro Lys Gln Leu Lys Asp Lys Thr Glu Phe Ser  
565 570 575

Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Asn Ala Ser Ala Trp Leu  
580 585 590

Thr Lys Asn Met Asp Pro Leu Asn Asp Asn Val Thr Ser Leu Leu Asn  
595 600 605

Ala Ser Ser Asp Lys Phe Val Ala Asp Leu Trp Lys Asp Val Asp Arg  
610 615 620

N3027PCT\_sequ.list.txt

I l e	V a l	G l y	L e u	A s p	G l n	M e t	A l a	L y s	M e t	T h r	G l u	S e r	S e r	L e u	P r o
625					630					635					640
S e r	A l a	S e r	L y s	T h r	L y s	L y s	G l y	M e t	P h e	A r g	T h r	V a l	G l y	G l n	L e u
				645					650					655	
T y r	L y s	G l u	G l n	L e u	G l y	L y s	L e u	M e t	T h r	T h r	L e u	A r g	A s n	T h r	T h r
			660					665					670		
P r o	A s n	P h e	V a l	A r g	C y s	I l e	I l e	P r o	A s n	H i s	G l u	L y s	A r g	S e r	G l y
		675					680					685			
L y s	L e u	A s p	A l a	P h e	L e u	V a l	L e u	G l u	G l n	L e u	A r g	C y s	A s n	G l y	V a l
	690					695					700				
L e u	G l u	G l y	I l e	A r g	I l e	C y s	A r g	G l n	G l y	P h e	P r o	A s n	A r g	I l e	V a l
705					710					715					720
P h e	G l n	G l u	P h e	A r g	G l n	A r g	T y r	G l u	I l e	L e u	A l a	A l a	A s n	A l a	I l e
				725					730					735	
P r o	L y s	G l y	P h e	M e t	A s p	G l y	L y s	G l n	A l a	C y s	I l e	L e u	M e t	I l e	L y s
			740					745					750		
A l a	L e u	G l u	L e u	A s p	P r o	A s n	L e u	T y r	A r g	I l e	G l y	G l n	S e r	L y s	I l e
		755					760					765			
P h e	P h e	A r g	T h r	G l y	V a l	L e u	A l a	H i s	L e u	G l u	G l u	G l u	A r g	A s p	L e u
	770					775					780				
L y s	I l e	T h r	A s p	V a l	I l e	M e t	A l a	P h e	G l n	A l a	M e t	C y s	A r g	G l y	T y r
785					790					795					800
L e u	A l a	A r g	L y s	A l a	P h e	A l a	L y s	A r g	G l n	G l n	G l n	L e u	T h r	A l a	M e t
				805					810					815	
L y s	V a l	I l e	G l n	A r g	A s n	C y s	A l a	A l a	T y r	L e u	L y s	L e u	A r g	A s n	T r p
			820					825					830		
G l n	T r p	T r p	A r g	L e u	P h e	T h r	L y s	V a l	L y s	P r o	L e u	L e u	G l n	V a l	T h r
	835						840					845			
A r g	G l n	G l u	G l u	G l u	M e t	G l n	A l a	L y s	G l u	A s p	G l u	L e u	G l n	L y s	T h r
	850					855					860				
L y s	G l u	A r g	G l n	G l n	L y s	A l a	G l u	A s n	G l u	L e u	L y s	G l u	L e u	G l u	G l n
865					870					875					880
L y s	H i s	S e r	G l n	L e u	T h r	G l u	G l u	L y s	A s n	L e u	L e u	G l n	G l u	G l n	L e u
				885					890					895	

G n A l a G u T h r G u L e u T y r A l a G u A l a G u G u M e t A r g V a l A r g  
 900 905 910  
 L e u A l a A l a L y s L y s G n G u L e u G u G u I l e L e u H i s G u M e t G u  
 915 920 925  
 A l a A r g L e u G u G u G u G u A s p A r g G y G n G n L e u G n A l a G u  
 930 935 940  
 A r g L y s L y s M e t A l a G n G n M e t L e u A s p L e u G u G u G n L e u G u  
 945 950 955 960  
 G u G u G u A l a A l a A r g G n L y s L e u G n L e u G u L y s V a l T h r A l a  
 965 970 975  
 G u A l a L y s I l e L y s L y s L e u G u A s p G u I l e L e u V a l M e t A s p A s p  
 980 985 990  
 G n A s n A s n L y s L e u S e r L y s G u A r g L y s L e u L e u G u G u A r g I l e  
 995 1000 1005  
 S e r A s p L e u T h r T h r A s n L e u A l a G u G u G u G u L y s A l a L y s  
 1010 1015 1020  
 A s n L e u T h r L y s L e u L y s A s n L y s H i s G u S e r M e t I l e S e r G u  
 1025 1030 1035  
 L e u G u V a l A r g L e u L y s L y s G u G u L y s S e r A r g G n G u L e u  
 1040 1045 1050  
 G u L y s L e u L y s A r g L y s L e u G u G y A s p A l a S e r A s p P h e H i s  
 1055 1060 1065  
 G u G n I l e A l a A s p L e u G n A l a G n I l e A l a G u L e u L y s M e t  
 1070 1075 1080  
 G n L e u A l a L y s L y s G u G u G u L e u G n A l a A l a L e u A l a A r g  
 1085 1090 1095  
 L e u A s p A s p G u I l e A l a G n L y s A s n A s n A l a L e u L y s L y s I l e  
 1100 1105 1110  
 A r g G u L e u G u G y H i s I l e S e r A s p L e u G n G u A s p L e u A s p  
 1115 1120 1125  
 S e r G u A r g A l a A l a A r g A s n L y s A l a G u L y s G n L y s A r g A s p  
 1130 1135 1140  
 L e u G y G u G u L e u G u A l a L e u L y s T h r G u L e u G u A s p T h r  
 1145 1150 1155  
 L e u A s p S e r T h r A l a T h r G n G n G u L e u A r g A l a L y s A r g G u  
 1160 1165 1170

1160														
G n	G u	Val	Thr	Val	Leu	Lys	Lys	Al a	Leu	Asp	G u	G u	Thr	Arg
1175						1180					1185			
Ser	Hi s	G u	Al a	G n	Val	G n	G u	Met	Arg	G n	Lys	Hi s	Al a	G n
1190						1195					1200			
Al a	Val	G u	G u	Leu	Thr	G u	G n	Leu	G u	G n	Phe	Lys	Arg	Al a
1205						1210					1215			
Lys	Al a	Asn	Leu	Asp	Lys	Asn	Lys	G n	Thr	Leu	G u	Lys	G u	Asn
1220						1225					1230			
Al a	Asp	Leu	Al a	G y	G u	Leu	Arg	Val	Leu	G y	G n	Al a	Lys	G n
1235						1240					1245			
G u	Val	G u	Hi s	Lys	Lys	Lys	Lys	Leu	G u	Al a	G n	Val	G n	G u
1250						1255					1260			
Leu	G n	Ser	Lys	Cys	Ser	Asp	G y	G u	Arg	Al a	Arg	Al a	G u	Leu
1265						1270					1275			
Asn	Asp	Lys	Val	Hi s	Lys	Leu	G n	Asn	G u	Val	G u	Ser	Val	Thr
1280						1285					1290			
G y	Met	Leu	Asn	G u	Al a	G u	G y	Lys	Al a	I l e	Lys	Leu	Al a	Lys
1295						1300					1305			
Asp	Val	Al a	Ser	Leu	Ser	Ser	G n	Leu	G n	Asp	Thr	G n	G u	Leu
1310						1315					1320			
Leu	G n	G u	G u	Thr	Arg	G n	Lys	Leu	Asn	Val	Ser	Thr	Lys	Leu
1325						1330					1335			
Arg	G n	Leu	G u	G u	G u	Arg	Asn	Ser	Leu	G n	Asp	G n	Leu	Asp
1340						1345					1350			
G u	G u	Met	G u	Al a	Lys	G n	Asn	Leu	G u	Arg	Hi s	I l e	Ser	Thr
1355						1360					1365			
Leu	Asn	I l e	G n	Leu	Ser	Asp	Ser	Lys	Lys	Lys	Leu	G n	Asp	Phe
1370						1375					1380			
Al a	Ser	Thr	Val	G u	Al a	Leu	G u	G u	G y	Lys	Lys	Arg	Phe	G n
1385						1390					1395			
Lys	G u	I l e	G u	Asn	Leu	Thr	G n	G n	Tyr	G u	G u	Lys	Al a	Al a
1400						1405					1410			
Al a	Tyr	Asp	Lys	Leu	G u	Lys	Thr	Lys	Asn	Arg	Leu	G n	G n	G u
1415						1420					1425			

N3027PCT\_sequ.list.txt

Leu	Asp	Asp	Leu	Val	Val	Asp	Leu	Asp	Asn	Gln	Arg	Gln	Leu	Val
	1430					1435					1440			
Ser	Asn	Leu	Glu	Lys	Lys	Gln	Arg	Lys	Phe	Asp	Gln	Leu	Leu	Ala
	1445					1450					1455			
Glu	Glu	Lys	Asn	Ile	Ser	Ser	Lys	Tyr	Ala	Asp	Glu	Arg	Asp	Arg
	1460					1465					1470			
Ala	Glu	Ala	Glu	Ala	Arg	Glu	Lys	Glu	Thr	Lys	Ala	Leu	Ser	Leu
	1475					1480					1485			
Ala	Arg	Ala	Leu	Glu	Glu	Ala	Leu	Glu	Ala	Lys	Glu	Glu	Leu	Glu
	1490					1495					1500			
Arg	Thr	Asn	Lys	Met	Leu	Lys	Ala	Glu	Met	Glu	Asp	Leu	Val	Ser
	1505					1510					1515			
Ser	Lys	Asp	Asp	Val	Gly	Lys	Asn	Val	His	Glu	Leu	Glu	Lys	Ser
	1520					1525					1530			
Lys	Arg	Ala	Leu	Glu	Thr	Gln	Met	Glu	Glu	Met	Lys	Thr	Gln	Leu
	1535					1540					1545			
Glu	Glu	Leu	Glu	Asp	Glu	Leu	Gln	Ala	Thr	Glu	Asp	Ala	Lys	Leu
	1550					1555					1560			
Arg	Leu	Glu	Val	Asn	Met	Gln	Ala	Leu	Lys	Gly	Gln	Phe	Glu	Arg
	1565					1570					1575			
Asp	Leu	Gln	Ala	Arg	Asp	Glu	Gln	Asn	Glu	Glu	Lys	Arg	Arg	Gln
	1580					1585					1590			
Leu	Gln	Arg	Gln	Leu	His	Glu	Tyr	Glu	Thr	Glu	Leu	Glu	Asp	Glu
	1595					1600					1605			
Arg	Lys	Gln	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Lys	Lys	Lys	Leu	Glu
	1610					1615					1620			
Gly	Asp	Leu	Lys	Asp	Leu	Glu	Leu	Gln	Ala	Asp	Ser	Ala	Ile	Lys
	1625					1630					1635			
Gly	Arg	Glu	Glu	Ala	Ile	Lys	Gln	Leu	Arg	Lys	Leu	Gln	Ala	Gln
	1640					1645					1650			
Met	Lys	Asp	Phe	Gln	Arg	Glu	Leu	Glu	Asp	Ala	Arg	Ala	Ser	Arg
	1655					1660					1665			
Asp	Glu	Ile	Phe	Ala	Thr	Ala	Lys	Glu	Asn	Glu	Lys	Lys	Ala	Lys
	1670					1675					1680			

N3027PCT\_sequ.list.txt

Ser Leu Gu Ala Asp Leu Met Gn Leu Gn Gu Asp Leu Ala Ala  
1685 1690 1695

Ala Gu Arg Ala Arg Lys Gn Ala Asp Leu Gu Lys Gu Gu Leu  
1700 1705 1710

Ala Gu Gu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gn  
1715 1720 1725

Asp Gu Lys Arg Arg Leu Gu Ala Arg Ile Ala Gn Leu Gu Gu  
1730 1735 1740

Gu Leu Gu Gu Gu Gn Gly Asn Met Gu Ala Met Ser Asp Arg  
1745 1750 1755

Val Arg Lys Ala Thr Gn Gn Ala Gu Gn Leu Ser Asn Gu Leu  
1760 1765 1770

Ala Thr Gu Arg Ser Thr Ala Gn Lys Asn Gu Ser Ala Arg Gn  
1775 1780 1785

Gn Leu Gu Arg Gn Asn Lys Gu Leu Arg Ser Lys Leu His Gu  
1790 1795 1800

Met Gu Gly Ala Val Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala  
1805 1810 1815

Leu Gu Ala Lys Ile Ala Gn Leu Gu Gu Gn Val Gu Gn Gu  
1820 1825 1830

Ala Arg Gu Lys Gn Ala Ala Thr Lys Ser Leu Lys Gn Lys Asp  
1835 1840 1845

Lys Lys Leu Lys Gu Ile Leu Leu Gn Val Gu Asp Gu Arg Lys  
1850 1855 1860

Met Ala Gu Gn Tyr Lys Gu Gn Ala Gu Lys Gly Asn Ala Arg  
1865 1870 1875

Val Lys Gn Leu Lys Arg Gn Leu Gu Gu Ala Gu Gu Gu Ser  
1880 1885 1890

Gn Arg Ile Asn Ala Asn Arg Arg Lys Leu Gn Arg Gu Leu Asp  
1895 1900 1905

Gu Ala Thr Gu Ser Asn Gu Ala Met Gly Arg Gu Val Asn Ala  
1910 1915 1920

Leu Lys Ser Lys Leu Arg Gly Pro Pro Pro Gn Gu Thr Ser Gn  
1925 1930 1935

<210> 79  
 <211> 6942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(6942)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SM2B

```

<400> 79
gggagatttg gacgctccgg cctgggaggt gcgtcagatc cgagctcgcc atccagtttc 60
ctctccacta gtccccccag ttggagatct gggaccaaca aggcaccatg gcgcagaagg 120
gccaactcag tgacgatgag aagttcctct ttgtggacaa aaacttcatc aacagcccag 180
tggcccaggc tgactgggccc gccaagagac tcgtctgggt cccctcggag aagcagggct 240
tcgaggcagc cagcattaag gaggagaagg gggatgaggt ggttgtggag ctggtggaga 300
atggcaagaa ggtcacggtt gggaaagatg acatccagaa gatgaacca cccaagttct 360
ccaagggtgga ggacatggcg gagctgacgt gcctcaacga agcctccgtg ctacacaacc 420
tgagggagcg gtacttctca gggctaatat atacgtactc tggcctcttc tgcgtggtgg 480
tcaaccctta taaacacctg cccatctact cggagaagat cgtcgacatg tacaagggca 540
agaagaggca cgagatgccg cctcacatct acgccatcgc agacacggcc taccggagca 600
tgcttcaaga tcgggaggac cagttcatctc tatgcacagg cgagtctgga gccgggaaaa 660
ccgaaaacac caagaaggctc attcagtagc ttggccgtggt ggcctcctcc cacaagggca 720
agaaagacac aagtatcacg caaggcccat cttttgccta cggagagctg gaaaagcagc 780
ttctacaagc aaacccgat tctggaggctt tcggcaacgc caaacagtg aagaacgaca 840
actcctcacg attcggcaaa ttcatccgca tcaacttcta cgtcacgggt t acatcgtgg 900
gagccaacat tgagacctat ctgctagaaa aatcacgggc aattcgccaa gccagagacg 960
agaggacatt ccacatcttt tactacatga ttgctggagc caaggagaag atgagaagtg 1020
acttgctttt ggagggcttc aacaactaca ccttctctc caatggcttt gtgccatcc 1080
cagcagccca ggatgatgag atgttccagg aaaccgtgga ggccatggca atcatgggtt 1140
tcagcgagga ggagcagcta tccatattga aggtggtatc atcggctctg cagcttggaa 1200
atatcgtctt caagaaggaa agaaacacag accaggcgtc catgccagat aacacagctg 1260
ctcagaaaagt ttgccacctc atgggaattat atgtgacaga ttccaccaga tccatcctca 1320
ctcctcgtat caaggttggg cgagatgtgg tacagaaaagc tcagacaaaa gaacaggctg 1380
actttgctgt agaggctttg gccaaggcaa catatgagcg ccttttccgc tggatactca 1440
cccgcgtgaa caaagccctg gacaagacct atcggcaagg ggcttcttct ctggggatcc 1500
tggatatagc tggatttgag atctttgagg tgaactcctt cgagcagctg tgcataact 1560
acaccaacga gaagctgcag cagctcttca accacacat gtatcatcctg gagcaggagg 1620
agtaccagcg cgagggcata gagtggaact tcatcgactt tgggctggac ctacagccct 1680

```

N3027PCT\_sequ. list.txt

gcat cgagct	cat cgagcga	ccgaacaacc	ct ccaggt gt	gct ggccct g	ct ggacgagg	1740
aat gct ggt t	ccccaaagcc	acggacaagt	ct t t cgt gga	gaagct gt gc	acggagcagg	1800
gcagccaccc	caagt t ccag	aagcccaagc	agct caagga	caagact gag	t t ct ccat ca	1860
t ccat t at gc	t gggaaggt g	gact at aat g	cgagt gcct g	gct gaccaag	aat at ggacc	1920
cgct gaat ga	caacgt gact	t ccct gct ca	at gcct cct c	cgacaagt t t	gt ggccgacc	1980
t gt ggaagga	cgt ggaccgc	at cgt gggcc	t ggaccagat	ggccaagat g	acggagagct	2040
cgct gcccag	cgcct ccaag	accaagaagg	gcat gt t ccg	cacagt gggg	cagct gt aca	2100
aggagcagct	gggcaagct g	at gaccacgc	t acgcaacac	cacgcccac	t t cgt gcgct	2160
gcat cat ccc	caaccacgag	aagaggt ccg	gcaagct gga	t gcgt t cct g	gt gct ggagc	2220
agct gcggt g	caat ggggt g	ct ggaaggca	t t cgcat ct g	ccggcagggc	t t ccccaacc	2280
ggat cgt ct t	ccaggagt t c	cgccaacgct	acgagat cct	ggcggcgaat	gccat cccca	2340
aaggct t cat	ggacgggaag	caggcct gca	t t ct cat gat	caaagccct g	gaact t gacc	2400
ccaact t at a	caggat aggg	cagagcaaaa	t ct t ct t ccg	aact ggcgt c	ct ggcccacc	2460
t agaggagga	gcgagat t t g	aagat caccg	at gt cat cat	ggcct t ccag	gcgat gt gt c	2520
gt ggct act t	ggccagaaaag	gct t t t gcc	agaggcagca	gcagct gacc	gccat gaagg	2580
t gat t cagag	gaact gcgcc	gcct acct ca	agct gcggaa	ct ggcagt gg	t ggaggct t t	2640
t caccaaagt	gaagccact g	ct gcaggt ga	cacggcagga	ggaggagat g	caggccaagg	2700
aggat gaact	gcagaagacc	aaggagcggc	agcagaaggc	agagaat gag	ct t aaggagc	2760
t ggaacagaa	gcact cgcag	ct gaccgagg	agaagaacct	gct acaggaa	cagct gcagg	2820
cagagacaga	gct gt at gca	gaggct gagg	agat gcgggt	gcggct ggcg	gccaagaagc	2880
aggagct gga	ggagat act g	cat gagat gg	aggcccgcct	ggaggaggag	gaagacaggg	2940
gccagcagct	acaggct gaa	aggaagaaga	t ggcccagca	gat gct ggac	ct t gaagaac	3000
agct ggagga	ggaggaagct	gccaggcaga	agct gcaact	t gagaaggt c	acggct gagg	3060
ccaagat caa	gaaact ggag	gat gagat cc	t ggt cat gga	t gat cagaac	aat aaact at	3120
caaaagaacg	aaaact cct t	gaggagagga	t t agt gact t	aacgacaaat	ct t gcagaag	3180
aggaagaaaa	ggccaagaat	ct t accaagc	t gaaaaacaa	gcat gaat ct	at gat t t cag	3240
aact ggaagt	gcggct aaag	aaggaagaga	agagccgaca	ggagct ggag	aagct gaaac	3300
ggaagct gga	gggt gat gcc	agcgact t cc	acgagcagat	cgct gacct c	caggcgcaga	3360
t cgcagagct	caagat gcag	ct ggccaaga	aggaggagga	gct gcaggcg	gccct ggcca	3420
ggct t gacga	t gaaat cgct	cagaagaaca	at gccct gaa	gaagat ccgg	gagct ggagg	3480
gccacat ct c	agacct ccag	gaggacct gg	act cagagcg	ggccgccagg	aacaaggct g	3540
aaaagcagaa	gcgagacct c	ggcgaggagc	t ggaggccct	aaagacagag	ct ggaagaca	3600
cact ggacag	cacagccact	cagcaggagc	t cagggccaa	gagggagcag	gaggt gacgg	3660
t gct gaagaa	ggccct ggat	gaagagacgc	ggc cccat ga	ggct caggt c	caggagat ga	3720
ggcagaaaca	cgcacaggcg	gt ggaggagc	t cacagagca	gct t gagcag	t t caagaggg	3780

N3027PCT\_sequ. list . . txt

ccaaggcgaa	cct agacaag	aat aagcaga	cgct ggagaa	agagaacgca	gacct ggccg	3840
gggagct gcg	ggt cct gggc	caggccaagc	aggaggt gga	acat aagaag	aagaagct gg	3900
aggcgcaggt	gcaggagct g	cagt ccaagt	gcagcgat gg	ggagcgggcc	cgggcggagc	3960
t caat gacaa	agt ccacaag	ct gcagaat g	aagt t gagag	cgt cacaggg	at gct t aacg	4020
aggccgaggg	gaaggccat t	aagct ggcca	aggacgt ggc	gt ccct cagt	t cccagct cc	4080
aggacaccca	ggagct gct t	caagaagaaa	cccggcagaa	gct caacgt g	t ct acgaagc	4140
t gcgccagct	ggaggaggag	cgaacagcc	t gcaagacca	gct ggacgag	gagat ggagg	4200
ccaagcagaa	cct ggagcgc	cacat ct cca	ct ct caacat	ccagct ct cc	gact cgaaga	4260
agaagct gca	ggact t t gcc	agcaccgt gg	aagct ct gga	agaggggaag	aagaggt t cc	4320
agaaggagat	cgagaacct c	accagcagt	acgaggagaa	ggcggccgct	t at gat aaac	4380
t ggaaaagac	caagaacagg	ct t cagcagg	agct ggacga	cct ggt t gt t	gat t t ggaca	4440
accagcggca	act cgt gt cc	aacct ggaaa	agaagcagag	gaaat t t gat	cagt t gt t ag	4500
ccgaggagaa	aaacat ct ct	t ccaaat acg	cggat gagag	ggacagagct	gaggcagaag	4560
ccagggagaa	ggaaaccaag	gccct gt ccc	t ggct cgggc	cct t gaagag	gcct t ggaag	4620
ccaaagagga	act cgagcgg	accaacaaaa	t gct caaagc	cgaaat ggaa	gacct ggt ca	4680
gct ccaagga	t gacgt gggc	aagaacgt cc	at gagct gga	gaagt ccaag	cgggccct gg	4740
agacccagat	ggaggagat g	aagacgcagc	t ggaagagct	ggaggacgag	ct gcaagcca	4800
cggaggacgc	caaact gcgg	ct ggaagt ca	acat gcaggc	gct caagggc	cagt t cgaaa	4860
gggat ct cca	agcccgggac	gagcagaat g	aggagaagag	gaggcaact g	cagagacagc	4920
t t cacgagt a	t gagacggaa	ct ggaagacg	agcgaaagca	acgt gccct g	gcagct gcag	4980
caaagaagaa	gct ggaaggg	gacct gaaag	acct ggagct	t caggccgac	t ct gccat ca	5040
aggggagggg	ggaagccat c	aagcagct ac	gcaaact gca	ggct cagat g	aaggact t t c	5100
aaagagagct	ggaagat gcc	cgt gcct cca	gagat gagat	ct t t gccaca	gccaaagaga	5160
at gagaagaa	agccaagagc	t t ggaagcag	acct cat gca	gct acaagag	gacct cgccg	5220
ccgct gagag	ggct cgcaaa	caagcggacc	t cgagaagga	ggaact ggca	gaggagct gg	5280
ccagt agcct	gt cggggaagg	aacgcact cc	aggacgagaa	gcgccgcct g	gaggcccgga	5340
t cgcccagct	ggaggaggag	ct ggaggagg	agcagggcaa	cat ggaggcc	at gagcgacc	5400
gggt ccgcaa	agccacacag	caggccgagc	agct cagcaa	cgagct ggcc	acagagcgca	5460
gcacggccca	gaagaat gag	agt gcccggc	agcagct cga	gcggcagaac	aaggagct cc	5520
ggagcaagct	ccacgagat g	gagggggccg	t caagt ccaa	gt t caagt cc	accat cgcg	5580
cgct ggaggc	caagat t gca	cagct ggagg	agcaggt cga	gcaggaggcc	agagagaaac	5640
aggcggccac	caagt cgct g	aagcagaaa	acaagaagct	gaaggaaat c	t t gct gcagg	5700
t ggaggacga	gcgcaagat g	gccgagcagt	acaaggagca	ggcagagaaa	ggcaat gcc	5760
gggt caagca	gct caagagg	cagct ggagg	aggcagagga	ggagt cccag	cgcat caacg	5820

N3027PCT\_sequ.list.txt

```

ccaaccgcag gaagctgcag cgggagctgg atgaggccac ggagagcaac gaggccatgg 5880
gccgcgaggt gaacgcactc aagagcaagc tcagagggcc ccccccacag gaaacttcgc 5940
agtgatgcac caggcgagga aacgagacct ctttcgttcc ttctagaagg tctggaggac 6000
gtagagttat tgaaaatgca gatggttctg aggaggaaac ggacactcga gacgcagact 6060
tcaatggaac caaggccagt gaataagcaa ctttctacag ttttgcacca cggcaagaaa 6120
acaaaaaacc aaaacaaaca aacaaaaaaa acccaacaac aaccagaac aaagcaaaac 6180
ccagcagact gtacttagca ttgtctaat ccatctcaa attccaaat a t c acagacac 6240
ccctcacaca aggaatat aa aaaccaccac cctccagcct gggcaacgt a gt aaacct c 6300
atctatacaa gaatttaaaa at aagctggg cgtggtggt a cacacctgt g gtcccagct a 6360
ctaggagggc tgagccagga agaacgctcc agcccaggac ttcgaggct g caatgagct a 6420
taattgcatc attgcactcc agcctgggca acagagaccc tgtctcaacc accaccacca 6480
ccaccacccc tactaccct gtattcaagg taaaaattga agtttgtat g atgt aagaga 6540
tgagaaaaac ccaacaggaa acacagacac atcctccagt tctatcaat g gat t gt gcag 6600
aactgagtt tttagaaaaa catatccacg gt aaccggt c cctggcaat t ctgtttacat 6660
gaaatgggga gaaagtcacc gaaatgggt g ccgccggccc ccactcccaa t t cat t ccct 6720
aacctgcaaa cctttccaac ttctcacgt c aggcctttga gaattctttc cccctctcct 6780
ggtttccaca ctcagacac gcacagttca ccaagtgcct tctgtagtca catgaattga 6840
aaaggagacg ctgctccac ggaggggagc aggaatgctg cactgtttac accctgactg 6900
tgcttaaaaa cactttcact aataaatggt tat aatcac aa 6942

```

<210> 80  
 <211> 1945  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1945)  
 <223> myosin, heavy chain 11, smooth muscle (MYH11), transcript variant SM2B

<400> 80

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
1          5          10
Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
20          25          30
Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
35          40          45
Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
50          55          60

```

N3027PCT\_sequ.list.txt

Asn 65	Gly	Lys	Lys	Val	Thr 70	Val	Gly	Lys	Asp 75	Asp	Ile	Gln	Lys	Met	Asn 80
Pro	Pro	Lys	Phe	Ser 85	Lys	Val	Glu	Asp	Met 90	Ala	Glu	Leu	Thr	Cys 95	Leu
Asn	Glu	Ala	Ser 100	Val	Leu	His	Asn	Leu 105	Arg	Glu	Arg	Tyr	Phe 110	Ser	Gly
Leu	Ile	Tyr 115	Thr	Tyr	Ser	Gly	Leu 120	Phe	Cys	Val	Val	Val 125	Asn	Pro	Tyr
Lys	His 130	Leu	Pro	Ile	Tyr	Ser 135	Glu	Lys	Ile	Val	Asp 140	Met	Tyr	Lys	Gly
Lys 145	Lys	Arg	His	Glu	Met 150	Pro	Pro	His	Ile	Tyr 155	Ala	Ile	Ala	Asp	Thr 160
Ala	Tyr	Arg	Ser	Met 165	Leu	Gln	Asp	Arg	Glu 170	Asp	Gln	Ser	Ile	Leu 175	Cys
Thr	Gly	Glu	Ser 180	Gly	Ala	Gly	Lys	Thr 185	Glu	Asn	Thr	Lys	Lys 190	Val	Ile
Gln	Tyr	Leu 195	Ala	Val	Val	Ala	Ser 200	Ser	His	Lys	Gly	Lys 205	Lys	Asp	Thr
Ser	Ile 210	Thr	Gln	Gly	Pro	Ser 215	Phe	Ala	Tyr	Gly	Glu 220	Leu	Glu	Lys	Gln
Leu 225	Leu	Gln	Ala	Asn	Pro 230	Ile	Leu	Glu	Ala	Phe 235	Gly	Asn	Ala	Lys	Thr 240
Val	Lys	Asn	Asp	Asn 245	Ser	Ser	Arg	Phe	Gly 250	Lys	Phe	Ile	Arg	Ile 255	Asn
Phe	Asp	Val	Thr 260	Gly	Tyr	Ile	Val	Gly 265	Ala	Asn	Ile	Glu	Thr 270	Tyr	Leu
Leu	Glu	Lys 275	Ser	Arg	Ala	Ile	Arg 280	Gln	Ala	Arg	Asp	Glu 285	Arg	Thr	Phe
His	Ile 290	Phe	Tyr	Tyr	Met	Ile 295	Ala	Gly	Ala	Lys	Glu 300	Lys	Met	Arg	Ser
Asp 305	Leu	Leu	Leu	Glu	Gly 310	Phe	Asn	Asn	Tyr	Thr 315	Phe	Leu	Ser	Asn	Gly 320
Phe	Val	Pro	Ile	Pro 325	Ala	Ala	Gln	Asp	Asp 330	Glu	Met	Phe	Gln	Glu 335	Thr
Val	Glu	Ala	Met	Ala	Ile	Met	Gly	Phe	Ser	Glu	Glu	Glu	Gln	Leu	Ser

340

345

350

```

I l e  L e u  L y s  V a l  V a l  S e r  S e r  V a l  L e u  G l n  L e u  G l y  A s n  I l e  V a l  P h e
355                                     360                                     365

L y s  L y s  G l u  A r g  A s n  T h r  A s p  G l n  A l a  S e r  M e t  P r o  A s p  A s n  T h r  A l a
370                                     375                                     380

A l a  G l n  L y s  V a l  C y s  H i s  L e u  M e t  G l y  I l e  A s n  V a l  T h r  A s p  P h e  T h r
385                                     390                                     395                                     400

A r g  S e r  I l e  L e u  T h r  P r o  A r g  I l e  L y s  V a l  G l y  A r g  A s p  V a l  V a l  G l n
405                                     410                                     415

L y s  A l a  G l n  T h r  L y s  G l u  G l n  A l a  A s p  P h e  A l a  V a l  G l u  A l a  L e u  A l a
420                                     425                                     430

L y s  A l a  T h r  T y r  G l u  A r g  L e u  P h e  A r g  T r p  I l e  L e u  T h r  A r g  V a l  A s n
435                                     440                                     445

L y s  A l a  L e u  A s p  L y s  T h r  H i s  A r g  G l n  G l y  A l a  S e r  P h e  L e u  G l y  I l e
450                                     455                                     460

L e u  A s p  I l e  A l a  G l y  P h e  G l u  I l e  P h e  G l u  V a l  A s n  S e r  P h e  G l u  G l n
465                                     470                                     475                                     480

L e u  C y s  I l e  A s n  T y r  T h r  A s n  G l u  L y s  L e u  G l n  G l n  L e u  P h e  A s n  H i s
485                                     490                                     495

T h r  M e t  P h e  I l e  L e u  G l u  G l n  G l u  G l u  T y r  G l n  A r g  G l u  G l y  I l e  G l u
500                                     505                                     510

T r p  A s n  P h e  I l e  A s p  P h e  G l y  L e u  A s p  L e u  G l n  P r o  C y s  I l e  G l u  L e u
515                                     520                                     525

I l e  G l u  A r g  P r o  A s n  A s n  P r o  P r o  G l y  V a l  L e u  A l a  L e u  L e u  A s p  G l u
530                                     535                                     540

G l u  C y s  T r p  P h e  P r o  L y s  A l a  T h r  A s p  L y s  S e r  P h e  V a l  G l u  L y s  L e u
545                                     550                                     555                                     560

C y s  T h r  G l u  G l n  G l y  S e r  H i s  P r o  L y s  P h e  G l n  L y s  P r o  L y s  G l n  L e u
565                                     570                                     575

L y s  A s p  L y s  T h r  G l u  P h e  S e r  I l e  I l e  H i s  T y r  A l a  G l y  L y s  V a l  A s p
580                                     585                                     590

T y r  A s n  A l a  S e r  A l a  T r p  L e u  T h r  L y s  A s n  M e t  A s p  P r o  L e u  A s n  A s p
595                                     600                                     605

A s n  V a l  T h r  S e r  L e u  L e u  A s n  A l a  S e r  S e r  A s p  L y s  P h e  V a l  A l a  A s p
610                                     615                                     620

```

N3027PCT\_sequ.list.txt

Leu Trp Lys Asp Val Asp Arg Ile Val Gly Leu Asp Gl n Met Ala Lys  
 625 630 635 640  
 Met Thr Gl u Ser Ser Leu Pro Ser Ala Ser Lys Thr Lys Lys Gly Met  
 645 650 655  
 Phe Arg Thr Val Gly Gl n Leu Tyr Lys Gl u Gl n Leu Gly Lys Leu Met  
 660 665 670  
 Thr Thr Leu Arg Asn Thr Thr Pro Asn Phe Val Arg Cys Ile Ile Pro  
 675 680 685  
 Asn His Gl u Lys Arg Ser Gly Lys Leu Asp Ala Phe Leu Val Leu Gl u  
 690 695 700  
 Gl n Leu Arg Cys Asn Gly Val Leu Gl u Gly Ile Arg Ile Cys Arg Gl n  
 705 710 715 720  
 Gly Phe Pro Asn Arg Ile Val Phe Gl n Gl u Phe Arg Gl n Arg Tyr Gl u  
 725 730 735  
 Ile Leu Ala Ala Asn Ala Ile Pro Lys Gly Phe Met Asp Gly Lys Gl n  
 740 745 750  
 Ala Cys Ile Leu Met Ile Lys Ala Leu Gl u Leu Asp Pro Asn Leu Tyr  
 755 760 765  
 Arg Ile Gly Gl n Ser Lys Ile Phe Phe Arg Thr Gly Val Leu Ala His  
 770 775 780  
 Leu Gl u Gl u Gl u Arg Asp Leu Lys Ile Thr Asp Val Ile Met Ala Phe  
 785 790 795 800  
 Gl n Ala Met Cys Arg Gly Tyr Leu Ala Arg Lys Ala Phe Ala Lys Arg  
 805 810 815  
 Gl n Gl n Gl n Leu Thr Ala Met Lys Val Ile Gl n Arg Asn Cys Ala Ala  
 820 825 830  
 Tyr Leu Lys Leu Arg Asn Trp Gl n Trp Trp Arg Leu Phe Thr Lys Val  
 835 840 845  
 Lys Pro Leu Leu Gl n Val Thr Arg Gl n Gl u Gl u Gl u Met Gl n Ala Lys  
 850 855 860  
 Gl u Asp Gl u Leu Gl n Lys Thr Lys Gl u Arg Gl n Gl n Lys Ala Gl u Asn  
 865 870 875 880  
 Gl u Leu Lys Gl u Leu Gl u Gl n Lys His Ser Gl n Leu Thr Gl u Gl u Lys  
 885 890 895

N3027PCT\_sequ.list.txt

Asn Leu Leu Gln Gu Gln Leu Gln Ala Gu Thr Gu Leu Tyr Ala Gu  
 900 905 910  
 Ala Gu Gu Met Arg Val Arg Leu Ala Ala Lys Lys Gln Gu Leu Gu  
 915 920 925  
 Gu Ile Leu His Gu Met Gu Ala Arg Leu Gu Gu Gu Gu Asp Arg  
 930 935 940  
 Gly Gln Gln Leu Gln Ala Gu Arg Lys Lys Met Ala Gln Gln Met Leu  
 945 950 955 960  
 Asp Leu Gu Gu Gln Leu Gu Gu Gu Gu Ala Ala Arg Gln Lys Leu  
 965 970 975  
 Gln Leu Gu Lys Val Thr Ala Gu Ala Lys Ile Lys Lys Leu Gu Asp  
 980 985 990  
 Gu Ile Leu Val Met Asp Asp Gln Asn Asn Lys Leu Ser Lys Gu Arg  
 995 1000 1005  
 Lys Leu Leu Gu Gu Arg Ile Ser Asp Leu Thr Thr Asn Leu Ala  
 1010 1015 1020  
 Gu Gu Gu Gu Lys Ala Lys Asn Leu Thr Lys Leu Lys Asn Lys  
 1025 1030 1035  
 His Gu Ser Met Ile Ser Gu Leu Gu Val Arg Leu Lys Lys Gu  
 1040 1045 1050  
 Gu Lys Ser Arg Gln Gu Leu Gu Lys Leu Lys Arg Lys Leu Gu  
 1055 1060 1065  
 Gly Asp Ala Ser Asp Phe His Gu Gln Ile Ala Asp Leu Gln Ala  
 1070 1075 1080  
 Gln Ile Ala Gu Leu Lys Met Gln Leu Ala Lys Lys Gu Gu Gu  
 1085 1090 1095  
 Leu Gln Ala Ala Leu Ala Arg Leu Asp Asp Gu Ile Ala Gln Lys  
 1100 1105 1110  
 Asn Asn Ala Leu Lys Lys Ile Arg Gu Leu Gu Gly His Ile Ser  
 1115 1120 1125  
 Asp Leu Gln Gu Asp Leu Asp Ser Gu Arg Ala Ala Arg Asn Lys  
 1130 1135 1140  
 Ala Gu Lys Gln Lys Arg Asp Leu Gly Gu Gu Leu Gu Ala Leu  
 1145 1150 1155

Lys Thr 1160 G u Leu G u Asp Thr 1165 Leu Asp Ser Thr Ala 1170 Thr G n G n  
 G u Leu 1175 Arg Ala Lys Arg G u 1180 G n G u Val Thr Val 1185 Leu Lys Lys  
 Ala Leu 1190 Asp G u G u Thr Arg 1195 Ser His G u Ala G n 1200 Val G n G u  
 Met Arg 1205 G n Lys His Ala G n 1210 Ala Val G u G u Leu 1215 Thr G u G n  
 Leu G u 1220 G n Phe Lys Arg Ala 1225 Lys Ala Asn Leu Asp 1230 Lys Asn Lys  
 G n Thr 1235 Leu G u Lys G u Asn 1240 Ala Asp Leu Ala Gly 1245 G u Leu Arg  
 Val Leu 1250 Gly G n Ala Lys G n 1255 G u Val G u His Lys 1260 Lys Lys Lys  
 Leu G u 1265 Ala G n Val G n G u 1270 Leu G n Ser Lys Cys 1275 Ser Asp Gly  
 G u Arg 1280 Ala Arg Ala G u Leu 1285 Asn Asp Lys Val His 1290 Lys Leu G n  
 Asn G u 1295 Val G u Ser Val Thr 1300 Gly Met Leu Asn G u 1305 Ala G u Gly  
 Lys Ala 1310 Ile Lys Leu Ala Lys 1315 Asp Val Ala Ser Leu 1320 Ser Ser G n  
 Leu G n 1325 Asp Thr G n G u Leu 1330 Leu G n G u G u Thr 1335 Arg G n Lys  
 Leu Asn 1340 Val Ser Thr Lys Leu 1345 Arg G n Leu G u G u 1350 G u Arg Asn  
 Ser Leu 1355 G n Asp G n Leu Asp 1360 G u G u Met G u Ala 1365 Lys G n Asn  
 Leu G u 1370 Arg His Ile Ser Thr 1375 Leu Asn Ile G n Leu 1380 Ser Asp Ser  
 Lys Lys 1385 Lys Leu G n Asp Phe 1390 Ala Ser Thr Val G u 1395 Ala Leu G u  
 G u Gly 1400 Lys Lys Arg Phe G n 1405 Lys G u Ile G u Asn 1410 Leu Thr G n  
 G n Tyr G u G u Lys Ala Ala Ala Tyr Asp Lys Leu G u Lys Thr

1415															
Lys	Asn	Arg	Leu	Gln	Gln	Glu	Leu	Asp	Asp	Leu	Val	Val	Asp	Leu	
1430						1435					1440				
Asp	Asn	Gln	Arg	Gln	Leu	Val	Ser	Asn	Leu	Glu	Lys	Lys	Gln	Arg	
1445						1450					1455				
Lys	Phe	Asp	Gln	Leu	Leu	Ala	Glu	Glu	Lys	Asn	Ile	Ser	Ser	Lys	
1460						1465					1470				
Tyr	Ala	Asp	Glu	Arg	Asp	Arg	Ala	Glu	Ala	Glu	Ala	Arg	Glu	Lys	
1475						1480					1485				
Glu	Thr	Lys	Ala	Leu	Ser	Leu	Ala	Arg	Ala	Leu	Glu	Glu	Ala	Leu	
1490						1495					1500				
Glu	Ala	Lys	Glu	Glu	Leu	Glu	Arg	Thr	Asn	Lys	Met	Leu	Lys	Ala	
1505						1510					1515				
Glu	Met	Glu	Asp	Leu	Val	Ser	Ser	Lys	Asp	Asp	Val	Gly	Lys	Asn	
1520						1525					1530				
Val	His	Glu	Leu	Glu	Lys	Ser	Lys	Arg	Ala	Leu	Glu	Thr	Gln	Met	
1535						1540					1545				
Glu	Glu	Met	Lys	Thr	Gln	Leu	Glu	Glu	Leu	Glu	Asp	Glu	Leu	Gln	
1550						1555					1560				
Ala	Thr	Glu	Asp	Ala	Lys	Leu	Arg	Leu	Glu	Val	Asn	Met	Gln	Ala	
1565						1570					1575				
Leu	Lys	Gly	Gln	Phe	Glu	Arg	Asp	Leu	Gln	Ala	Arg	Asp	Glu	Gln	
1580						1585					1590				
Asn	Glu	Glu	Lys	Arg	Arg	Gln	Leu	Gln	Arg	Gln	Leu	His	Glu	Tyr	
1595						1600					1605				
Glu	Thr	Glu	Leu	Glu	Asp	Glu	Arg	Lys	Gln	Arg	Ala	Leu	Ala	Ala	
1610						1615					1620				
Ala	Ala	Lys	Lys	Lys	Leu	Glu	Gly	Asp	Leu	Lys	Asp	Leu	Glu	Leu	
1625						1630					1635				
Gln	Ala	Asp	Ser	Ala	Ile	Lys	Gly	Arg	Glu	Glu	Ala	Ile	Lys	Gln	
1640						1645					1650				
Leu	Arg	Lys	Leu	Gln	Ala	Gln	Met	Lys	Asp	Phe	Gln	Arg	Glu	Leu	
1655						1660					1665				
Glu	Asp	Ala	Arg	Ala	Ser	Arg	Asp	Glu	Ile	Phe	Ala	Thr	Ala	Lys	
1670						1675					1680				

N3027PCT\_sequ.list.txt

G u	Asn	G u	Lys	Lys	Al a	Lys	Ser	Leu	G u	Al a	Asp	Leu	Met	G n
	1685					1690					1695			
Leu	G n	G u	Asp	Leu	Al a	Al a	Al a	G u	Arg	Al a	Arg	Lys	G n	Al a
	1700					1705					1710			
Asp	Leu	G u	Lys	G u	G u	Leu	Al a	G u	G u	Leu	Al a	Ser	Ser	Leu
	1715					1720					1725			
Ser	G y	Arg	Asn	Al a	Leu	G n	Asp	G u	Lys	Arg	Arg	Leu	G u	Al a
	1730					1735					1740			
Arg	I l e	Al a	G n	Leu	G u	G u	G u	Leu	G u	G u	G u	G n	G y	Asn
	1745					1750					1755			
Met	G u	Al a	Met	Ser	Asp	Arg	Val	Arg	Lys	Al a	Thr	G n	G n	Al a
	1760					1765					1770			
G u	G n	Leu	Ser	Asn	G u	Leu	Al a	Thr	G u	Arg	Ser	Thr	Al a	G n
	1775					1780					1785			
Lys	Asn	G u	Ser	Al a	Arg	G n	G n	Leu	G u	Arg	G n	Asn	Lys	G u
	1790					1795					1800			
Leu	Arg	Ser	Lys	Leu	H i s	G u	Met	G u	G y	Al a	Val	Lys	Ser	Lys
	1805					1810					1815			
Phe	Lys	Ser	Thr	I l e	Al a	Al a	Leu	G u	Al a	Lys	I l e	Al a	G n	Leu
	1820					1825					1830			
G u	G u	G n	Val	G u	G n	G u	Al a	Arg	G u	Lys	G n	Al a	Al a	Thr
	1835					1840					1845			
Lys	Ser	Leu	Lys	G n	Lys	Asp	Lys	Lys	Leu	Lys	G u	I l e	Leu	Leu
	1850					1855					1860			
G n	Val	G u	Asp	G u	Arg	Lys	Met	Al a	G u	G n	Tyr	Lys	G u	G n
	1865					1870					1875			
Al a	G u	Lys	G y	Asn	Al a	Arg	Val	Lys	G n	Leu	Lys	Arg	G n	Leu
	1880					1885					1890			
G u	G u	Al a	G u	G u	G u	Ser	G n	Arg	I l e	Asn	Al a	Asn	Arg	Arg
	1895					1900					1905			
Lys	Leu	G n	Arg	G u	Leu	Asp	G u	Al a	Thr	G u	Ser	Asn	G u	Al a
	1910					1915					1920			
Met	G y	Arg	G u	Val	Asn	Al a	Leu	Lys	Ser	Lys	Leu	Arg	G y	Pro
	1925					1930					1935			

N3027PCT\_sequ.list.txt

Pro Pro G n G u Thr Ser G n  
1940 1945

<210> 81  
<211> 5992  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_f eature  
<222> (1)..(5992)  
<223> myosin, heavy chain 13, skeletal muscle (MYH13)

<400> 81  
aaat t gct gt gaccgcagca t ct ct aggaa gacgct t t at t cct gaagga cact gact gt 60  
cact t gggaa ccaagaagcc ct ct gcagt c at gagct ct g acgcagaaat ggccat t t t t 120  
ggagaagcag ct ccct acct ccggaaacca gagaaggaga gaat cgaggc t caaaat cgt 180  
ccat t cgat t ccaagaaagc ct gct t t gt a gcggat aat a aggaaat gt a t gt gaaaggc 240  
at gat ccaga ct agggaaaa t gacaaagt c at agt caaga ccct cgat ga ccggat gct c 300  
act ct gaaca at gaccaggt ct t ccccat g aaccct ccca aat t t gacaa gat cgaggac 360  
at ggccat ga t gact cacct gcat gaacct gct gt t ct gt acaacct caa agagcgct at 420  
gcagcct gga t gat ct acac ct act caggc ct ct t ct gt g t caccgt caa ccct acaag 480  
t ggct gccgg t gt acaagcc cgaggt ggt g gct gcct aca gaggcaaaaa gcgccaggag 540  
gccccgcccc acat ct t ct c cat ct ct gac aat gcct at c agt t cat gct gact gat cga 600  
gacaaccagt ct at cct cat caccggagaa t ccggggct g ggaagact gt gaacaccaag 660  
cgt gt cat cc agt at t t t gc aacaat t gca gt t accgggg acaagaagaa ggagacacag 720  
ccaggcaaaaa t gcagggaac cct agaggat cagat cat cc aggccaaccc act gct ggag 780  
gcct t t ggaa at gccaagac t gt gaggaat gacaact cct caagat t t gg gaagt t cat t 840  
cggat t cat t t t ggagccac aggaaagct g gcat cggcag acat cgaaac t t at ct gt t a 900  
gaaaaat cca gagt gacgt t t caat t at cc agt gagagaa gct at cat at t t t ct accaa 960  
at t at gt caa acaagaagcc agaact aat t gacct gct t c t gat ct ccac caaccct t c 1020  
gact t cccct t cgt gagcca aggagaggt c acggt agcca gt at cgat ga cagt gaagaa 1080  
ct gct ggcga cagat aat gc cat t gacat c ct gggct t ca gct cagagga gaaagt cggg 1140  
at ct acaaac t gacgggagc cgt gat gcat t at gggaaca t gaagt t caa gcagaagcag 1200  
cgt gaggagc aggcggagcc agacggcacc gaagt ggct g acaaagccgg at acct gat g 1260  
ggact gaat t ct gcagaaat gct gaagggc ct gt gct gt c caagggt gaa ggt t ggcaat 1320  
gaat at gt ca ct aaagggca aaat gt ccag caggt gacca at t cggg ggg t gct ct ggcc 1380  
aaagccgt ct acgagaagat gt t cct gt gg at ggt caccg gcat caacca gcagct ggac 1440  
accaagcagc ccaggcagt a ct t cat cggg gt ct t ggaca t t gct ggct t t gagat ct t t 1500  
gat t t caaca gcct ggagca gct gt gcat c aact t cacca at gagaaact gcaacagt t t 1560

N3027PCT\_sequ. list . . txt

t t caaccacc	acat gt t cgt	gct ggagcag	gaagagt aca	agaaggaagg	cat cgagt gg	1620
gagt t cat t g	act t cggaat	ggacct ggct	gcct gcat cg	agct cat cga	gaagcct at g	1680
ggcat ct t ct	ccat cct gga	agaggagt gc	at gt t cccca	aggcaacaga	cacct cct t c	1740
aagaacaagc	t gt at gacca	gcat ct t gga	aaat ccaaca	act t ccagaa	gcccgaagcct	1800
gccaaaggca	aggct gaggc	t cact t ct cg	ct ggt gcact	at gccggcac	cgt ggact ac	1860
aacat cgccg	gct ggct gga	caaaaacaag	gacccct ga	acgagact gt	ggg ggggct g	1920
t accagaagt	ct t cgct gaa	gct t ct ct cc	t t cct t t t t t	ccaact at gc	t ggt gcagag	1980
acaggcgact	ccggaggaag	caagaagggc	gggaagaaga	agggct cct c	t t t ccagacc	2040
gt gt cggccg	t gt t cagga	aaat t t aaac	aaat t gat ga	ct aact t aag	gagcaccac	2100
cct cact t t g	t acgat gt ct	gat t cccaat	gagaccaaga	ct cct ggt gt	gat ggaccac	2160
t act t ggt ca	t gcaccagct	gcgct gt aac	ggggct cct cg	agggcat ccg	gat t t gcagg	2220
aagggat t cc	ccagccggat	cct ct at gct	gact t caagc	agcggg accg	gat cct caat	2280
gccagt gct a	t ccct gaagg	gcagt t cat t	gacagcaaaa	at gcct caga	gaagct cct c	2340
aact ccat cg	at gt ggaccg	ggagcagt t c	aggt t cggca	acaccaaggt	gt t t t t caaa	2400
gct gggct cc	t gggact t t t	ggaggagat g	agagat gaga	agct ggt gac	gct gat gaca	2460
agcacgcagg	cggg gt gcag	ggggg acct g	at gcgggt gg	agt t caagaa	gat gat ggag	2520
aggagggact	ccat ct t ct g	cat ccagt ac	aacat ccgct	ct t t t at gaa	cgt caagcac	2580
t ggccct gga	t gaacct gt t	ct t caaaat c	aagccct gc	t gaagagt gc	agaggccgag	2640
aaggagat gg	ccacat gaa	ggaagact t t	gagaggacca	aggaagaact	ggcccgat ct	2700
gaggct cgcc	ggaaggagct	ggaggagaaa	at ggt ct ccc	t cct gcagga	gaagaat gac	2760
ct ccaat t gc	aggt ccagt c	t gaaacagaa	aat ct gat gg	acgct gagga	acggg gt gaa	2820
ggact cat ca	aaagcaagat	cct act ggaa	gcaaaagt ca	aggagct gac	ggagagat t g	2880
gaagaggaag	aggagat gaa	t t ct gaat t g	gt t gccaaga	agaggaat ct	ggaagat aaa	2940
t gct cct ct c	t caagagaga	cat t gat gac	ct ggagct ga	cct t gacgaa	agt t gaaaag	3000
gagaagcat g	ccacagagaa	caaggt aaag	aat ct t t ccg	aagaaat gac	agcact t gaa	3060
gaaaacat t t	ccaaat t gac	caaagaaaag	aaat ct ct ac	aggaggccca	t cagcaaaca	3120
ct ggat gat c	t t caggt gga	agaagat aaa	gt caat ggt c	t aat caaaat	aaat gccaaag	3180
ct t gaacagc	aaacagat ga	t ct t gagggg	t cct t agagc	aggagaagaa	act gcgggcg	3240
gact t ggaaa	gggcgaagag	gaagct ggaa	ggagat ct ga	aaat gt ccca	ggaat ccat t	3300
at ggat ct ag	aaaat gacaa	gcagcaaat a	gaagagaaat	t gaaaaagaa	ggagt t t gaa	3360
ct cagt cagt	t acaagccaa	aat agat gac	gaacaagt cc	acagt t t gca	gt t t caaaag	3420
aagat t aaag	aact gcaagc	ccgcat agaa	gagct ggagg	aggaaat t ga	agcggaacac	3480
acgct cagag	ccaagat t ga	gaagcagcgc	t cagat ct gg	ccagggaact	ggaggagat c	3540
agcgagaggc	t ggaagaagc	cagt gggggc	act t cagccc	agat t gagat	gaacaagaag	3600
agggaggct g	agt t ccagaa	aat gcgcagg	gacct ggagg	aggccaccct	gcagcacgaa	3660

N3027PCT\_sequ. list . . txt

gccacagcag	ccaccctgag	gaagaagcaa	gcagat agt g	t ggccgagct	t ggggagcag	3720
at t gacaacc	t gcagcgggt	gaagcagaag	ct ggagaagg	agaagagcga	gct gaagat g	3780
gagat t gacg	acat ggccag	caacat cgag	gct ct ct cca	agt caaagag	t aacat agaa	3840
agaacgt gcc	ggacggt aga	agat caat t t	agt gaaat ca	aagccaagga	cgagcaacag	3900
acacagt t ga	t ccat gat ct	gaacat gcag	aaagcaagac	t gcagaccca	aaat ggggag	3960
ct gagccacc	gagt ggaaga	gaaggagt ct	ct gat t t cac	agct gaccaa	aagcaagcag	4020
gccct cacc	agcagct gga	ggagct t aag	aggcaaat gg	aagaagaaac	caaggccaag	4080
aacgccat gg	cgcacgccct	gcagt cct cc	cgccacgact	gt gacct gct	gcgggaacag	4140
t at gaggagg	agcaggaagc	caaggccgag	ct gcagaggg	cgct gt ccaa	ggccaacagt	4200
gaggt t gccc	agt ggaggac	caaat acgag	acggacgcca	t t cagcgcac	agaggagct g	4260
gaggaggcca	agaaaaaact	ggcccagagg	ct ccaggaag	cagaggagaa	cacggagacg	4320
gcgaact cca	agt gcgcat c	gt t ggagaaa	accaagcaga	ggct gcaggg	agaggt ggag	4380
gat ct gat gc	gggat ct gga	gcgct cccac	accgcct gt g	ccacact gga	caagaagcag	4440
aggaact t cg	acaaggt cct	t gcagagt gg	aagcaaaagc	t ggacgaaag	ccaggct gag	4500
t t ggaagct g	ct cagaagga	gt ccaggt ca	ct cagcact g	aact ct t caa	gat gaggaat	4560
gcct at gagg	aggt ggt gga	ccagt t agag	acact gaggc	gagagaacaa	aaat ct gcaa	4620
gaagagat t t	ccgact t aac	t gagcagat t	gcagaaact g	gcaagaat ct	t caggaagcg	4680
gaaaagacca	agaagct agt	ggagcaggaa	aagt cagat c	t gcaggt cgc	ct t agaagaa	4740
gt ggagggt t	cct t ggaaca	cgaggagagc	aagat ct t gc	gcgt gcagct	agagct gacg	4800
caggt gaaat	ccgagct aga	ccgcaaggt c	at t gagaagg	at gaagaaat	cgagcagct a	4860
aaaagaaaca	gccagcgggc	agcagaggcc	ct gcagagcg	t gct ggat gc	t gaaat ccgc	4920
agccggaacg	acgccct gag	gct aaagaag	aagat ggagg	gagacct t aa	t gagat ggag	4980
at t cagct gg	gccact ccaa	ccgccagat g	gcagagaccc	agaagcat ct	gcgcacggt c	5040
cagggccagc	t caaggact c	ccagct gcat	ct cgat gacg	ccct gaggag	caat gaggac	5100
ct caaggagc	agct ggccat	cgt ggagcgc	aggaat ggcc	t cct gct gga	ggagct ggag	5160
gaaat gaagg	t ggccct gga	acagacggag	cggacccgca	ggct gt caga	gcaggagct g	5220
ct ggacgcca	gcgaccgcgt	gcagct cct g	cact cccaga	acacaagcct	gat aaat acc	5280
aagaaaaaac	t ggaggct ga	cat agct cag	t gccaggcag	aggt ggagaa	ct cgat ccag	5340
gagt ccagga	acgcagagga	gaaggccaag	aaggccat ca	cggat gct gc	cat gat ggct	5400
gaggagct aa	agaaggaaca	ggacaccagc	gccacct gg	agcggat gaa	gaagaacct g	5460
gagcagacgg	t gaaggacct	gcagcaccgt	ct agat gagg	ct gaacaact	ggcgct gaag	5520
ggcggaaga	agcagat cca	gaaact ggag	aaccgggt gc	gggagct gga	aaat gagct t	5580
gat gt ggaac	agaagagggg	agct gaagcc	ct gaagggag	cccacaagt a	cgaacgcaaa	5640
gt caaggaga	t gact t acca	ggct gaggag	gaccacaaga	at at cct t ag	gct ccaggac	5700

N3027PCT\_sequ.list.txt

ct ggt ggaca agct gcaggc caaagt gaag tct tacaaga ggcaggct ga ggaggcggag 5760  
gagcaggcca acacgcagct gt ccagat gc cggagagt cc agcat gagct agaggaggcc 5820  
gcggagaggg cggacat cgc t gagt cccag gt caacaagc t gagggccaa gagccgagac 5880  
gt gggcagcc agaagat gga agaat gaggc t cacct gat g ct cgt t gcca t gggacacct 5940  
ccgagagagt ggagggaaaa t gt gt gagaa at aaat t ct c ct aaat act c gg 5992

<210> 82  
<211> 1938  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(1938)  
<223> myosin, heavy chain 13, skeletal muscle (MYH13)  
<400> 82

Met Ser Ser Asp Ala Glu Met Ala Ile Phe Gly Glu Ala Ala Pro Tyr  
1 5 10 15  
Leu Arg Lys Pro Glu Lys Glu Arg Ile Glu Ala Gln Asn Arg Pro Phe  
20 25 30  
Asp Ser Lys Lys Ala Cys Phe Val Ala Asp Asn Lys Glu Met Tyr Val  
35 40 45  
Lys Gly Met Ile Gln Thr Arg Glu Asn Asp Lys Val Ile Val Lys Thr  
50 55 60  
Leu Asp Asp Arg Met Leu Thr Leu Asn Asn Asp Gln Val Phe Pro Met  
65 70 75 80  
Asn Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Met Thr His  
85 90 95  
Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala  
100 105 110  
Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro  
115 120 125  
Tyr Lys Trp Leu Pro Val Tyr Lys Pro Glu Val Val Ala Ala Tyr Arg  
130 135 140  
Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp  
145 150 155 160  
Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Asp Asn Gln Ser Ile Leu  
165 170 175  
Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Asp Lys Lys Lys Glu  
 195 200 205  
 Thr Gln Pro Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile Gln  
 210 215 220  
 Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn  
 225 230 235 240  
 Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala  
 245 250 255  
 Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys  
 260 265 270  
 Ser Arg Val Thr Phe Gln Leu Ser Ser Glu Arg Ser Tyr His Ile Phe  
 275 280 285  
 Tyr Gln Ile Met Ser Asn Lys Lys Pro Glu Leu Ile Asp Leu Leu Leu  
 290 295 300  
 Ile Ser Thr Asn Pro Phe Asp Phe Pro Phe Val Ser Gln Gly Glu Val  
 305 310 315 320  
 Thr Val Ala Ser Ile Asp Asp Ser Glu Glu Leu Leu Ala Thr Asp Asn  
 325 330 335  
 Ala Ile Asp Ile Leu Gly Phe Ser Ser Glu Glu Lys Val Gly Ile Tyr  
 340 345 350  
 Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys Gln  
 355 360 365  
 Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala Asp  
 370 375 380  
 Lys Ala Gly Tyr Leu Met Gly Leu Asn Ser Ala Glu Met Leu Lys Gly  
 385 390 395 400  
 Leu Cys Cys Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly  
 405 410 415  
 Gln Asn Val Gln Gln Val Thr Asn Ser Val Gly Ala Leu Ala Lys Ala  
 420 425 430  
 Val Tyr Glu Lys Met Phe Leu Trp Met Val Thr Arg Ile Asn Gln Gln  
 435 440 445  
 Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile  
 450 455 460

N3027PCT\_sequ.list.txt

Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys Ile  
465 470 475 480

Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe  
485 490 495

Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Glu Phe  
500 505 510

Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu Lys  
515 520 525

Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys  
530 535 540

Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Asp Gln His Leu Gly  
545 550 555 560

Lys Ser Asn Asn Phe Gln Lys Pro Lys Pro Ala Lys Gly Lys Ala Glu  
565 570 575

Ala His Phe Ser Leu Val His Tyr Ala Gly Thr Val Asp Tyr Asn Ile  
580 585 590

Ala Gly Trp Leu Asp Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val  
595 600 605

Gly Leu Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Phe Leu Phe Ser  
610 615 620

Asn Tyr Ala Gly Ala Glu Thr Gly Asp Ser Gly Gly Ser Lys Lys Gly  
625 630 635 640

Gly Lys Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Val Phe Arg  
645 650 655

Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His  
660 665 670

Phe Val Arg Cys Leu Ile Pro Asn Glu Thr Lys Thr Pro Gly Val Met  
675 680 685

Asp His Tyr Leu Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu  
690 695 700

Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu Tyr Ala  
705 710 715 720

Asp Phe Lys Gln Arg Tyr Arg Ile Leu Asn Ala Ser Ala Ile Pro Glu  
725 730 735

N3027PCT\_sequ.list.txt

G l y   G l n   P h e   I l e   A s p   S e r   L y s   A s n   A l a   S e r   G l u   L y s   L e u   L e u   A s n   S e r  
                     740                                    745                                    750

I l e   A s p   V a l   A s p   A r g   G l u   G l n   P h e   A r g   P h e   G l y   A s n   T h r   L y s   V a l   P h e  
                     755                                    760                                    765

P h e   L y s   A l a   G l y   L e u   L e u   G l y   L e u   L e u   G l u   G l u   M e t   A r g   A s p   G l u   L y s  
                     770                                    775                                    780

L e u   V a l   T h r   L e u   M e t   T h r   S e r   T h r   G l n   A l a   V a l   C y s   A r g   G l y   T y r   L e u  
                     785                                    790                                    795                                    800

M e t   A r g   V a l   G l u   P h e   L y s   L y s   M e t   M e t   G l u   A r g   A r g   A s p   S e r   I l e   P h e  
                                     805                                    810                                    815

C y s   I l e   G l n   T y r   A s n   I l e   A r g   S e r   P h e   M e t   A s n   V a l   L y s   H i s   T r p   P r o  
                     820                                    825                                    830

T r p   M e t   A s n   L e u   P h e   P h e   L y s   I l e   L y s   P r o   L e u   L e u   L y s   S e r   A l a   G l u  
                     835                                    840                                    845

A l a   G l u   L y s   G l u   M e t   A l a   T h r   M e t   L y s   G l u   A s p   P h e   G l u   A r g   T h r   L y s  
                     850                                    855                                    860

G l u   G l u   L e u   A l a   A r g   S e r   G l u   A l a   A r g   A r g   L y s   G l u   L e u   G l u   G l u   L y s  
                     865                                    870                                    875                                    880

M e t   V a l   S e r   L e u   L e u   G l n   G l u   L y s   A s n   A s p   L e u   G l n   L e u   G l n   V a l   G l n  
                                     885                                    890                                    895

S e r   G l u   T h r   G l u   A s n   L e u   M e t   A s p   A l a   G l u   G l u   A r g   C y s   G l u   G l y   L e u  
                     900                                    905                                    910

I l e   L y s   S e r   L y s   I l e   L e u   L e u   G l u   A l a   L y s   V a l   L y s   G l u   L e u   T h r   G l u  
                     915                                    920                                    925

A r g   L e u   G l u   G l u   G l u   G l u   G l u   M e t   A s n   S e r   G l u   L e u   V a l   A l a   L y s   L y s  
                     930                                    935                                    940

A r g   A s n   L e u   G l u   A s p   L y s   C y s   S e r   S e r   L e u   L y s   A r g   A s p   I l e   A s p   A s p  
                     945                                    950                                    955                                    960

L e u   G l u   L e u   T h r   L e u   T h r   L y s   V a l   G l u   L y s   G l u   L y s   H i s   A l a   T h r   G l u  
                                     965                                    970                                    975

A s n   L y s   V a l   L y s   A s n   L e u   S e r   G l u   G l u   M e t   T h r   A l a   L e u   G l u   G l u   A s n  
                     980                                    985                                    990

I l e   S e r   L y s   L e u   T h r   L y s   G l u   L y s   L y s   S e r   L e u   G l n   G l u   A l a   H i s   G l n  
                     995                                    1000                                    1005

G n Thr 1010 Leu Asp Asp Leu G n 1015 Val G u G u Asp Lys 1020 Val Asn G y  
 Leu Ile 1025 Lys Ile Asn Ala Lys 1030 Leu G u G n G n Thr 1035 Asp Asp Leu  
 G u G y 1040 Ser Leu G u G n G u 1045 Lys Lys Leu Arg Ala 1050 Asp Leu G u  
 Arg Ala 1055 Lys Arg Lys Leu G u 1060 G y Asp Leu Lys Met 1065 Ser G n G u  
 Ser Ile 1070 Met Asp Leu G u Asn 1075 Asp Lys G n G n Ile 1080 G u G u Lys  
 Leu Lys 1085 Lys Lys G u Phe G u 1090 Leu Ser G n Leu G n 1095 Ala Lys Ile  
 Asp Asp 1100 G u G n Val His Ser 1105 Leu G n Phe G n Lys 1110 Lys Ile Lys  
 G u Leu 1115 G n Ala Arg Ile G u 1120 G u Leu G u G u G u 1125 Ile G u Ala  
 G u His 1130 Thr Leu Arg Ala Lys 1135 Ile G u Lys G n Arg 1140 Ser Asp Leu  
 Ala Arg 1145 G u Leu G u G u Ile 1150 Ser G u Arg Leu G u 1155 G u Ala Ser  
 G y Ala 1160 Thr Ser Ala G n Ile 1165 G u Met Asn Lys Lys 1170 Arg G u Ala  
 G u Phe 1175 G n Lys Met Arg Arg 1180 Asp Leu G u G u Ala 1185 Thr Leu G n  
 His G u 1190 Ala Thr Ala Ala Thr 1195 Leu Arg Lys Lys G n 1200 Ala Asp Ser  
 Val Ala 1205 G u Leu G y G u G n 1210 Ile Asp Asn Leu G n 1215 Arg Val Lys  
 G n Lys 1220 Leu G u Lys G u Lys 1225 Ser G u Leu Lys Met 1230 G u Ile Asp  
 Asp Met 1235 Ala Ser Asn Ile G u 1240 Ala Leu Ser Lys Ser 1245 Lys Ser Asn  
 Ile G u 1250 Arg Thr Cys Arg Thr 1255 Val G u Asp G n Phe 1260 Ser G u Ile  
 Lys Ala Lys Asp G u G n G n Thr G n Leu Ile His Asp Leu Asn



N3027PCT\_sequ.list.txt

Lys	Lys	Leu	Val	Glu	Gln	Glu	Lys	Ser	Asp	Leu	Gln	Val	Ala	Leu
	1535					1540					1545			
Glu	Glu	Val	Glu	Gly	Ser	Leu	Glu	His	Glu	Glu	Ser	Lys	Ile	Leu
	1550					1555					1560			
Arg	Val	Gln	Leu	Glu	Leu	Ser	Gln	Val	Lys	Ser	Glu	Leu	Asp	Arg
	1565					1570					1575			
Lys	Val	Ile	Glu	Lys	Asp	Glu	Glu	Ile	Glu	Gln	Leu	Lys	Arg	Asn
	1580					1585					1590			
Ser	Gln	Arg	Ala	Ala	Glu	Ala	Leu	Gln	Ser	Val	Leu	Asp	Ala	Glu
	1595					1600					1605			
Ile	Arg	Ser	Arg	Asn	Asp	Ala	Leu	Arg	Leu	Lys	Lys	Lys	Met	Glu
	1610					1615					1620			
Gly	Asp	Leu	Asn	Glu	Met	Glu	Ile	Gln	Leu	Gly	His	Ser	Asn	Arg
	1625					1630					1635			
Gln	Met	Ala	Glu	Thr	Gln	Lys	His	Leu	Arg	Thr	Val	Gln	Gly	Gln
	1640					1645					1650			
Leu	Lys	Asp	Ser	Gln	Leu	His	Leu	Asp	Asp	Ala	Leu	Arg	Ser	Asn
	1655					1660					1665			
Glu	Asp	Leu	Lys	Glu	Gln	Leu	Ala	Ile	Val	Glu	Arg	Arg	Asn	Gly
	1670					1675					1680			
Leu	Leu	Leu	Glu	Glu	Leu	Glu	Glu	Met	Lys	Val	Ala	Leu	Glu	Gln
	1685					1690					1695			
Thr	Glu	Arg	Thr	Arg	Arg	Leu	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Ala
	1700					1705					1710			
Ser	Asp	Arg	Val	Gln	Leu	Leu	His	Ser	Gln	Asn	Thr	Ser	Leu	Ile
	1715					1720					1725			
Asn	Thr	Lys	Lys	Lys	Leu	Glu	Ala	Asp	Ile	Ala	Gln	Cys	Gln	Ala
	1730					1735					1740			
Glu	Val	Glu	Asn	Ser	Ile	Gln	Glu	Ser	Arg	Asn	Ala	Glu	Glu	Lys
	1745					1750					1755			
Ala	Lys	Lys	Ala	Ile	Thr	Asp	Ala	Ala	Met	Met	Ala	Glu	Glu	Leu
	1760					1765					1770			
Lys	Lys	Glu	Gln	Asp	Thr	Ser	Ala	His	Leu	Glu	Arg	Met	Lys	Lys
	1775					1780					1785			

N3027PCT\_sequ.list.txt

Asn Leu Glu Gln Thr Val Lys Asp Leu Gln His Arg Leu Asp Glu  
1790 1795 1800

Ala Glu Gln Leu Ala Leu Lys Gly Gly Lys Lys Gln Ile Gln Lys  
1805 1810 1815

Leu Glu Asn Arg Val Arg Glu Leu Glu Asn Glu Leu Asp Val Glu  
1820 1825 1830

Gln Lys Arg Gly Ala Glu Ala Leu Lys Gly Ala His Lys Tyr Glu  
1835 1840 1845

Arg Lys Val Lys Glu Met Thr Tyr Gln Ala Glu Glu Asp His Lys  
1850 1855 1860

Asn Ile Leu Arg Leu Gln Asp Leu Val Asp Lys Leu Gln Ala Lys  
1865 1870 1875

Val Lys Ser Tyr Lys Arg Gln Ala Glu Glu Ala Glu Glu Gln Ala  
1880 1885 1890

Asn Thr Gln Leu Ser Arg Cys Arg Arg Val Gln His Glu Leu Glu  
1895 1900 1905

Glu Ala Ala Glu Arg Ala Asp Ile Ala Glu Ser Gln Val Asn Lys  
1910 1915 1920

Leu Arg Ala Lys Ser Arg Asp Val Gly Ser Gln Lys Met Glu Glu  
1925 1930 1935

<210> 83  
<211> 6831  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(6831)  
<223> myosin, heavy chain 14 (MYH14), transcript variant 1

<400> 83  
ctctttctcc ccaggccgaa gcctcgggac ggccctggaa gccgaccatg gcagccgtga 60  
ccatgtcggg gcccgggcgg aaggcgcccc ccaggccggg cccagtcccc gaggcggccc 120  
agccgttcct gttcacgccc cgcgggcccc gcgcgggtgg cgggcctggc tccggcacct 180  
ccccgcaggt ggagtggacg gcccggcgtc tcgtgtgggt gccttcggag cttcacgggt 240  
tcgaggcggc ggcgctgcgg gacgaaggcg aggaggaggc ggaggtggag ctggcggaga 300  
gcgggaggcg gctgcgactg ccgcgggacc agatccagcg catgaaccg cccaagt tca 360  
gcaaggccga ggacatggcc gagctgacct gcctcaacga ggcctcggc ctgcacaacc 420  
tccgggagcg gtactactcc ggcctcatct acacgtactc cggccttttc tgtgtggtca 480

N3027PCT\_sequ. list.txt

t caacccgt a caagcagct t cccat ct aca cagaagccat t gt ggagat g t accggggca	540
agaagcgcca cgaggt gccacacgt gt acgcagt gac cgagggggcc t at cggagca	600
t gct gcagga t cgt gaggac cagt ccat t c t ct gcaact gg agagt ct gga gct gggaaga	660
cggaaaacac caagaaggt c at ccagt acc t cgcccacgt ggcgt cgt ct ccaaagggca	720
ggaaggagcc ggggt gt cccc gcct ccgt ca gcaccgt gt c t t at ggt gag ct ggagcggc	780
agct gct t ca ggccaacccc at cct agagg cct t t ggcaa t gccaaagaca gt gaagaat g	840
acaact cct c ccgat t cggc aaat t cat cc gcat caact t t gat gt t gcc ggggt acat cg	900
t gggcgccaa cat t gagacc t acct gct gg agaagt cgcg ggccat ccgc caggccaagg	960
acgagt gcag ct t ccacat c t t ct accagc t gct gggggg cgct ggagag cagct caaag	1020
ccgacct cct cct cgagccc t gct cccact accggt t cct gaccaacggg ccgt cat cct	1080
ct cccggcca ggagcgggaa ct ct t ccagg agacgct gga gt cgct gcgg gt cct gggat	1140
t cagccacga ggaaat cat c t ccat gct gc ggat ggt ct c agcagt t ct c cagt t t ggca	1200
acat t gcct t gaagagagaa cggaacaccg at caagccac cat gcct gac aacacagct g	1260
cacagaagct ct gccgcct c t t gggact gg ggggt gacgga t t t ct cccga gcct t gct ca	1320
cccct cgcat caaagt t ggc cgagact at g t gcagaaagc ccagact aag gaacaggct g	1380
act t cgcgct ggaggccct g gccaaaggcca cct acgagcg cct ct t ccgc t ggct ggt t c	1440
t gcgcct caa ccgggcct t g gaccgcagcc cccgccaagg cgcct cct t c ct gggcat cc	1500
t ggacat cgc gggct t t gag at ct t ccagc t gaact cct t cgagcagct c t gcat caact	1560
acaccaacga gaagct gcag cagct ct t ca accacaccat gt t cgt gct g gagcaggagg	1620
agt accagcg t gagggcct c ccct ggacct t cct cgact t t ggcct cgac ct gcagccct	1680
gcat cgacct cat cgagcgg ccggccaacc cccct ggact cct ggccct g ct ggat gagg	1740
agt gct ggt t cccgaaggcc acagacaagt cgt t t gt gga gaaggt agcc caggagcagg	1800
gcggccaccc caagt t ccag cggccgaggc acct gcggga t caggccgac t t cagt gt t c	1860
t ccaact acgc gggcaaggt c gact acaagg ccaacgagt g gct gat gaaa aacat ggacc	1920
ct ct gaat ga caacgt cgca gcct t gct cc accagagcac agaccggct g acggcagaga	1980
t ct ggaaaga cgt ggagggc at cgt ggggc t ggaacaggt gagcagcct g ggcgacggcc	2040
caccaggt gg ccgccccgt cgggggt at gt t ccggacagt gggacagct c t acaaggagt	2100
ccct gagccg cct cat ggcc acact cagca acaccaaccc cagt t t t gt c cgct gcat t g	2160
t cccaacca cgagaagagg gccgggaagc t ggagccacg gct ggt gct g gaccagct t c	2220
gct gcaacgg ggt cct ggag ggcat ccgca t ct gt cgcca gggct t cccc aaccgcat cc	2280
t ct t ccagga gt t ccggcag cgat acgaga t cct gacacc caat gccat c cccaagggct	2340
t cat ggat gg gaagcaggcc t gt gaaaaga t gat ccaggc gct ggaact g gacccaacc	2400
t ct accgct gggacagagc aagat ct t ct t ccgggct gg ggt cct ggcc cagct ggaag	2460
aggagcgaga cct gaaggt c accgacat ca t cgt ct cct t ccaggcagct gcccggggat	2520
acct ggct cg cagggcct t c cagaagcgcc agcagcagca gagcgccct g aggggt gat gc	2580

N3027PCT\_sequ. list . . txt

agcggaact g	cgcgccct ac	ct caagct ga	gacact ggca	gt ggt ggcgg	ct gt t t acca	2640
aggt gaagcc	act gct gcag	gt gacgcggc	aggat gaggt	gct gcaggca	cgggcccagg	2700
agct gcagaa	agt gcaggag	ct acagcagc	agagcgcccc	cgaagt t ggg	gagct ccagg	2760
gccgagt ggc	acagct ggaa	gaggagcgcg	cccgccct ggc	agagcaat t g	cgagcagagg	2820
cagaact gt g	t gcagaggcc	gaggagacgc	gggggaggct	ggcagcccg	aagcaggagc	2880
t ggagct ggt	ggt gt cagag	ct ggaggct c	gcgt gggcga	ggaggaggag	t gcagccgt c	2940
aaat gcaaac	cgagaagaag	aggct gcagc	agcacaat aca	ggagct agag	gcccacct t g	3000
aggct gagga	gggt gcgcgg	cagaagct gc	agct ggagaa	ggt gacgaca	gaggcaaaaa	3060
t gaagaaat t	t gaagaggac	ct gct gct cc	t ggaagacca	gaat t ccaag	ct gagcaagg	3120
agcggaagct	gct ggaagat	cgt ct ggccg	agt t ct cat c	ccaggcagct	gaggaggagg	3180
agaaggt caa	gagcct caat	aagct acggc	t caaat at ga	ggccacaat c	gcagacat gg	3240
aggaccgcct	acggaaggag	gagaagggt c	gccaggagct	ggagaagct g	aagcggaggc	3300
t ggat gggga	gagct cagag	ct gcaggagc	agat ggt gga	gcagcaacag	cgggcagagg	3360
agct gcgggc	ccagct gggc	cggaaggagg	aggagct gca	ggct gccct g	gccagggcag	3420
aagacgaggg	t gggggcccg	gccagct gc	t gaaat ccct	gcgggaggct	caagcagccc	3480
t ggccgaggc	ccaggaggac	ct ggagt ct g	agcgt gt ggc	caggaccaag	gcggagaagc	3540
agcgccggga	cct gggcgag	gagct ggagg	cgct gcgggg	cgagct ggag	gacacgct gg	3600
act ccaccaa	cgcacagcag	gagct ccggt	ccaagaggga	acaggaggt g	acggagct ga	3660
agaagact ct	ggaggaggag	act cgcat cc	acgaggcggc	agt gcaggag	ct gaggcagc	3720
gccacggcca	ggccct gggg	gagct ggcgg	agcagct gga	gcaggccccg	aggggcaaag	3780
gt gcat ggg	gaagaccgg	ct ggccct gg	aggccgaggt	gt ccgagct g	cgggcagaac	3840
t gagcagcct	gcagact gca	cgt caggagg	gt gagcagcg	gaggcgccgc	ct ggagt t ac	3900
agct gcagga	ggt gcagggc	cgggct ggt g	at ggggagag	ggcacgagcg	gaggct gct g	3960
agaagct gca	gcgagcccag	gct gaact gg	agaat gt gt c	t ggggcgct g	aacgaggct g	4020
agt ccaaaac	cat ccgt ct t	agcaaggagc	t gagcagcac	agaagcccag	ct gcacgat g	4080
cccaggagct	gct gcaggag	gagaccagg	cgaaat t ggc	ct t ggggt cc	cggtt gcgag	4140
ccat ggaggc	t gaggcagcc	gggct gcgt g	agcagct gga	ggaggaggca	gct gccaggg	4200
aacgggcggg	ccgt gaact g	cagact gcc	aggcccagct	t t ccgagt gg	cggcggcgcc	4260
aggaggagga	ggcaggggca	ct ggaggcag	gggaggaggc	acggcgccgg	gcagcccggg	4320
aggccgaggc	cct gacccag	cgctt ggcag	aaaagacaga	gaccgt ggat	cggct ggagc	4380
ggggccgccc	ccggct gcag	caggagct gg	acgacgccac	cat ggacct g	gagcagcagc	4440
ggcagct t gt	gagcaccct g	gagaagaagc	agcgcaagt t	t gaccagct t	ct ggcagagg	4500
agaaggcagc	t gt act t cgg	gcagt ggagg	aacgt gagcg	ggccgaggca	gagggccggg	4560
agcgt gaggc	t cgggccct g	t cact gacac	gggcact gga	ggaggagcag	gaggcacgt g	4620

N3027PCT\_sequ. list .txt

aggagct gga gcggcagaac cgggccct gc gggct gagct ggaggcact g ct gagcagca	4680
aggat gacgt cggcaagagc gt gcat gagc t ggaacgagc ct gccgggt a gcagaacagg	4740
cagccaat ga t ct gcgagca caggt gacag aact ggagga t gagct gaca gcggccgagg	4800
at gccaagct gcgt ct ggag gt gact gt gc aggct ct caa gact cagcat gagcgt gacc	4860
t gcagggccg t gat gaggct ggt gaagaga ggcggaggca gct ggccaag cagct gagag	4920
at gcagaggt ggagcgggat gaggagcggga agcagcgcac t ct ggccgt g gct gcccga	4980
agaagct gga gggagagct g gaggagct ga aggct cagat ggcct ct gcc ggccagggca	5040
aggaggaggc ggt gaagcag ct t cgcaaga t gcaggccca gat gaaggag ct at ggcggg	5100
aggt ggagga gacacgcacc t cccgggagg agat ct t ct c ccagaat cgg gaaagt gaaa	5160
agcgcct caa gggcct ggag gct gaggt gc t gcggct gca ggaggaact g gccgcct cgg	5220
accgt gct cg gcggcaggcc cagcaggacc gggat gagat ggcagat gag gt ggccaat g	5280
gt aacct t ag caaggcagcc at t ct ggagg agaagcgt ca gct ggagggg cgcct ggggc	5340
agt t ggagga agagct ggag gaggagcaga gcaact cgga gct gct caat gaccgt acc	5400
gcaagct gct cct gcaggt a gagt cact ga ccacagagct gt cagct gag cgcagt t t ct	5460
cagccaaggc agagagcggg cggcagcagc t ggaacggca gat ccaggag ct acggggac	5520
gcct gggg ga ggaggat gct gggggccgt g cccgccacaa gat gaccat t gct gccct t g	5580
agt ct aagt t ggcccaggct gaggagcagc t agagcaaga gaccagagag cgcct cct ct	5640
ct ggaaagct ggt ggcgaga gct gagaagc ggct t aaaga ggt ggt gct c caggt ggagg	5700
aggagcggag ggt ggct gac cagct ccggg accagct gga gaagggaaac ct t cgagt ca	5760
agcagct gaa gcggcagct g gaggaggccg aggaggaggc at cccgggct caggccggcc	5820
gccggaggct gcagcgt gag ct ggaagat g t cacagagt c ggccgagt cc at gaaccgt g	5880
aagt gaccac act gaggaac cggct t cgac gcggccccct cacct t cacc acccgcacgg	5940
t gcgccaggt ct t ccgact a gaggagggcg t ggcat ccga cgaggaggca gaggaagcac	6000
agcct gggg c t gggccat cc ccggagcct g aggggt cccc accagcccac cccagt gac	6060
cct accct gt ccccagat gc act aacagat ggggcccagc cccct t cct c cct ggacccc	6120
acgggccccct gt cccaggaa ccccgccct c t gact t ct t g ccct t t ggaa at ggt gcagc	6180
act ct ggcat t t at cacccc cacct gggg c ccct gcaacc t cccat caaa ggat gacccc	6240
t aaacacaga ggagcggggc aggcaggag gcaat gact g gagct acct t gct t gt t ggg	6300
ggact gggg a cagt t ggcaa gct gt gt t t c cat cagct cc ct gt cct cct t t ct t ccct c	6360
gt t at t gat c t at agacat t aggaagggag t gagacggct cct ccacat cct cagccag	6420
t gcaacccat t ccct ct gct t ct ct ct ct c t ct ct ct ct c t ccct ccct c t cct t ccct a	6480
ccct ct cacc at ct t t ct t g gcct ct ct ga gggg ct ct ct gt gcat ct t t t t aggaat ct	6540
cgct ct cact ct ct acgt ag ccact ct cct t ccccat t t ct gcgt ccac ccct gaact c	6600
ct gagcgaca gaagccccag gcct ccacca gcct t gaacc ct t gcaaagg ggcaggacaa	6660
ggggacccct ct cact cct g ct gct gccca t gct ct gcc t ccct t ct gg t t gct ct gag	6720

N3027PCT\_sequ.list.txt

gggttcggagc ttccctctgg gactaaagga gtgtccttta ccctcccagc ctccaggctc 6780  
tggcagaaat aaactccaac ccgactggac cataaaaaaa aaaaaaaaaa a 6831

<210> 84  
<211> 2003  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MSC\_FEATURE  
<222> (1)..(2003)  
<223> myosin, heavy chain 14 (MYH14), transcript variant 1

<400> 84

Met Ala Ala Val Thr Met Ser Val Pro Gly Arg Lys Ala Pro Pro Arg  
1 5 10 15

Pro Gly Pro Val Pro Glu Ala Ala Gn Pro Phe Leu Phe Thr Pro Arg  
20 25 30

Gly Pro Ser Ala Gly Gly Gly Pro Gly Ser Gly Thr Ser Pro Gn Val  
35 40 45

Glu Trp Thr Ala Arg Arg Leu Val Trp Val Pro Ser Glu Leu His Gly  
50 55 60

Phe Glu Ala Ala Ala Leu Arg Asp Glu Gly Glu Glu Glu Ala Glu Val  
65 70 75 80

Glu Leu Ala Glu Ser Gly Arg Arg Leu Arg Leu Pro Arg Asp Gn Ile  
85 90 95

Gn Arg Met Asn Pro Pro Lys Phe Ser Lys Ala Glu Asp Met Ala Glu  
100 105 110

Leu Thr Cys Leu Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg  
115 120 125

Tyr Tyr Ser Gly Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val  
130 135 140

Ile Asn Pro Tyr Lys Gn Leu Pro Ile Tyr Thr Glu Ala Ile Val Glu  
145 150 155 160

Met Tyr Arg Gly Lys Lys Arg His Glu Val Pro Pro His Val Tyr Ala  
165 170 175

Val Thr Glu Gly Ala Tyr Arg Ser Met Leu Gn Asp Arg Glu Asp Gn  
180 185 190

Ser Ile Leu Cys Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr  
195 200 205

N3027PCT\_sequ.list.txt

Lys Lys Val Ile Gln Tyr Leu Ala His Val Ala Ser Ser Pro Lys Gly  
 210 215 220  
 Arg Lys Glu Pro Gly Val Pro Ala Ser Val Ser Thr Val Ser Tyr Gly  
 225 230 235 240  
 Glu Leu Glu Arg Gln Leu Leu Gln Ala Asn Pro Ile Leu Glu Ala Phe  
 245 250 255  
 Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser Arg Phe Gly Lys  
 260 265 270  
 Phe Ile Arg Ile Asn Phe Asp Val Ala Gly Tyr Ile Val Gly Ala Asn  
 275 280 285  
 Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Ile Arg Gln Ala Lys  
 290 295 300  
 Asp Glu Cys Ser Phe His Ile Phe Tyr Gln Leu Leu Gly Gly Ala Gly  
 305 310 315 320  
 Glu Gln Leu Lys Ala Asp Leu Leu Leu Glu Pro Cys Ser His Tyr Arg  
 325 330 335  
 Phe Leu Thr Asn Gly Pro Ser Ser Ser Pro Gly Gln Glu Arg Glu Leu  
 340 345 350  
 Phe Gln Glu Thr Leu Glu Ser Leu Arg Val Leu Gly Phe Ser His Glu  
 355 360 365  
 Glu Ile Ile Ser Met Leu Arg Met Val Ser Ala Val Leu Gln Phe Gly  
 370 375 380  
 Asn Ile Ala Leu Lys Arg Glu Arg Asn Thr Asp Gln Ala Thr Met Pro  
 385 390 395 400  
 Asp Asn Thr Ala Ala Gln Lys Leu Cys Arg Leu Leu Gly Leu Gly Val  
 405 410 415  
 Thr Asp Phe Ser Arg Ala Leu Leu Thr Pro Arg Ile Lys Val Gly Arg  
 420 425 430  
 Asp Tyr Val Gln Lys Ala Gln Thr Lys Glu Gln Ala Asp Phe Ala Leu  
 435 440 445  
 Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu Phe Arg Trp Leu Val  
 450 455 460  
 Leu Arg Leu Asn Arg Ala Leu Asp Arg Ser Pro Arg Gln Gly Ala Ser  
 465 470 475 480

N3027PCT\_sequ.list.txt

Phe Leu Gly Ile Leu Asp Ile Ala Gly Phe Glu Ile Phe Gln Leu Asn  
485 490 495

Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn Glu Lys Leu Gln Gln  
500 505 510

Leu Phe Asn His Thr Met Phe Val Leu Glu Gln Glu Glu Tyr Gln Arg  
515 520 525

Glu Gly Ile Pro Trp Thr Phe Leu Asp Phe Gly Leu Asp Leu Gln Pro  
530 535 540

Cys Ile Asp Leu Ile Glu Arg Pro Ala Asn Pro Pro Gly Leu Leu Ala  
545 550 555 560

Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala Thr Asp Lys Ser Phe  
565 570 575

Val Glu Lys Val Ala Gln Glu Gln Gly Gly His Pro Lys Phe Gln Arg  
580 585 590

Pro Arg His Leu Arg Asp Gln Ala Asp Phe Ser Val Leu His Tyr Ala  
595 600 605

Gly Lys Val Asp Tyr Lys Ala Asn Glu Trp Leu Met Lys Asn Met Asp  
610 615 620

Pro Leu Asn Asp Asn Val Ala Ala Leu Leu His Gln Ser Thr Asp Arg  
625 630 635 640

Leu Thr Ala Glu Ile Trp Lys Asp Val Glu Gly Ile Val Gly Leu Glu  
645 650 655

Gln Val Ser Ser Leu Gly Asp Gly Pro Pro Gly Gly Arg Pro Arg Arg  
660 665 670

Gly Met Phe Arg Thr Val Gly Gln Leu Tyr Lys Glu Ser Leu Ser Arg  
675 680 685

Leu Met Ala Thr Leu Ser Asn Thr Asn Pro Ser Phe Val Arg Cys Ile  
690 695 700

Val Pro Asn His Glu Lys Arg Ala Gly Lys Leu Glu Pro Arg Leu Val  
705 710 715 720

Leu Asp Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile Cys  
725 730 735

Arg Gln Gly Phe Pro Asn Arg Ile Leu Phe Gln Glu Phe Arg Gln Arg  
740 745 750

Tyr Glu Ile Leu Thr Pro Asn Ala Ile Pro Lys Gly Phe Met Asp Gly  
 755 760 765  
 Lys Gln Ala Cys Gu Lys Met Ile Gln Ala Leu Gu Leu Asp Pro Asn  
 770 775 780  
 Leu Tyr Arg Val Gly Gln Ser Lys Ile Phe Phe Arg Ala Gly Val Leu  
 785 790 795 800  
 Ala Gln Leu Gu Gu Gu Arg Asp Leu Lys Val Thr Asp Ile Ile Val  
 805 810 815  
 Ser Phe Gln Ala Ala Ala Arg Gly Tyr Leu Ala Arg Arg Ala Phe Gln  
 820 825 830  
 Lys Arg Gln Gln Gln Gln Ser Ala Leu Arg Val Met Gln Arg Asn Cys  
 835 840 845  
 Ala Ala Tyr Leu Lys Leu Arg His Trp Gln Trp Trp Arg Leu Phe Thr  
 850 855 860  
 Lys Val Lys Pro Leu Leu Gln Val Thr Arg Gln Asp Gu Val Leu Gln  
 865 870 875 880  
 Ala Arg Ala Gln Gu Leu Gln Lys Val Gln Gu Leu Gln Gln Gln Ser  
 885 890 895  
 Ala Arg Gu Val Gly Gu Leu Gln Gly Arg Val Ala Gln Leu Gu Gu  
 900 905 910  
 Gu Arg Ala Arg Leu Ala Gu Gln Leu Arg Ala Gu Ala Gu Leu Cys  
 915 920 925  
 Ala Gu Ala Gu Gu Thr Arg Gly Arg Leu Ala Ala Arg Lys Gln Gu  
 930 935 940  
 Leu Gu Leu Val Val Ser Gu Leu Gu Ala Arg Val Gly Gu Gu Gu  
 945 950 955 960  
 Gu Cys Ser Arg Gln Met Gln Thr Gu Lys Lys Arg Leu Gln Gln His  
 965 970 975  
 Ile Gln Gu Leu Gu Ala His Leu Gu Ala Gu Gu Gly Ala Arg Gln  
 980 985 990  
 Lys Leu Gln Leu Gu Lys Val Thr Thr Gu Ala Lys Met Lys Lys Phe  
 995 1000 1005  
 Gu Gu Asp Leu Leu Leu Leu Gu Asp Gln Asn Ser Lys Leu Ser  
 1010 1015 1020  
 Lys Gu Arg Lys Leu Leu Gu Asp Arg Leu Ala Gu Phe Ser Ser  
 Page 409

1025														
G n	Al a	Al a	G u	G u	G u	G u	Lys	Val	Lys	Ser	Leu	Asn	Lys	Leu
1040						1045					1050			
Arg	Leu	Lys	Tyr	G u	Al a	Thr	I l e	Al a	Asp	Met	G u	Asp	Arg	Leu
1055						1060					1065			
Arg	Lys	G u	G u	Lys	G y	Arg	G n	G u	Leu	G u	Lys	Leu	Lys	Arg
1070						1075					1080			
Arg	Leu	Asp	G y	G u	Ser	Ser	G u	Leu	G n	G u	G n	Met	Val	G u
1085						1090					1095			
G n	G n	G n	Arg	Al a	G u	G u	Leu	Arg	Al a	G n	Leu	G y	Arg	Lys
1100						1105					1110			
G u	G u	G u	Leu	G n	Al a	Al a	Leu	Al a	Arg	Al a	G u	Asp	G u	G y
1115						1120					1125			
G y	Al a	Arg	Al a	G n	Leu	Leu	Lys	Ser	Leu	Arg	G u	Al a	G n	Al a
1130						1135					1140			
Al a	Leu	Al a	G u	Al a	G n	G u	Asp	Leu	G u	Ser	G u	Arg	Val	Al a
1145						1150					1155			
Arg	Thr	Lys	Al a	G u	Lys	G n	Arg	Arg	Asp	Leu	G y	G u	G u	Leu
1160						1165					1170			
G u	Al a	Leu	Arg	G y	G u	Leu	G u	Asp	Thr	Leu	Asp	Ser	Thr	Asn
1175						1180					1185			
Al a	G n	G n	G u	Leu	Arg	Ser	Lys	Arg	G u	G n	G u	Val	Thr	G u
1190						1195					1200			
Leu	Lys	Lys	Thr	Leu	G u	G u	G u	Thr	Arg	I l e	H i s	G u	Al a	Al a
1205						1210					1215			
Val	G n	G u	Leu	Arg	G n	Arg	H i s	G y	G n	Al a	Leu	G y	G u	Leu
1220						1225					1230			
Al a	G u	G n	Leu	G u	G n	Al a	Arg	Arg	G y	Lys	G y	Al a	Trp	G u
1235						1240					1245			
Lys	Thr	Arg	Leu	Al a	Leu	G u	Al a	G u	Val	Ser	G u	Leu	Arg	Al a
1250						1255					1260			
G u	Leu	Ser	Ser	Leu	G n	Thr	Al a	Arg	G n	G u	G y	G u	G n	Arg
1265						1270					1275			
Arg	Arg	Arg	Leu	G u	Leu	G n	Leu	G n	G u	Val	G n	G y	Arg	Al a
1280						1285					1290			

N3027PCT\_sequ.list.txt

Gly Asp 1295 Gly Gu Arg Ala Arg 1300 Ala Gu Ala Ala Gu 1305 Lys Leu Gn  
 Arg Ala 1310 Gn Ala Gu Leu Gu 1315 Asn Val Ser Gly Ala 1320 Leu Asn Gu  
 Ala Gu 1325 Ser Lys Thr Ile Arg 1330 Leu Ser Lys Gu Leu 1335 Ser Ser Thr  
 Gu Ala 1340 Gn Leu His Asp Ala 1345 Gn Gu Leu Leu Gn 1350 Gu Gu Thr  
 Arg Ala 1355 Lys Leu Ala Leu Gly 1360 Ser Arg Val Arg Ala 1365 Met Gu Ala  
 Gu Ala 1370 Ala Gly Leu Arg Gu 1375 Gn Leu Gu Gu Gu 1380 Ala Ala Ala  
 Arg Gu 1385 Arg Ala Gly Arg Gu 1390 Leu Gn Thr Ala Gn 1395 Ala Gn Leu  
 Ser Gu 1400 Trp Arg Arg Arg Gn 1405 Gu Gu Gu Ala Gly 1410 Ala Leu Gu  
 Ala Gly 1415 Gu Gu Ala Arg Arg 1420 Arg Ala Ala Arg Gu 1425 Ala Gu Ala  
 Leu Thr 1430 Gn Arg Leu Ala Gu 1435 Lys Thr Gu Thr Val 1440 Asp Arg Leu  
 Gu Arg 1445 Gly Arg Arg Arg Leu 1450 Gn Gn Gu Leu Asp 1455 Asp Ala Thr  
 Met Asp 1460 Leu Gu Gn Gn Arg 1465 Gn Leu Val Ser Thr 1470 Leu Gu Lys  
 Lys Gn 1475 Arg Lys Phe Asp Gn 1480 Leu Leu Ala Gu Gu 1485 Lys Ala Ala  
 Val Leu 1490 Arg Ala Val Gu Gu 1495 Arg Gu Arg Ala Gu 1500 Ala Gu Gly  
 Arg Gu 1505 Arg Gu Ala Arg Ala 1510 Leu Ser Leu Thr Arg 1515 Ala Leu Gu  
 Gu Gu 1520 Gn Gu Ala Arg Gu 1525 Gu Leu Gu Arg Gn 1530 Asn Arg Ala  
 Leu Arg 1535 Ala Gu Leu Gu Ala 1540 Leu Leu Ser Ser Lys 1545 Asp Asp Val

N3027PCT\_sequ.list.txt

G y Lys Ser Val His G u Leu G u Arg Ala Cys Arg Val Ala G u  
 1550 1555 1560  
 G n Ala Ala Asn Asp Leu Arg Ala G n Val Thr G u Leu G u Asp  
 1565 1570 1575  
 G u Leu Thr Ala Ala G u Asp Ala Lys Leu Arg Leu G u Val Thr  
 1580 1585 1590  
 Val G n Ala Leu Lys Thr G n His G u Arg Asp Leu G n G y Arg  
 1595 1600 1605  
 Asp G u Ala G y G u G u Arg Arg Arg G n Leu Ala Lys G n Leu  
 1610 1615 1620  
 Arg Asp Ala G u Val G u Arg Asp G u G u Arg Lys G n Arg Thr  
 1625 1630 1635  
 Leu Ala Val Ala Ala Arg Lys Lys Leu G u G y G u Leu G u G u  
 1640 1645 1650  
 Leu Lys Ala G n Met Ala Ser Ala G y G n G y Lys G u G u Ala  
 1655 1660 1665  
 Val Lys G n Leu Arg Lys Met G n Ala G n Met Lys G u Leu Trp  
 1670 1675 1680  
 Arg G u Val G u G u Thr Arg Thr Ser Arg G u G u Ile Phe Ser  
 1685 1690 1695  
 G n Asn Arg G u Ser G u Lys Arg Leu Lys G y Leu G u Ala G u  
 1700 1705 1710  
 Val Leu Arg Leu G n G u G u Leu Ala Ala Ser Asp Arg Ala Arg  
 1715 1720 1725  
 Arg G n Ala G n G n Asp Arg Asp G u Met Ala Asp G u Val Ala  
 1730 1735 1740  
 Asn G y Asn Leu Ser Lys Ala Ala Ile Leu G u G u Lys Arg G n  
 1745 1750 1755  
 Leu G u G y Arg Leu G y G n Leu G u G u G u Leu G u G u G u  
 1760 1765 1770  
 G n Ser Asn Ser G u Leu Leu Asn Asp Arg Tyr Arg Lys Leu Leu  
 1775 1780 1785  
 Leu G n Val G u Ser Leu Thr Thr G u Leu Ser Ala G u Arg Ser  
 1790 1795 1800

Phe Ser Ala Lys Ala Gu Ser Gly Arg Gln Gln Leu Gu Arg Gln  
 1805 1810 1815  
 Ile Gln Gu Leu Arg Gly Arg Leu Gly Gu Gu Asp Ala Gly Ala  
 1820 1825 1830  
 Arg Ala Arg His Lys Met Thr Ile Ala Ala Leu Gu Ser Lys Leu  
 1835 1840 1845  
 Ala Gln Ala Gu Gu Gln Leu Gu Gln Gu Thr Arg Gu Arg Ile  
 1850 1855 1860  
 Leu Ser Gly Lys Leu Val Arg Arg Ala Gu Lys Arg Leu Lys Gu  
 1865 1870 1875  
 Val Val Leu Gln Val Gu Gu Gu Arg Arg Val Ala Asp Gln Leu  
 1880 1885 1890  
 Arg Asp Gln Leu Gu Lys Gly Asn Leu Arg Val Lys Gln Leu Lys  
 1895 1900 1905  
 Arg Gln Leu Gu Gu Ala Gu Gu Gu Ala Ser Arg Ala Gln Ala  
 1910 1915 1920  
 Gly Arg Arg Arg Leu Gln Arg Gu Leu Gu Asp Val Thr Gu Ser  
 1925 1930 1935  
 Ala Gu Ser Met Asn Arg Gu Val Thr Thr Leu Arg Asn Arg Leu  
 1940 1945 1950  
 Arg Arg Gly Pro Leu Thr Phe Thr Thr Arg Thr Val Arg Gln Val  
 1955 1960 1965  
 Phe Arg Leu Gu Gu Gly Val Ala Ser Asp Gu Gu Ala Gu Gu  
 1970 1975 1980  
 Ala Gln Pro Gly Ser Gly Pro Ser Pro Gu Pro Gu Gly Ser Pro  
 1985 1990 1995  
 Pro Ala His Pro Gln  
 2000

<210> 85  
 <211> 6807  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(6807)  
 <223> myosin, heavy chain 14 (MYH14), transcript variant 2

<400> 85  
 ctctttctcc ccaggccgaa gcctcgggac ggccctggaa gccgaccatg gcagccgtga  
 Page 413

N3027PCT\_sequ. list . . txt

ccat gt cggt	gccccgggcgg	aaggcgcccc	ccaggccggg	cccagt gccc	gaggcggccc	120
agccgt t cct	gt t cacgccc	cgcgggccca	gcgcgggt gg	cgggcct ggc	t cgggcacct	180
ccccgcaggt	ggagt ggacg	gccccggcgt c	t cgt gt ggg	gcct t cggag	ct t cacgggt	240
t cgaggcggc	ggcgct gcgg	gacgaaggcg	aggaggaggc	ggaggt ggag	ct ggcggaga	300
gcgggaggcg	gct gcgact g	ccgcgggacc	agat ccagcg	cat gaacccg	cccaagt t ca	360
gcaaggccga	ggacat ggcc	gagct gacct	gcct caacga	ggcct cgggt c	ct gcacaacc	420
t ccgggagcg	gt act act cc	ggcct cat ct	acacgt act c	cggcct t t t c	t gt gt ggt ca	480
t caacccgt a	caagcagct t	cccat ct aca	cagaagccat	t gt ggagat g	t accggggca	540
agaagcgcca	cgaggt gcc	ccccacgt gt	acgcagt gac	cgagggggcc	t at cggagca	600
t gct gcagga	t cgt gaggac	cagt ccat t c	t ct gcact gg	agagt ct gga	gct gggaaga	660
cggaaaacac	caagaaggt c	at ccagt acc	t cgcccacgt	ggcgt cgt ct	ccaaagggca	720
ggaaggagcc	gggt gt cccc	ggt gagct gg	agcggcagct	gct t caggcc	aaccccat cc	780
t agaggcct t	t ggcaat gcc	aagacagt ga	agaat gacaa	ct cct cccga	t t cggcaaat	840
t cat ccgcat	caact t t gat	gt t gccgggt	acat cgt ggg	cgccaacat t	gagacct acc	900
t gct ggagaa	gt cgcgggcc	at ccgccagg	ccaaggacga	gt gcagct t c	cacat ct t ct	960
accagct gct	ggggggcgct	ggagagcagc	t caaagccga	cct cct cct c	gagccct gct	1020
cccact accg	gt t cct gacc	aacggggcgt	cat cct ct cc	cggccaggag	cgggaact ct	1080
t ccaggagac	gct ggagt cg	ct gcgggt cc	t gggat t cag	ccacgaggaa	at cat ct cca	1140
t gct gcggat	gggt ct cagca	gt t ct ccagt	t t ggcaacat	t gcct t gaag	agagaacgga	1200
acaccgat ca	agccacat g	cct gacaaca	cagct gcaca	gaagct ct gc	cgcct ct t gg	1260
gact gggggt	gacggat t t c	t cccgagcct	t gct caccoc	t cgcat caaa	gt t ggccgag	1320
act at gt gca	gaaagcccag	act aaggaac	aggct gact t	cgcgct ggag	gccct ggcca	1380
aggccacct a	cgagcgct c	t t ccgct ggc	t ggt t ct gcg	cct caaccgg	gcct t ggacc	1440
gcagcccccg	ccaaggcgcc	t cct t cct gg	gcat cct gga	cat cgcgggc	t t t gagat ct	1500
t ccagct gaa	ct cct t cgag	cagct ct gca	t caact acac	caacgagaag	ct gcagcagc	1560
t ct t caacca	cacat gt t c	gt gct ggagc	aggaggagt a	ccagcgt gag	ggcat cccct	1620
ggacct t cct	cgact t t ggc	ct cgacct gc	agccct gcat	cgacct cat c	gagcggccgg	1680
ccaaccccc	t ggact cct g	gccct gct gg	at gaggagt g	ct ggt t cccg	aaggccacag	1740
acaagt cgt t	t gt ggagaag	gt agcccagg	agcagggcgg	ccacccaag	t t ccagcggc	1800
cgaggcacct	gcgggat cag	gccgact t ca	gt gt t ct cca	ct acgcgggc	aaggt cgact	1860
acaaggccaa	cgagt ggct g	at gaaaaaca	t ggacct ct	gaat gacaac	gt cgcagcct	1920
t gct ccacca	gagcacagac	cggct gacgg	cagagat ct g	gaaagacgt g	gagggcat cg	1980
t ggggct gga	acaggt gacg	agcct gggcg	acggcccacc	aggt ggccgc	ccccgt cggg	2040
gt at gt t ccg	gacagt ggga	cagct ct aca	aggagt ccct	gagccgcct c	at ggccacac	2100

N3027PCT\_sequ. list.txt

t cagcaacac caaccccagt t t t gt ccgct gcat t gt ccc caaccacgag aagagggccg	2160
ggaagct gga gccacggct g gt gct ggacc agct t cgct g caacggggc c ct ggagggca	2220
t ccgcat ct g t cgccagggc t t ccccaacc gcat cct ct t ccaggagt t c cggcagcgat	2280
acgagat cct gacacccaat gccat cccca agggct t cat ggat gggaag caggcct gt g	2340
aaaagat gat ccaggcgct g gaact ggacc ccaacct ct a ccgcgt ggga cagagcaaga	2400
t ct t ct t ccg ggct ggggt c ct ggcccagc t ggaagagga gcgagacct g aaggt caccg	2460
acat cat cgt ct cct t ccag gcagct gccc ggggat acct ggct cgcagg gcct t ccaga	2520
agcgccagca gcagcagagc gccct gaggg t gat gcagcg gaact gcgcg gcct acct ca	2580
agct gagaca ct ggcagt gg t ggccgct gt t t accaaggt gaagccact g ct gcaggt ga	2640
cgcggcagga t gaggt gct g caggcacggg cccaggagct gcagaaagt g caggagct ac	2700
agcagcagag cgcccgcgaa gt t ggggagc t ccaggggccg agt ggcacag ct ggaagagg	2760
agcgcgcccc cct ggcagag caat t gcgag cagaggcaga act gt gt gca gaggccgagg	2820
agacgcgggg gaggt ggca gcccgaagc aggagct gga gct ggt ggt g t cagagct gg	2880
aggct cgcgt gggcgaggag gaggt gca gccgt caaat gcaaaccgag aagaagaggc	2940
t gcagcagca cat acaggag ct agaggccc acct t gaggc t gaggagggg gcgcggcaga	3000
agct gcagct ggagaaggt g acgacagagg caaaaat gaa gaaat t t gaa gaggacct gc	3060
t gct cct gga agaccagaat t ccaagct ga gcaaggagcg gaagct gct g gaagat cgt c	3120
t ggccgagt t ct cat ccag gcagct gagg aggaggagaa ggt caagagc ct caat aagc	3180
t acggct caa at at gagggc acaat cgcag acat ggagga ccgcct acgg aaggaggaga	3240
agggt cgcca ggagct ggag aagct gaagc ggaggct gga t ggggagagc t cagagct gc	3300
aggagcagat ggt ggagcag caacagcggg cagaggagct gcgggcccag ct gggccgga	3360
aggaggagga gct gcaggct gccct ggcca gggcagaaga cgagggt ggg gcccgggccc	3420
agct gct gaa at ccct gcgg gaggt caag cagccct ggc cgaggcccag gaggacct gg	3480
agt ct gagcg t gt ggccagg accaaggcgg agaagcagcg ccgggacct g ggcgaggagc	3540
t ggaggcgct gcggggcgag ct ggaggaca cgct ggact c caccaacgca cagcaggagc	3600
t ccggt ccaa gagggaacag gaggt gacgg agct gaagaa gact ct ggag gaggagact c	3660
gcat ccacga ggcggcagt g caggagct ga ggcagcgcca cggccaggcc ct gggggagc	3720
t ggcggagca gct ggagcag gcccgaggg gcaaaggt gc at gggagaag acccggt gg	3780
ccct ggaggc cgaggt gt cc gagct gcggg cagaact gag cagcct gcag act gcacgt c	3840
aggaggggt ga gcagcggagg cgccgcct gg agt t acagct gcaggaggt g cagggccggg	3900
ct ggt gat gg ggagagggca cgagcggagg ct gct gagaa gct gcagcga gccaggct g	3960
aact ggagaa t gt gt ct ggg gcgct gaacg aggct gact c caaaacat c cgt ct t agca	4020
aggagct gag cagcacagaa gccagct gc acgat gccc ggagct gct g caggaggaga	4080
ccagggcgaa at t ggcct t g ggggt cccggg t gcgagccat ggaggct gag gcagccgggc	4140
t gcgt gagca gct ggaggag gaggcagct g ccagggaacg ggcgggcccgt gaact gcaga	4200

N3027PCT\_sequ. list . . txt

ct gcccaggc	ccagct t t cc	gagt ggcggc	ggcgccagga	ggaggaggca	ggggcact gg	4260
aggcagggga	ggaggcacgg	cgccggggcag	cccgggaggc	cgaggccct g	accagcgcc	4320
t ggcagaaaa	gacagagacc	gt ggat cggc	t ggagcgggg	cgcgcgccgg	ct gcagcagg	4380
agct ggacga	cgccaccat g	gacct ggagc	agcagcggca	gct t gt gagc	accct ggaga	4440
agaagcagcg	caagt t t gac	cagct t ct gg	cagaggagaa	ggcagct gt a	ct t cgggcag	4500
t ggaggaacg	t gagcggggc	gaggcagagg	gccgggagcg	t gaggct cgg	gccct gt cac	4560
t gacacgggc	act ggaggag	gagcaggagg	cacgt gagga	gct ggagcgg	cagaaccggg	4620
ccct gcgggc	t gagct ggag	gcact gct ga	gcagcaagga	t gacgt cggc	aagagcgt gc	4680
at gagct gga	acgagcct gc	cgggt agcag	aacaggcagc	caat gat ct g	cgagcacagg	4740
t gacagaact	ggaggat gag	ct gacagcgg	ccgaggat gc	caagct gcgt	ct ggaggt ga	4800
ct gt gcaggc	t ct caagact	cagcat gagc	gt gacct gca	gggccgt gat	gaggct ggt g	4860
aagagaggcg	gaggcagct g	gccaagcagc	t gagagat gc	agaggt ggag	cgggat gagg	4920
agcggaagca	gcgcact ct g	gccgt ggct g	cccgaagaa	gct ggaggga	gagct ggagg	4980
agct gaaggc	t cagat ggcc	t ct gccggcc	agggaagga	ggaggcggg g	aagcagct t c	5040
gcaagat gca	ggcccagat g	aaggagct at	ggcgggaggt	ggaggagaca	cgcacct ccc	5100
gggaggagat	ct t ct cccag	aat cgggaaa	gt gaaaagcg	cct caagggc	ct ggaggct g	5160
aggt gct gcg	gct gcaggag	gaact ggccg	cct cggaccg	t gct cggcgg	caggcccagc	5220
aggaccggga	t gagat ggca	gat gaggt gg	ccaat ggt aa	cct t agcaag	gcagccat t c	5280
t ggaggagaa	gcgt cagct g	gaggggccc	t ggggcagt t	ggaggaagag	ct ggaggagg	5340
agcagagcaa	ct cggagct g	ct caat gacc	gct accgcaa	gct gct cct g	cagggt agagt	5400
cact gaccac	agagct gt ca	gct gagcgca	gt t t ct cagc	caaggcagag	agcgggcggc	5460
agcagct gga	acggcagat c	caggagct ac	ggggacgcct	gggt gaggag	gat gct gggg	5520
cccgt gcccg	ccacaagat g	accat t gct g	ccct t gagt c	t aagt t ggcc	caggct gagg	5580
agcagct aga	gcaagagacc	agagagcgca	t cct ct ct gg	aaagct ggt g	cgcagagct g	5640
agaagcggct	t aaagaggt g	gt gct ccagg	t ggaggagga	gcggagggt g	gct gaccagc	5700
t ccgggacca	gct ggagaag	ggaaacct t c	gagt caagca	gct gaagcgg	cagct ggagg	5760
aggccgagga	ggaggcat cc	cgggct cagg	ccggccgccg	gaggct gcag	cgt gagct gg	5820
aagat gt cac	agagt cggcc	gagt ccat ga	accgt gaagt	gaccacact g	aggaaccggc	5880
t t cgacgcgg	ccccct cacc	t t caccaccc	gcacggt gcg	ccaggt ct t c	cgact agagg	5940
agggcgt ggc	at ccgacgag	gaggcagagg	aagcacagcc	t ggggt ct ggg	ccat ccccgg	6000
agcct gaggg	gt ccccacca	gcccaccccc	agt gacct a	ccct gt cccc	agat gcact a	6060
acagat gggg	cccagcccc	t t cct ccct g	gacccacgg	gcccct gt cc	caggaacccc	6120
gccct ct gac	t t ct t gccct	t t ggaaat gg	t gcagcact c	t ggcat t t at	cacccccacc	6180
t ggggt cccct	gcaacct ccc	at caaaggat	gacctt aaa	cacagaggag	cggggcaggc	6240

N3027PCT\_sequ.list.txt

```

aggaggagcaa t gactggagc t accttgctt gttgggggac tgggtacagt tggcaagct g 6300
tgtttccatc agctccctgt cctcctttct tccctcgttat t gatctata gacattagga 6360
agggagt gag acggctcctc caccatcctc agccagt gca acccat tccc tctgcttctc 6420
tctctctctc tctctctccc tccctctcct tccctaccct ct caccatct t tcttggcct 6480
ctctgaggggt ctctctgtgc atcttttttag gaatctcgct ct cactctct acgt agccac 6540
tctccttccc ccat t tctgc gtccaccct gaactcctga gcgacagaag cccaggcct 6600
ccaccagcct tgaacccttg caaaggggca ggacaagggg acccctctca ct cctgctgc 6660
tgcccatgct ctgccctccc t tctgggtgc tctgaggggt cggagcttcc ctctgggact 6720
aaaggagtgt cctttaccct cccagcctcc aggctctggc agaaat aaac tccaaccga 6780
ctggaccata aaaaaaaaaa aaaaaaa 6807

```

<210> 86  
 <211> 1995  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> M SC\_FEATURE  
 <222> (1).(1995)  
 <223> myosin, heavy chain 14 (MYH14), transcript variant 2

<400> 86

```

Met Ala Ala Val Thr Met Ser Val Pro Gly Arg Lys Ala Pro Pro Arg
1          5          10          15

Pro Gly Pro Val Pro Glu Ala Ala Gln Pro Phe Leu Phe Thr Pro Arg
20          25          30

Gly Pro Ser Ala Gly Gly Gly Pro Gly Ser Gly Thr Ser Pro Gln Val
35          40          45

Glu Trp Thr Ala Arg Arg Leu Val Trp Val Pro Ser Glu Leu His Gly
50          55          60

Phe Glu Ala Ala Ala Leu Arg Asp Glu Gly Glu Glu Ala Glu Val
65          70          75          80

Glu Leu Ala Glu Ser Gly Arg Arg Leu Arg Leu Pro Arg Asp Gln Ile
85          90          95

Gln Arg Met Asn Pro Pro Lys Phe Ser Lys Ala Glu Asp Met Ala Glu
100         105         110

Leu Thr Cys Leu Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg
115         120         125

Tyr Tyr Ser Gly Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val
130         135         140

```

N3027PCT\_sequ.list.txt

Ile Asn Pro Tyr Lys Gln Leu Pro Ile Tyr Thr Glu Ala Ile Val Glu  
145 150 155 160

Met Tyr Arg Gly Lys Lys Arg His Glu Val Pro Pro His Val Tyr Ala  
165 170 175

Val Thr Glu Gly Ala Tyr Arg Ser Met Leu Gln Asp Arg Glu Asp Gln  
180 185 190

Ser Ile Leu Cys Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr  
195 200 205

Lys Lys Val Ile Gln Tyr Leu Ala His Val Ala Ser Ser Pro Lys Gly  
210 215 220

Arg Lys Glu Pro Gly Val Pro Gly Glu Leu Glu Arg Gln Leu Leu Gln  
225 230 235 240

Ala Asn Pro Ile Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Lys Asn  
245 250 255

Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val  
260 265 270

Ala Gly Tyr Ile Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys  
275 280 285

Ser Arg Ala Ile Arg Gln Ala Lys Asp Glu Cys Ser Phe His Ile Phe  
290 295 300

Tyr Gln Leu Leu Gly Gly Ala Gly Glu Gln Leu Lys Ala Asp Leu Leu  
305 310 315 320

Leu Glu Pro Cys Ser His Tyr Arg Phe Leu Thr Asn Gly Pro Ser Ser  
325 330 335

Ser Pro Gly Gln Glu Arg Glu Leu Phe Gln Glu Thr Leu Glu Ser Leu  
340 345 350

Arg Val Leu Gly Phe Ser His Glu Glu Ile Ile Ser Met Leu Arg Met  
355 360 365

Val Ser Ala Val Leu Gln Phe Gly Asn Ile Ala Leu Lys Arg Glu Arg  
370 375 380

Asn Thr Asp Gln Ala Thr Met Pro Asp Asn Thr Ala Ala Gln Lys Leu  
385 390 395 400

Cys Arg Leu Leu Gly Leu Gly Val Thr Asp Phe Ser Arg Ala Leu Leu  
405 410 415

Thr Pro Arg Ile Lys Val Gly Arg Asp Tyr Val Gln Lys Ala Gln Thr  
 420 425 430  
 Lys Glu Gln Ala Asp Phe Ala Leu Glu Ala Leu Ala Lys Ala Thr Tyr  
 435 440 445  
 Glu Arg Leu Phe Arg Trp Leu Val Leu Arg Leu Asn Arg Ala Leu Asp  
 450 455 460  
 Arg Ser Pro Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala  
 465 470 475 480  
 Gly Phe Glu Ile Phe Gln Leu Asn Ser Phe Glu Gln Leu Cys Ile Asn  
 485 490 495  
 Tyr Thr Asn Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Val  
 500 505 510  
 Leu Glu Gln Glu Glu Tyr Gln Arg Glu Gly Ile Pro Trp Thr Phe Leu  
 515 520 525  
 Asp Phe Gly Leu Asp Leu Gln Pro Cys Ile Asp Leu Ile Glu Arg Pro  
 530 535 540  
 Ala Asn Pro Pro Gly Leu Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe  
 545 550 555 560  
 Pro Lys Ala Thr Asp Lys Ser Phe Val Glu Lys Val Ala Gln Glu Gln  
 565 570 575  
 Gly Gly His Pro Lys Phe Gln Arg Pro Arg His Leu Arg Asp Gln Ala  
 580 585 590  
 Asp Phe Ser Val Leu His Tyr Ala Gly Lys Val Asp Tyr Lys Ala Asn  
 595 600 605  
 Glu Trp Leu Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Ala Ala  
 610 615 620  
 Leu Leu His Gln Ser Thr Asp Arg Leu Thr Ala Glu Ile Trp Lys Asp  
 625 630 635 640  
 Val Glu Gly Ile Val Gly Leu Glu Gln Val Ser Ser Leu Gly Asp Gly  
 645 650 655  
 Pro Pro Gly Gly Arg Pro Arg Arg Gly Met Phe Arg Thr Val Gly Gln  
 660 665 670  
 Leu Tyr Lys Glu Ser Leu Ser Arg Leu Met Ala Thr Leu Ser Asn Thr  
 675 680 685  
 Asn Pro Ser Phe Val Arg Cys Ile Val Pro Asn His Glu Lys Arg Ala  
 Page 419

690

695

700

Gly Lys Leu Glu Pro Arg Leu Val Leu Asp Gln Leu Arg Cys Asn Gly  
705 710 715 720

Val Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile  
725 730 735

Leu Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Thr Pro Asn Ala  
740 745 750

Ile Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Glu Lys Met Ile  
755 760 765

Gln Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Val Gly Gln Ser Lys  
770 775 780

Ile Phe Phe Arg Ala Gly Val Leu Ala Gln Leu Glu Glu Glu Arg Asp  
785 790 800

Leu Lys Val Thr Asp Ile Ile Val Ser Phe Gln Ala Ala Ala Arg Gly  
805 810 815

Tyr Leu Ala Arg Arg Ala Phe Gln Lys Arg Gln Gln Gln Gln Ser Ala  
820 825 830

Leu Arg Val Met Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg His  
835 840 845

Trp Gln Trp Trp Arg Leu Phe Thr Lys Val Lys Pro Leu Leu Gln Val  
850 855 860

Thr Arg Gln Asp Glu Val Leu Gln Ala Arg Ala Gln Glu Leu Gln Lys  
865 870 875 880

Val Gln Glu Leu Gln Gln Gln Ser Ala Arg Glu Val Gly Glu Leu Gln  
885 890 895

Gly Arg Val Ala Gln Leu Glu Glu Glu Arg Ala Arg Leu Ala Glu Gln  
900 905 910

Leu Arg Ala Glu Ala Glu Leu Cys Ala Glu Ala Glu Glu Thr Arg Gly  
915 920 925

Arg Leu Ala Ala Arg Lys Gln Glu Leu Glu Leu Val Val Ser Glu Leu  
930 935 940

Glu Ala Arg Val Gly Glu Glu Glu Glu Cys Ser Arg Gln Met Gln Thr  
945 950 955 960

Glu Lys Lys Arg Leu Gln Gln His Ile Gln Glu Leu Glu Ala His Leu  
965 970 975

N3027PCT\_sequ.list.txt

G u A l a G u G u G y A l a A r g G n L y s L e u G n L e u G u L y s V a l T h r  
 980 985 990  
 T h r G u A l a L y s M e t L y s L y s P h e G u G u A s p L e u L e u L e u L e u G u  
 995 1000 1005  
 A s p G n A s n S e r L y s L e u S e r L y s G u A r g L y s L e u L e u G u A s p  
 1010 1015 1020  
 A r g L e u A l a G u P h e S e r S e r G n A l a A l a G u G u G u G u L y s  
 1025 1030 1035  
 V a l L y s S e r L e u A s n L y s L e u A r g L e u L y s T y r G u A l a T h r I l e  
 1040 1045 1050  
 A l a A s p M e t G u A s p A r g L e u A r g L y s G u G u L y s G y A r g G n  
 1055 1060 1065  
 G u L e u G u L y s L e u L y s A r g A r g L e u A s p G y G u S e r S e r G u  
 1070 1075 1080  
 L e u G n G u G n M e t V a l G u G n G n G n A r g A l a G u G u L e u  
 1085 1090 1095  
 A r g A l a G n L e u G y A r g L y s G u G u G u L e u G n A l a A l a L e u  
 1100 1105 1110  
 A l a A r g A l a G u A s p G u G y G y A l a A r g A l a G n L e u L e u L y s  
 1115 1120 1125  
 S e r L e u A r g G u A l a G n A l a A l a L e u A l a G u A l a G n G u A s p  
 1130 1135 1140  
 L e u G u S e r G u A r g V a l A l a A r g T h r L y s A l a G u L y s G n A r g  
 1145 1150 1155  
 A r g A s p L e u G y G u G u L e u G u A l a L e u A r g G y G u L e u G u  
 1160 1165 1170  
 A s p T h r L e u A s p S e r T h r A s n A l a G n G n G u L e u A r g S e r L y s  
 1175 1180 1185  
 A r g G u G n G u V a l T h r G u L e u L y s L y s T h r L e u G u G u G u  
 1190 1195 1200  
 T h r A r g I l e H i s G u A l a A l a V a l G n G u L e u A r g G n A r g H i s  
 1205 1210 1215  
 G y G n A l a L e u G y G u L e u A l a G u G n L e u G u G n A l a A r g  
 1220 1225 1230

N3027PCT\_sequ.list.txt

Arg	Gly	Lys	Gly	Ala	Trp	Glu	Lys	Thr	Arg	Leu	Ala	Leu	Glu	Ala
1235						1240					1245			
Glu	Val	Ser	Glu	Leu	Arg	Ala	Glu	Leu	Ser	Ser	Leu	Gln	Thr	Ala
1250						1255					1260			
Arg	Gln	Glu	Gly	Glu	Gln	Arg	Arg	Arg	Arg	Leu	Glu	Leu	Gln	Leu
1265						1270					1275			
Gln	Glu	Val	Gln	Gly	Arg	Ala	Gly	Asp	Gly	Glu	Arg	Ala	Arg	Ala
1280						1285					1290			
Glu	Ala	Ala	Glu	Lys	Leu	Gln	Arg	Ala	Gln	Ala	Glu	Leu	Glu	Asn
1295						1300					1305			
Val	Ser	Gly	Ala	Leu	Asn	Glu	Ala	Glu	Ser	Lys	Thr	Ile	Arg	Leu
1310						1315					1320			
Ser	Lys	Glu	Leu	Ser	Ser	Thr	Glu	Ala	Gln	Leu	His	Asp	Ala	Gln
1325						1330					1335			
Glu	Leu	Leu	Gln	Glu	Glu	Thr	Arg	Ala	Lys	Leu	Ala	Leu	Gly	Ser
1340						1345					1350			
Arg	Val	Arg	Ala	Met	Glu	Ala	Glu	Ala	Ala	Gly	Leu	Arg	Glu	Gln
1355						1360					1365			
Leu	Glu	Glu	Glu	Ala	Ala	Ala	Arg	Glu	Arg	Ala	Gly	Arg	Glu	Leu
1370						1375					1380			
Gln	Thr	Ala	Gln	Ala	Gln	Leu	Ser	Glu	Trp	Arg	Arg	Arg	Gln	Glu
1385						1390					1395			
Glu	Glu	Ala	Gly	Ala	Leu	Glu	Ala	Gly	Glu	Glu	Ala	Arg	Arg	Arg
1400						1405					1410			
Ala	Ala	Arg	Glu	Ala	Glu	Ala	Leu	Thr	Gln	Arg	Leu	Ala	Glu	Lys
1415						1420					1425			
Thr	Glu	Thr	Val	Asp	Arg	Leu	Glu	Arg	Gly	Arg	Arg	Arg	Leu	Gln
1430						1435					1440			
Gln	Glu	Leu	Asp	Asp	Ala	Thr	Met	Asp	Leu	Glu	Gln	Gln	Arg	Gln
1445						1450					1455			
Leu	Val	Ser	Thr	Leu	Glu	Lys	Lys	Gln	Arg	Lys	Phe	Asp	Gln	Leu
1460						1465					1470			
Leu	Ala	Glu	Glu	Lys	Ala	Ala	Val	Leu	Arg	Ala	Val	Glu	Glu	Arg
1475						1480					1485			

G u Arg Ala G u Ala G u G y Arg G u Arg G u Ala Arg Ala Leu  
 1490 1495 1500  
 Ser Leu Thr Arg Ala Leu G u G u G u G n G u Ala Arg G u G u  
 1505 1510 1515  
 Leu G u Arg G n Asn Arg Ala Leu Arg Ala G u Leu G u Ala Leu  
 1520 1525 1530  
 Leu Ser Ser Lys Asp Asp Val G y Lys Ser Val Hi s G u Leu G u  
 1535 1540 1545  
 Arg Ala Cys Arg Val Ala G u G n Ala Ala Asn Asp Leu Arg Ala  
 1550 1555 1560  
 G n Val Thr G u Leu G u Asp G u Leu Thr Ala Ala G u Asp Ala  
 1565 1570 1575  
 Lys Leu Arg Leu G u Val Thr Val G n Ala Leu Lys Thr G n Hi s  
 1580 1585 1590  
 G u Arg Asp Leu G n G y Arg Asp G u Ala G y G u G u Arg Arg  
 1595 1600 1605  
 Arg G n Leu Ala Lys G n Leu Arg Asp Ala G u Val G u Arg Asp  
 1610 1615 1620  
 G u G u Arg Lys G n Arg Thr Leu Ala Val Ala Ala Arg Lys Lys  
 1625 1630 1635  
 Leu G u G y G u Leu G u G u Leu Lys Ala G n Met Ala Ser Ala  
 1640 1645 1650  
 G y G n G y Lys G u G u Ala Val Lys G n Leu Arg Lys Met G n  
 1655 1660 1665  
 Ala G n Met Lys G u Leu Trp Arg G u Val G u G u Thr Arg Thr  
 1670 1675 1680  
 Ser Arg G u G u Ile Phe Ser G n Asn Arg G u Ser G u Lys Arg  
 1685 1690 1695  
 Leu Lys G y Leu G u Ala G u Val Leu Arg Leu G n G u G u Leu  
 1700 1705 1710  
 Ala Ala Ser Asp Arg Ala Arg Arg G n Ala G n G n Asp Arg Asp  
 1715 1720 1725  
 G u Met Ala Asp G u Val Ala Asn G y Asn Leu Ser Lys Ala Ala  
 1730 1735 1740  
 Ile Leu G u G u Lys Arg G n Leu G u G y Arg Leu G y G n Leu

1745

1750

1755

G u G u G u Leu G u G u G u G n Ser Asn Ser G u Leu Leu Asn  
1760 1765 1770

Asp Arg Tyr Arg Lys Leu Leu Leu G n Val G u Ser Leu Thr Thr  
1775 1780 1785

G u Leu Ser Ala G u Arg Ser Phe Ser Ala Lys Ala G u Ser Gly  
1790 1795 1800

Arg G n G n Leu G u Arg G n Ile G n G u Leu Arg Gly Arg Leu  
1805 1810 1815

G y G u G u Asp Ala G y Ala Arg Ala Arg His Lys Met Thr Ile  
1820 1825 1830

Ala Ala Leu G u Ser Lys Leu Ala G n Ala G u G u G n Leu G u  
1835 1840 1845

G n G u Thr Arg G u Arg Ile Leu Ser Gly Lys Leu Val Arg Arg  
1850 1855 1860

Ala G u Lys Arg Leu Lys G u Val Val Leu G n Val G u G u G u  
1865 1870 1875

Arg Arg Val Ala Asp G n Leu Arg Asp G n Leu G u Lys Gly Asn  
1880 1885 1890

Leu Arg Val Lys G n Leu Lys Arg G n Leu G u G u Ala G u G u  
1895 1900 1905

G u Ala Ser Arg Ala G n Ala Gly Arg Arg Arg Leu G n Arg G u  
1910 1915 1920

Leu G u Asp Val Thr G u Ser Ala G u Ser Met Asn Arg G u Val  
1925 1930 1935

Thr Thr Leu Arg Asn Arg Leu Arg Arg Gly Pro Leu Thr Phe Thr  
1940 1945 1950

Thr Arg Thr Val Arg G n Val Phe Arg Leu G u G u Gly Val Ala  
1955 1960 1965

Ser Asp G u G u Ala G u G u Ala G n Pro Gly Ser Gly Pro Ser  
1970 1975 1980

Pro G u Pro G u Gly Ser Pro Pro Ala His Pro G n  
1985 1990 1995

&lt;210&gt; 87

&lt;211&gt; 7074

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(7074)  
 <223> myosin, heavy chain 15 (MYH15)

<400> 87  
 cat t t c t a c t t c a t a t g a t c a t t t t a a t t g t a t t t a c c t c a t c t t a c c a a a a g a t c a t g 60  
 g t t g a a t c t t g c c t a c t c a c g t t t a g g g c c t t t t t t t g g t g g a t t g c t t t a a t a a g a t g 120  
 g a t c t g t c a g a c c t t g g a g a g c c g c a g c c t t c c t c a g a a g a a g t g a a g c t g a g c t g c t t 180  
 c t a c t a c a g g c c a c a g c c t t g g a t g g g a a g a a g a a t g c t g g a t t c c t g a t g g t g a g a a t 240  
 g c t t a t a t c g a g g c t g a g g t a a a a g g g a g t g a a g a t g a t g g a a c a g t a a t t g t t g a g a c a 300  
 g c a g a t g g a g a g a g t c t g a g c a t a a a g g a g g a c a a a a t c c a g c a g a t g a a t c c t c c a g a g 360  
 t t t g a a a t g a t t g a a g a c a t g g c a a t g c t g a c t c a c c t c a a t g a g g c a t c c g t g c t g c a t 420  
 a c c c t g a a g c g g c g c t a t g g c c a g t g g a t g a t c t a t a c a t a t t c a g g t c t c t t c t g t g t g 480  
 a c c a t a a a c c c t t a c a a a t g g c t t c c c g t g t a t c a g a a a g a a g t c a t g g c c g c c t a c a a a 540  
 g g g a a g a g g c g a t c a g a g g c t c c c c c t c a c a t c t t t g c t g t t g c c a a t a a c g c c t t t c a g 600  
 g a c a t g c t t c a c a a t c g a g a a a t c a g t c t a t a c t c t t c a c a g g a g a a t c t g g t g c t g g a 660  
 a a g a c t g t g a a c a g c a a a c a t a t t a t c c a g t a t t t t g c c a c c a t a g c a g c c a t g a t t g a a 720  
 t c c a g g a a a a g c a g g g g g c g t t a g a a g a t c a a a t c a t g c a a g c g a a t a c t a t c t t g g a a 780  
 g c a t t t g g a a a t g c t a a a c c c t g a g a a t g a c a a c t c c t c t c g t t t t g g c a a a t t c a t c 840  
 a g g a t g c a c t t t g g t g c c a g a g g c a t g c t g t c a t c t g t g g a c a t t g a t a t c t a t t t g c t t 900  
 g a a a a g t c c a g g g t g a t t t t c c a g c a g g c t g g a g a g a g g a a c t a c c a c a t a t t c t a t c a a 960  
 a t t c t a t c t g g a c a a a a g a g c t t c a t g a c c t g c t c c t g g t a t c t g c a a a t c c c t c a g a c 1020  
 t t c c a c t t t t g c t c c t g t g g a g c a g t t a c t g t g g a g a g c t t g g a t g a t g c t g a a g a a t t g 1080  
 c t g g c c a c a g a a c a a g c c a t g g a c a t c t t g g c t t t c t t c c t g a t g a g a a g t a t g g a t g c 1140  
 t a t a a a c t c a c t g g a g c c a t c a t g c a c t t t g g a a a t a t g a a a t t a a c a g a a c c t a g a 1200  
 g a a g a g c a a c t g g a a g c a g a t g g c a c a g a a a a t g c t g a c a a g c t g c t t t c c t c a t g g g c 1260  
 a t t a a c t c c t c t g a g t t g g t a a a g t g c t t g a t c c a t c c t a g a a t c a a a g t t g g t a a c g a a 1320  
 t a t g t t a c c a g a g g t c a a a c t a t a g a a c a g g t a a c c t g t g c t g t c g g t g c c c t g t c c a a g 1380  
 t c a a t g t a t g a a a g g a t g t t t a a g t g g c t a g t g g c a c g g a t c a a c a g g g c c c t g g a t g c c 1440  
 a a g c t g t c a a g g c a g t t c t t c a t t g g c a t t c t t g a c a t c a c t g g t t t t g a a a t c c t t g a g 1500  
 t a t a a t a g c c t t g a g c a a c t t t g c a t t a a t t t t a c c a a t g a a a a t t a c a a c a a t t c t t c 1560  
 a a t t g g c a c a t g t t t g t t c t g g a g c a a g a g g a a t a t a g a a a g a a g c a t t g a a t g g g t g 1620  
 t c t a t t g g c t t t g g t c t g g a t t t g c a a g c t t g c a t a g a t c t c a t t g a g a a g c c a a t g g g c 1680  
 a t c c t t t c c a t c c t t g a a g a g a g t g t a t g t t t c c t a a g g c t a c a g a c c t g a c t t t c a a g 1740  
 a c c a a a c t c t t t g a c a a c c a t t t t t g g a a a g t c g g t t c a t c t c c a g a a g c c c a a g c c t g a t 1800

N3027PCT\_sequ.list.txt

aagaagaaat	ttgaagctca	ttttgaactt	gtccattatg	caggagt ggt	accttat aat	1860
atcagt ggtt	ggctggaaaa	gaacaaagac	ctcctta atg	aaacagt ggt	agctgt attt	1920
cagaagt ctt	ccaacagact	cctggcgagc	ctttttgaaa	attacat gag	tactgacagt	1980
gctat accat	ttggggagaa	gaaacgaaag	aaaggagctt	cat t ccaaac	ggt t gcat ct	2040
ctgcat aaag	aaaacct gaa	t aaat t gat g	actaat ct ga	aat caacagc	acct cat ttt	2100
gtgagat gca	t aaat cccaa	tgt gaacaaa	at accaggt a	t act ggaccc	tt act t ggt t	2160
ctacagcagt	tgcgctgt aa	t ggt gt ctt g	gaagggact a	ggat at gccg	t gaaggt ttt	2220
ccaaaccgac	tgcagt at gc	t gat ttt aaa	caaaggt act	gcatt ct gaa	t ccaaggacc	2280
ttt ccaaaga	gcaagt ttt gt	gagcagcaga	aaagcagct g	aagaat t act	t ggct cct t g	2340
gagat agacc	at acccagt a	ccgat ttt gga	at cact aagg	tgt ttttt aa	agct ggggt t t	2400
ctgggccaac	t ggaagcaat	aagagat gag	agact at cta	aagt ct t cac	at t gt t ccaa	2460
gccagagcac	agggcaaact	gat gcgaat c	aaat t ccaga	agat t ct gga	agaaagggat	2520
gcact t attt	t gat ccaat g	gaacat aaga	gct t t cat gg	ct gt gaagaa	ct ggccct gg	2580
atgaggct ct	t ctt caagat	caagcct ctt	gt t aaat ctt	cagaagt agg	agaagaagt a	2640
gct ggact ga	aggaagagt g	tgcacaat ta	cagaaagcct	t ggagaaat c	agagt t t cag	2700
agggaggaac	t gaaagcaaa	gcaagt at cc	ct cact cagg	aaaaaaat ga	cct gat t ctt	2760
cagct t cagg	ct gagcaaga	gacact ggca	aat gt t gaag	agcagt gcga	gt ggct gat t	2820
aaat ccaaga	t ccagct gga	ggccagagt a	aaggagct gt	cggagaggggt	ggaggaagaa	2880
gaggagat aa	at t ct gagct	gact gccagg	gggcggaaac	t cgaagat ga	at gt ttt gag	2940
tt gaagaaag	aaat cgat ga	cct ggaaaca	at gt t ggt ga	agt cagagaa	ggagaagcgt	3000
act acagagc	acaaggt caa	gaact t gact	gaggaagt ag	agt t t ct aaa	t gaggat at c	3060
agcaaact t a	acagagcagc	caaggt t gt g	caggaggccc	at cagcagac	cct ggat gac	3120
ctgcacat gg	aggaggagaa	gct cagcagc	ct gagcaaaag	caaat ct gaa	gct ggaacag	3180
caagt t gat g	agct t gaggg	t gccct t gag	caggagagaa	aagcgagaat	gaact gt gaa	3240
agggaact gc	acaaact gga	gggcaat t t a	aagct gaat c	gggaaagt at	ggagaacct g	3300
gaaagcagcc	agcgacacct	ggcagaagag	ct gaggaaaa	aagaat t aga	at t gagt cag	3360
at gaat t caa	aagt ggagaa	t gagaaaggc	ct ggt agct c	agct t cagaa	gacggt t aaa	3420
gagct t caga	ct caaat aaa	ggat t t gaaa	gagaaact ag	aagct gaaag	gaccact cga	3480
gccaagat gg	aaaggagag	agct gacct c	acccaagacc	t ggct gact t	gaat gagagg	3540
ctggaggagg	taggaggat c	cagt t t ggct	cagct ggaaa	t aact aagaa	acaggaaacc	3600
aaat t ccaga	agct gcaccg	agacat ggaa	gaggccact c	t gcact t t ga	gacaact t ct	3660
gcat ctt t ga	agaagagaca	tgcagacagc	ct ggct gagg	t cgagggcca	ggt agaaaat	3720
ctacagcagg	tcaagcagaa	act ggaaaaa	gacaagagt g	act t gcagct	agaagt agat	3780
gacct cct ga	cccgt gt t ga	gcagat gaca	agagct aagg	caaat gct ga	gaaact ct gt	3840

N3027PCT\_sequ. list.txt

act ct at at g aagagcgct t gcat gaagca act gcaaagc t agat aaggt gact cagt t g	3900
gcaaat gacc t ggcagcaca aaagacaaaag ct gt ggagt g agagt ggcga gt t cct acgg	3960
aggct t gaag agaaggaggc t ct gat aaac caact t t cca gggaaaagag caact t cact	4020
cggcagat t g aagacct gag agggcagct g gaaaaggaga ccaaat ccca gagt gccct g	4080
gccccat gccc t gcagaaggc t cagcgt gac t gt gacct t c t acgagagca gt at gaggaa	4140
gaacaagagg t caaggct ga gct gcaccgg acct t at cca aagt caat gc t gaaat ggt g	4200
caat ggagaa t gaagt at ga aaacaat gt c at ccagagaa cagaagact t ggaggat gcc	4260
aagaaggaac t ggcaat t ag at t gcaggag gcagccgaag ccat ggggggt ggccaat gcc	4320
agaaat gcct cct t ggagag agccaggcac cagct gcagc t ggagct cgg ggacgccct g	4380
t ct gacct cg ggaaggt ccg ct ct gcagca gccaggct gg accagaagca gct gcagt ct	4440
ggcaaggccc t t gccgact g gaagcagaag cagcaggagt cccaggcgt t gct ggat gcc	4500
t ct cagaagg aagt t caggc t ct cagt aca gagct cct ca agct caagaa cacct at gag	4560
gagagcat cg t gggccagga gacact cagg agggagaaca agaacct cca agaagagat t	4620
t ct aat ct ga caaaccaggt t agagaaggg accaagaact t aact gaaat ggaaaaggt c	4680
aagaaact aa t t gaagaaga gaagacagaa gt ccaggt ga cact ggaaga aacagagggga	4740
gccct ggaac gt aat gaaag caagat t ct t cat t t ccagc t t gaact ct t ggaagct aaa	4800
gcagaact t g aaagaaagct t t cagagaaa gat gaagaaa t agaaaat t t t aggaggaag	4860
cagcagt gt a ccat t gact c cct gcagt ct agt ct ggat t ct gaagct aa gagcagaat t	4920
gaggt t accc ggct gaagaa gaagat ggaa gaggacct ca at gagat gga act ccagct t	4980
agct gt gcca accggcaggt gt cagaagca accaaat ccc t gggccagct t cagat t caa	5040
at caaggacc t t caaat gca gct ggat gac agcacacaac t gaacagt ga t ct gaaggag	5100
caggt ggct g t ggct gagcg gcgcaact ct ct t ct t cagt ct gaact aga ggat ct aagg	5160
t cct gcaag agcagacaga gcgt ggccgc aggct gt cag aagaagagct cct ggaagca	5220
acagaaagaa t caat ct t t t ct at acccag aacacaagcc t cct cagcca gaagaagaaa	5280
ct ggaggct g at gt t gcccg gat gcagaaa gaagct gaag aggt ggt gca ggagt gt caa	5340
aat gcagaag agaaggccaa gaaggcagcc at t gaggcag caaact t gt c agaagaact g	5400
aagaagaagc aagacaccat t gccact t g gaaaggacaa gagaaaat at ggagcagaca	5460
at t acagact t acagaaaag gct ggct gaa gct gaacaga t ggccct gat ggggagt aga	5520
aagcaaat cc agaaact aga at ccagggt t cgt gaact gg aaggt gaact ggagggt gaa	5580
at ccgt cgca gt gcagaggc ccagagggga gcccgcagac t t gagcgat g cat caaagag	5640
ct gacct at c aggcagagga agacaagaag aat ct gagca ggat gcaaac t cagat ggat	5700
aaact t cagc t aaaagt gca aaat t acaag cagcaagt cg aggt ggcgga aacacaagcc	5760
aat caat acc t t t ccaagt a t aagaaacag caacat gagt t gaat gaagt gaaggaaagg	5820
gcagaggt gg cagaat ct ca agt caat aaa ct caaaat t a aagcaagaga gt t t gggaaa	5880
aaggt t caag aagaat agca t cccct gct t t gaaaggaca acagct ggag aagt acaagg	5940

N3027PCT\_sequ.list.txt

```

aaggtgctgt ttcatggcca aaaacttagg ttgcatggaa acatTTTTaa aaacatgttt 6000
aaattgcttt t cacaccata taaacaaggc aattagaaaa ataat aaag ggaat at cat 6060
tgcttccaca gttaatgggg attttttgat cctcaaatgc aagt aaact a ccttctaatg 6120
cttcacatga cagattaaat aaatggaaga accttttcaa ttctgatgtt taaaaaatga 6180
ataaatactt gatcctttgt ccatatttcc tcttaatggg taggactcat agaagatgtc 6240
cttagaccag tcacgcttca tggggactag ggcatgttgg tgaatggttt ttactaaagt 6300
taggcaactt tggcttgatt caccctaaa tctatgaatg tatattgtga gccagcagt g 6360
gtagaatgga agtcataga tctcctcagc attgtgat at aaat at agct at agt taggc 6420
aat tt gaaca t gt aggcaaa actctcctaa tcaacacaca t gt aggct at at gct ggt ac 6480
atgctttaaa catggaggt a accccacacg agacattcag tgacaggtaa tatgctggat 6540
ttgtgcagta ccgatttggc tcagctggag gaacatgtcc cggaattcct ctctctcatg 6600
gttctggatt ggagt aggtc ataaagaaat ttgcattaat ttgatcagca gctattttat 6660
actcat aagg tcagtgtaca gaccaagca tggtgacagc ttgaaaat at gactccaggc 6720
caaaaagggg agctagaaga gaccagagac agctccctgg acccagagct ctccagctc 6780
ctgccagcct cctccttcag ctttgcaaag tactggccag gtgtgtgtgc agctccatgg 6840
caaccagcat cagcttttcc tgagatcaca cacagcattg cagtggaggc cgtgagacag 6900
acatgggttc tgtttgttct tatggacttc ccttcatcct tgctgcattc acagt cgacc 6960
tacagt gact tcaggcccag aaccagatgc agaggaaca gcctggccta gacttctcca 7020
ccagcaccca caattgtgta aggctgaagc tctataat aa atctttattc tgtc 7074

```

<210> 88  
 <211> 1946  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1946)  
 <223> myosin, heavy chain 15 (MYH15)

<400> 88

Met Val Glu Ser Cys Leu Leu Thr Phe Arg Ala Phe Phe Trp Trp Ile  
 1 5 10 15

Ala Leu Ile Lys Met Asp Leu Ser Asp Leu Gly Glu Ala Ala Ala Phe  
 20 25 30

Leu Arg Arg Ser Glu Ala Glu Leu Leu Leu Glu Ala Thr Ala Leu  
 35 40 45

Asp Gly Lys Lys Lys Cys Trp Ile Pro Asp Gly Glu Asn Ala Tyr Ile  
 50 55 60

N3027PCT\_sequ.list.txt

G u A l a G u V a l L y s G y S e r G u A s p A s p G y T h r V a l I l e V a l G u  
 65 70 75 80  
 T h r A l a A s p G y G u S e r L e u S e r I l e L y s G u A s p L y s I l e G n G n  
 85 90 95  
 M e t A s n P r o P r o G u P h e G u M e t I l e G u A s p M e t A l a M e t L e u T h r  
 100 105 110  
 H i s L e u A s n G u A l a S e r V a l L e u H i s T h r L e u L y s A r g A r g T y r G y  
 115 120 125  
 G n T r p M e t I l e T y r T h r T y r S e r G y L e u P h e C y s V a l T h r I l e A s n  
 130 135 140  
 P r o T y r L y s T r p L e u P r o V a l T y r G n L y s G u V a l M e t A l a A l a T y r  
 145 150 155 160  
 L y s G y L y s A r g A r g S e r G u A l a P r o P r o H i s I l e P h e A l a V a l A l a  
 165 170 175  
 A s n A s n A l a P h e G n A s p M e t L e u H i s A s n A r g G u A s n G n S e r I l e  
 180 185 190  
 L e u P h e T h r G y G u S e r G y A l a G y L y s T h r V a l A s n S e r L y s H i s  
 195 200 205  
 I l e I l e G n T y r P h e A l a T h r I l e A l a A l a M e t I l e G u S e r A r g L y s  
 210 215 220  
 L y s G n G y A l a L e u G u A s p G n I l e M e t G n A l a A s n T h r I l e L e u  
 225 230 235 240  
 G u A l a P h e G y A s n A l a L y s T h r L e u A r g A s n A s p A s n S e r S e r A r g  
 245 250 255  
 P h e G y L y s P h e I l e A r g M e t H i s P h e G y A l a A r g G y M e t L e u S e r  
 260 265 270  
 S e r V a l A s p I l e A s p I l e T y r L e u L e u G u L y s S e r A r g V a l I l e P h e  
 275 280 285  
 G n G n A l a G y G u A r g A s n T y r H i s I l e P h e T y r G n I l e L e u S e r  
 290 295 300  
 G y G n L y s G u L e u H i s A s p L e u L e u L e u V a l S e r A l a A s n P r o S e r  
 305 310 315 320  
 A s p P h e H i s P h e C y s S e r C y s G y A l a V a l T h r V a l G u S e r L e u A s p  
 325 330 335  
 A s p A l a G u G u L e u L e u A l a T h r G u G n A l a M e t A s p I l e L e u G y  
 Page 429

340

345

350

Phe Leu Pro Asp Glu Lys Tyr Gly Cys Tyr Lys Leu Thr Gly Ala Ile  
 355 360 365  
 Met His Phe Gly Asn Met Lys Phe Lys Gln Lys Pro Arg Glu Glu Gln  
 370 375 380  
 Leu Glu Ala Asp Gly Thr Glu Asn Ala Asp Lys Ala Ala Phe Leu Met  
 385 390 395 400  
 Gly Ile Asn Ser Ser Glu Leu Val Lys Cys Leu Ile His Pro Arg Ile  
 405 410 415  
 Lys Val Gly Asn Glu Tyr Val Thr Arg Gly Gln Thr Ile Glu Gln Val  
 420 425 430  
 Thr Cys Ala Val Gly Ala Leu Ser Lys Ser Met Tyr Glu Arg Met Phe  
 435 440 445  
 Lys Trp Leu Val Ala Arg Ile Asn Arg Ala Leu Asp Ala Lys Leu Ser  
 450 455 460  
 Arg Gln Phe Phe Ile Gly Ile Leu Asp Ile Thr Gly Phe Glu Ile Leu  
 465 470 475 480  
 Glu Tyr Asn Ser Leu Glu Gln Leu Cys Ile Asn Phe Thr Asn Glu Lys  
 485 490 495  
 Leu Gln Gln Phe Phe Asn Trp His Met Phe Val Leu Glu Gln Glu Glu  
 500 505 510  
 Tyr Lys Lys Glu Ser Ile Glu Trp Val Ser Ile Gly Phe Gly Leu Asp  
 515 520 525  
 Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met Gly Ile Leu Ser  
 530 535 540  
 Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr Asp Leu Thr Phe  
 545 550 555 560  
 Lys Thr Lys Leu Phe Asp Asn His Phe Gly Lys Ser Val His Leu Gln  
 565 570 575  
 Lys Pro Lys Pro Asp Lys Lys Lys Phe Glu Ala His Phe Glu Leu Val  
 580 585 590  
 His Tyr Ala Gly Val Val Pro Tyr Asn Ile Ser Gly Trp Leu Glu Lys  
 595 600 605  
 Asn Lys Asp Leu Leu Asn Glu Thr Val Val Ala Val Phe Gln Lys Ser  
 610 615 620

N3027PCT\_sequ.list.txt

Ser Asn Arg Leu Leu Ala Ser Leu Phe Glu Asn Tyr Met Ser Thr Asp  
625 630 635 640

Ser Ala Ile Pro Phe Gly Glu Lys Lys Arg Lys Lys Gly Ala Ser Phe  
645 650 655

Gln Thr Val Ala Ser Leu His Lys Glu Asn Leu Asn Lys Leu Met Thr  
660 665 670

Asn Leu Lys Ser Thr Ala Pro His Phe Val Arg Cys Ile Asn Pro Asn  
675 680 685

Val Asn Lys Ile Pro Gly Ile Leu Asp Pro Tyr Leu Val Leu Gln Gln  
690 695 700

Leu Arg Cys Asn Gly Val Leu Glu Gly Thr Arg Ile Cys Arg Glu Gly  
705 710 715 720

Phe Pro Asn Arg Leu Gln Tyr Ala Asp Phe Lys Gln Arg Tyr Cys Ile  
725 730 735

Leu Asn Pro Arg Thr Phe Pro Lys Ser Lys Phe Val Ser Ser Arg Lys  
740 745 750

Ala Ala Glu Glu Leu Leu Gly Ser Leu Glu Ile Asp His Thr Gln Tyr  
755 760 765

Arg Phe Gly Ile Thr Lys Val Phe Phe Lys Ala Gly Phe Leu Gly Gln  
770 775 780

Leu Glu Ala Ile Arg Asp Glu Arg Leu Ser Lys Val Phe Thr Leu Phe  
785 790 795 800

Gln Ala Arg Ala Gln Gly Lys Leu Met Arg Ile Lys Phe Gln Lys Ile  
805 810 815

Leu Glu Glu Arg Asp Ala Leu Ile Leu Ile Gln Trp Asn Ile Arg Ala  
820 825 830

Phe Met Ala Val Lys Asn Trp Pro Trp Met Arg Leu Phe Phe Lys Ile  
835 840 845

Lys Pro Leu Val Lys Ser Ser Glu Val Gly Glu Glu Val Ala Gly Leu  
850 855 860

Lys Glu Glu Cys Ala Gln Leu Gln Lys Ala Leu Glu Lys Ser Glu Phe  
865 870 875 880

Gln Arg Glu Glu Leu Lys Ala Lys Gln Val Ser Leu Thr Gln Glu Lys  
885 890 895

N3027PCT\_sequ.list.txt

Asn Asp Leu Ile Leu Gln Leu Gln Ala Glu Gln Glu Thr Leu Ala Asn  
900 905 910

Val Glu Glu Gln Cys Glu Trp Leu Ile Lys Ser Lys Ile Gln Leu Glu  
915 920 925

Ala Arg Val Lys Glu Leu Ser Glu Arg Val Glu Glu Glu Glu Glu Ile  
930 935 940

Asn Ser Glu Leu Thr Ala Arg Gly Arg Lys Leu Glu Asp Glu Cys Phe  
945 950 955 960

Glu Leu Lys Lys Glu Ile Asp Asp Leu Glu Thr Met Leu Val Lys Ser  
965 970 975

Glu Lys Glu Lys Arg Thr Thr Glu His Lys Val Lys Asn Leu Thr Glu  
980 985 990

Glu Val Glu Phe Leu Asn Glu Asp Ile Ser Lys Leu Asn Arg Ala Ala  
995 1000 1005

Lys Val Val Gln Glu Ala His Gln Gln Thr Leu Asp Asp Leu His  
1010 1015 1020

Met Glu Glu Glu Lys Leu Ser Ser Leu Ser Lys Ala Asn Leu Lys  
1025 1030 1035

Leu Glu Gln Gln Val Asp Glu Leu Glu Gly Ala Leu Glu Gln Glu  
1040 1045 1050

Arg Lys Ala Arg Met Asn Cys Glu Arg Glu Leu His Lys Leu Glu  
1055 1060 1065

Gly Asn Leu Lys Leu Asn Arg Glu Ser Met Glu Asn Leu Glu Ser  
1070 1075 1080

Ser Gln Arg His Leu Ala Glu Glu Leu Arg Lys Lys Glu Leu Glu  
1085 1090 1095

Leu Ser Gln Met Asn Ser Lys Val Glu Asn Glu Lys Gly Leu Val  
1100 1105 1110

Ala Gln Leu Gln Lys Thr Val Lys Glu Leu Gln Thr Gln Ile Lys  
1115 1120 1125

Asp Leu Lys Glu Lys Leu Glu Ala Glu Arg Thr Thr Arg Ala Lys  
1130 1135 1140

Met Glu Arg Glu Arg Ala Asp Leu Thr Gln Asp Leu Ala Asp Leu  
1145 1150 1155

Asn G u Arg Leu G u G u Val G y G y Ser Ser Leu Ala G n Leu  
 1160 1165 1170  
 G u I l e Thr Lys Lys G n G u Thr Lys Phe G n Lys Leu H i s Arg  
 1175 1180 1185  
 Asp Met G u G u Ala Thr Leu H i s Phe G u Thr Thr Ser Ala Ser  
 1190 1195 1200  
 Leu Lys Lys Arg H i s Ala Asp Ser Leu Ala G u Leu G u G y G n  
 1205 1210 1215  
 Val G u Asn Leu G n G n Val Lys G n Lys Leu G u Lys Asp Lys  
 1220 1225 1230  
 Ser Asp Leu G n Leu G u Val Asp Asp Leu Leu Thr Arg Val G u  
 1235 1240 1245  
 G n Met Thr Arg Ala Lys Ala Asn Ala G u Lys Leu Cys Thr Leu  
 1250 1255 1260  
 Tyr G u G u Arg Leu H i s G u Ala Thr Ala Lys Leu Asp Lys Val  
 1265 1270 1275  
 Thr G n Leu Ala Asn Asp Leu Ala Ala G n Lys Thr Lys Leu Trp  
 1280 1285 1290  
 Ser G u Ser G y G u Phe Leu Arg Arg Leu G u G u Lys G u Ala  
 1295 1300 1305  
 Leu I l e Asn G n Leu Ser Arg G u Lys Ser Asn Phe Thr Arg G n  
 1310 1315 1320  
 I l e G u Asp Leu Arg G y G n Leu G u Lys G u Thr Lys Ser G n  
 1325 1330 1335  
 Ser Ala Leu Ala H i s Ala Leu G n Lys Ala G n Arg Asp Cys Asp  
 1340 1345 1350  
 Leu Leu Arg G u G n Tyr G u G u G u G n G u Val Lys Ala G u  
 1355 1360 1365  
 Leu H i s Arg Thr Leu Ser Lys Val Asn Ala G u Met Val G n Trp  
 1370 1375 1380  
 Arg Met Lys Tyr G u Asn Asn Val I l e G n Arg Thr G u Asp Leu  
 1385 1390 1395  
 G u Asp Ala Lys Lys G u Leu Ala I l e Arg Leu G n G u Ala Ala  
 1400 1405 1410  
 G u Ala Met G y Val Ala Asn Ala Arg Asn Ala Ser Leu G u Arg

1415														
Ala	Arg	His	Gln	Leu	Gln	Leu	Glu	Leu	Gly	Asp	Ala	Leu	Ser	Asp
1430						1435					1440			
Leu	Gly	Lys	Val	Arg	Ser	Ala	Ala	Ala	Arg	Leu	Asp	Gln	Lys	Gln
1445						1450					1455			
Leu	Gln	Ser	Gly	Lys	Ala	Leu	Ala	Asp	Trp	Lys	Gln	Lys	His	Glu
1460						1465					1470			
Glu	Ser	Gln	Ala	Leu	Leu	Asp	Ala	Ser	Gln	Lys	Glu	Val	Gln	Ala
1475						1480					1485			
Leu	Ser	Thr	Glu	Leu	Leu	Lys	Leu	Lys	Asn	Thr	Tyr	Glu	Glu	Ser
1490						1495					1500			
Ile	Val	Gly	Gln	Glu	Thr	Leu	Arg	Arg	Glu	Asn	Lys	Asn	Leu	Gln
1505						1510					1515			
Glu	Glu	Ile	Ser	Asn	Leu	Thr	Asn	Gln	Val	Arg	Glu	Gly	Thr	Lys
1520						1525					1530			
Asn	Leu	Thr	Glu	Met	Glu	Lys	Val	Lys	Lys	Leu	Ile	Glu	Glu	Glu
1535						1540					1545			
Lys	Thr	Glu	Val	Gln	Val	Thr	Leu	Glu	Glu	Thr	Glu	Gly	Ala	Leu
1550						1555					1560			
Glu	Arg	Asn	Glu	Ser	Lys	Ile	Leu	His	Phe	Gln	Leu	Glu	Leu	Leu
1565						1570					1575			
Glu	Ala	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Leu	Ser	Glu	Lys	Asp	Glu
1580						1585					1590			
Glu	Ile	Glu	Asn	Phe	Arg	Arg	Lys	Gln	Gln	Cys	Thr	Ile	Asp	Ser
1595						1600					1605			
Leu	Gln	Ser	Ser	Leu	Asp	Ser	Glu	Ala	Lys	Ser	Arg	Ile	Glu	Val
1610						1615					1620			
Thr	Arg	Leu	Lys	Lys	Lys	Met	Glu	Glu	Asp	Leu	Asn	Glu	Met	Glu
1625						1630					1635			
Leu	Gln	Leu	Ser	Cys	Ala	Asn	Arg	Gln	Val	Ser	Glu	Ala	Thr	Lys
1640						1645					1650			
Ser	Leu	Gly	Gln	Leu	Gln	Ile	Gln	Ile	Lys	Asp	Leu	Gln	Met	Gln
1655						1660					1665			
Leu	Asp	Asp	Ser	Thr	Gln	Leu	Asn	Ser	Asp	Leu	Lys	Glu	Gln	Val
1670						1675					1680			

N3027PCT\_sequ.list.txt

Ala	Val	Ala	Glu	Arg	Arg	Asn	Ser	Leu	Leu	Gln	Ser	Glu	Leu	Glu
	1685					1690					1695			
Asp	Leu	Arg	Ser	Leu	Gln	Glu	Gln	Thr	Glu	Arg	Gly	Arg	Arg	Leu
	1700					1705					1710			
Ser	Glu	Glu	Glu	Leu	Leu	Glu	Ala	Thr	Glu	Arg	Ile	Asn	Leu	Phe
	1715					1720					1725			
Tyr	Thr	Gln	Asn	Thr	Ser	Leu	Leu	Ser	Gln	Lys	Lys	Lys	Leu	Glu
	1730					1735					1740			
Ala	Asp	Val	Ala	Arg	Met	Gln	Lys	Glu	Ala	Glu	Glu	Val	Val	Gln
	1745					1750					1755			
Glu	Cys	Gln	Asn	Ala	Glu	Glu	Lys	Ala	Lys	Lys	Ala	Ala	Ile	Glu
	1760					1765					1770			
Ala	Ala	Asn	Leu	Ser	Glu	Glu	Leu	Lys	Lys	Lys	Gln	Asp	Thr	Ile
	1775					1780					1785			
Ala	His	Leu	Glu	Arg	Thr	Arg	Glu	Asn	Met	Glu	Gln	Thr	Ile	Thr
	1790					1795					1800			
Asp	Leu	Gln	Lys	Arg	Leu	Ala	Glu	Ala	Glu	Gln	Met	Ala	Leu	Met
	1805					1810					1815			
Gly	Ser	Arg	Lys	Gln	Ile	Gln	Lys	Leu	Glu	Ser	Arg	Val	Arg	Glu
	1820					1825					1830			
Leu	Glu	Gly	Glu	Leu	Glu	Gly	Glu	Ile	Arg	Arg	Ser	Ala	Glu	Ala
	1835					1840					1845			
Gln	Arg	Gly	Ala	Arg	Arg	Leu	Glu	Arg	Cys	Ile	Lys	Glu	Leu	Thr
	1850					1855					1860			
Tyr	Gln	Ala	Glu	Glu	Asp	Lys	Lys	Asn	Leu	Ser	Arg	Met	Gln	Thr
	1865					1870					1875			
Gln	Met	Asp	Lys	Leu	Gln	Leu	Lys	Val	Gln	Asn	Tyr	Lys	Gln	Gln
	1880					1885					1890			
Val	Glu	Val	Ala	Glu	Thr	Gln	Ala	Asn	Gln	Tyr	Leu	Ser	Lys	Tyr
	1895					1900					1905			
Lys	Lys	Gln	Gln	His	Glu	Leu	Asn	Glu	Val	Lys	Glu	Arg	Ala	Glu
	1910					1915					1920			
Val	Ala	Glu	Ser	Gln	Val	Asn	Lys	Leu	Lys	Ile	Lys	Ala	Arg	Glu
	1925					1930					1935			

N3027PCT\_sequ.list.txt

Phe Gly Lys Lys Val Gln Gu Gu  
1940 1945

<210> 89  
<211> 11876  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_feat ure  
<222> (1)..(11876)  
<223> unconv ent i onal myosi n- 15

<400> 89  
gggct gggcc t ccct t cccc at aacact ga gct gct ct gc t gggccaacc gt gct cct gg 60  
gccagccaga ggacccccat gaggcggcat gcaggcgggg agcaggccac agaacgcagg 120  
gt gaaaccca aggcgct ct a gaggagat ga at t at ggat c cgccct cccg gaat cct ggc 180  
t cggccct cc ccacgccacc cagggccagt cgggt ct gct cacagcccga ggaggccgcg 240  
t gt ccagccg cgggcaagag accgagcagg t ccct gt gt c t ccaagt ccc t gagcccgt g 300  
acaccggccc caggccct gt agagagcagg cagccaccat ggccaaggag gaagat gagg 360  
agaagaaagc caagaaaggg aagaagggga agaaggcacc ggagccggag aagcccaaac 420  
ggagcct gaa ggggacgt cg cggct gt t ca t gggct t ccg cgaccgt aca cccaagat ct 480  
ccaagaaggg ccagt t ccgc agcgcct cgg cct t ct t ct g gggcct ccac accggccccc 540  
agaagaccaa gcgcaagagg aaggcccgca ccgt gct caa gt ccacgt ca aagct cat ga 600  
cgcagat gcg cat gggcaag aagaagcggg cgat gaaggg caagaagccg t cct t cat gg 660  
t gat ccgct t cccaggccgc cgt ggct acg gccgcct gcg gccgcgcgcc cggc cact ca 720  
gcaaagcgt c cacggccat c aact ggct ca caaaaaagt t cct cct caag aaggccgagg 780  
agt cgggcag cgaacaggcc acagt ggacg cct ggct gca gcgct cgagc t cccgcat gg 840  
gct cccgcaa act cccct t c ccgt cgggt g ccgagat cct gcggcct ggg ggccggct cc 900  
ggagggt t ccc ccgcagccgc agcat ct acg cgt caggcga gcccct gggc t t cct gccct 960  
t cgaggacga ggccccat t c cat cact cgg gct cccgcaa gt cgct gt ac gggct t gagg 1020  
gct t ccagga cct gggcgag t at t at gact at caccgcga cggcgacgac t act acgacc 1080  
ggcagt cact ccaccgct ac gaggagcagg aaccct acct ggcgggcct c ggcccct aca 1140  
gcccggcct g gccaccct ac ggcgaccact act acgggt a cccgcccagag gat ccct acg 1200  
act act acca ccccgact at t acggt ggcc cct t t gat cc ggggt acacc t acggct acg 1260  
gct acgacga t t acgaaccc ccat at gcgc ccccgct cggg gt act cgt ct cct t acagct 1320  
accacgat gg gt acgagggc gaggcgcacc ct t at ggct a ct acct ggat ccct at gcgc 1380  
cgt acgacgc gccat accca ccct at gacc t cccat acca cact ccct ac gat gt accct 1440  
act t t gat cc ct acggagt c cact acaccg t cccct at gc cgaaggcgt c t at ggcgggt g 1500  
gggacgaggc cat ct acccc cccgaggt gc cct at t t t t a cccggaggag t cggct t cgg 1560

N3027PCT\_sequ. list.txt

cct t t gt gt a	cccc t ggg t a	ccaccgcccc	t cccgt cgcc	ccacaaccg	t at gcccacg	1620
ccat ggat ga	cat cgccgag	ct ggaggaac	cagaggacgc	gggcgt agag	cgt cagggga	1680
cct cct t ccg	cct gcccagc	gccgcct t ct	t cgagcagca	aggcat ggat	aagcccgcc	1740
gg t ccaagct	gt ccc t cat c	cgcaagt t cc	gcct ct t ccc	gcgaccccag	gt gaagct gt	1800
t t gggaagga	gaagct ggag	gt gcccct gc	caccct ct ct	ggacat t cct	ct cccct t gg	1860
gggat gcgga	cgaagaagag	gacgaggagg	agct gcccc	gg t t t ccgct	gt gccct acg	1920
gccaccct t t	ct ggggct t c	ct cacgccgc	gccagcgcaa	cct ccagcgc	gcgct gt cgg	1980
cct t cggcgc	ccaccggggc	ct gggct t cg	gccct gagt t	t ggccgcccc	gt gcct cgcc	2040
ct gccacct c	gct t gcgcgg	t t cct caaga	agacgct gt c	ggagaagaag	cccat cgcg	2100
ggct cagggg	cagccagaag	acccggggcg	gcggccct gc	t gt cagggag	gcggcct aca	2160
aacgct t cgg	ct acaagct g	gct ggcat gg	accccgagaa	gcccggcacg	cccat cgt gc	2220
t gaggagggc	ccagccgcgc	gct cgcagca	gcaacgacgc	gcgcccgcg	cccgcgccac	2280
agcccgcgcc	caggaccct c	t cccact gga	gcgcgct cct	gt ct ccgccc	gt gccccgc	2340
ggccccaaag	ct ccggggcc	ccgcccgcgc	cgccgct ct c	cccggcgct c	t cgggcct gc	2400
cccggccggc	ct cgccct ac	ggct cct cc	gccgccacc	gccgcct gg	gccgcccag	2460
cgcacgt gcc	accggcgccg	caggccagcg	gg t gggcct t	cgt ggagccc	cct gccgt ga	2520
gcccggaggt	gcccccgac	ct act agcct	t cccagggcc	ccgaccct cg	t t caggggct	2580
cccggccggag	aggggcggct	t t cggct t cc	ccggggcct c	t ccacgggcg	t cgcggaggc	2640
gagct t ggt c	accgct ggcc	t cgccccagc	cct cgct gag	gagct cgccg	ggcct cggct	2700
act gct cacc	ct t ggcgccc	ccgt cgcct c	agct gt cct t	gcgcacgggc	ccct t ccagc	2760
cgccct t cct	gcccccgcc	cgccggcccc	gct cgct gca	ggagt ccca	gccccacgcc	2820
gagccgct gg	gcgcct gggc	ccaccgggct	cgccgct gcc	gggct cacc	aggccgcct	2880
cgccgccccct	ggggct ct gc	cacagcccgc	ggcgcagct c	cct gaat ct g	ccct cgcgcc	2940
t cccgcacac	gt ggcgggcg	ct cagcgagc	caccact cg	ggct gt gaag	ccgcaagt gc	3000
gcct gccct t	ccaccgaccg	cccagggccg	gggcct ggcg	ggcgcccct g	gaacaccggg	3060
agagcccgcg	agaaccgag	gact cagaga	cgccct ggac	t gt gccccca	ct ggccccca	3120
gct gggacgt	ggacat gcct	cccacccaac	gcccaccct c	cccct ggcca	ggaggt gcag	3180
gcagccgccg	aggct t t t cc	aggccacccc	ct gt gccgga	aaaccct t t	ct ccagct cc	3240
t gggccct gt	gccat cccc	accct ccagc	ct gaggat cc	agct gct gat	at gaccaggg	3300
t ct t cct ggg	cagacacat	gagccggggc	ct ggacagct	caccaa t ca	gct ggcccaa	3360
cccct gagaa	gcct gaagaa	gaggccaccc	t gggggaccc	ccagct gcca	gcagagacca	3420
agcct ccaac	cccagcacct	ccaaggat g	t cact cccc	caaggat at c	act cccccca	3480
aggat gt cct	cccagagcaa	aagacat t aa	ggcccagcct	ct cat accca	ct ggct gcgt	3540
gt gaccagac	cagggccaca	t ggccacat	ggcaccgct g	gggaacact g	ccccaagccg	3600
cagccccct t	ggcgcccat c	agggccccag	agccct gcc	caaggggggt	gaacggcgcc	3660

N3027PCT\_sequ. list . . txt

aggcagcccc	tgggcgtttt	gctgtggtca	tgcctcgtgt	gcagaagctg	agctctttcc	3720
agcgagttgg	gcctgcaacc	ctgaagcctc	aagtcagacc	catcaggac	cccaagccaa	3780
gagcctgtag	tcttcgctgg	tcttgcctct	ggcttcgggc	agatgcctat	ggaccctggc	3840
cacgagtaca	cacccatccc	cagtcctgcc	acctgggccc	tggagctgcc	tgcctgtccc	3900
ttaggggctc	ctgggaggag	gtcggcccg	caagctggcg	gaacaagatg	cactccatcc	3960
gcaacctgcc	atccatgcgg	ttccgtgagc	agcacgggga	ggatggtgtg	gaggacatga	4020
cacagctgga	agacctccag	gaaaccactg	tgctgtccaa	cctcaagatt	agatttgaac	4080
ggaacctcat	ctacacatac	attgggagca	tcttgggtgtc	ggtgaacca	taccaaagt	4140
ttggaatcta	tgggccggag	caggtgcagc	agtacaacgg	acgggccctg	ggagagaatc	4200
ccccgcacct	ctttgctgtt	gcaaactctcg	ccttcgcca	aatgctcgat	gccaaacaga	4260
accagtgcac	aatcattagt	ggagagagcg	gctctggcaa	aactgaggcc	accaagctga	4320
ttctgcgcta	cctggccgcc	atgaaccaga	aacgggaggt	catgcagcag	ataagatcc	4380
tggaggcaac	accctcttg	gagtccttcg	gtaatgcaa	aaccgtcagg	aacgacaact	4440
ccagccgctt	tgggaagttt	gtggaaactc	ttctggaagg	gggcgtgatc	tctggtgcca	4500
taacctccca	gtacctgctt	gagaaatcca	ggatcgtgtt	tcaggccaaa	aacgagagga	4560
attaccacat	cttctacgag	ttgctggccg	ggttgcctgc	ccagctcagg	caggccttta	4620
gcctgcaaga	ggctgagacc	tactactatc	tgaaccaggg	tgggaactgt	gagatagcag	4680
gaaagagcga	tgcagatgac	tttcgccggc	tcttggctgc	catggaggtg	ttgggcttca	4740
gcagtgagga	ccaggacagc	atcttccgca	tcttggcctc	catcctgcac	ctgggcaacg	4800
tctactttga	gaagtatgag	acggatgcac	aggaggtggc	ctcagtggtg	agtccccgag	4860
agatccaggc	cgtggcagag	ctgctgcaga	tctcccctga	gggcctgcag	aaggccatca	4920
ccttcaaagt	gaccgagaca	atgcgagaga	agatcttcac	gcccctaa	gtggagagcg	4980
ctgtggatgc	cagggaacgc	atcgccaagg	tcttgtatgc	actgctgttc	agctggctca	5040
tcaccaggg	caacgcgctg	gtgtccccaa	ggcaggacac	actgtccatc	gccatcctgg	5100
acatctatgg	tttcgaggac	ctgagcttca	acagctttga	gcagctgtgt	attaaactacg	5160
caaacgagaa	ccttcagtac	cttttcaaca	agatcgtctt	ccaggaggag	caggaggagt	5220
acatccgtga	gcagatagac	tggcaggaga	tcacctttgc	tgacaaccag	ccccgcacat	5280
acctcatctc	actgaagcct	tatggcatcc	tgcggatcct	tgacgaccag	tgttgctttc	5340
cccaggctac	agaccacacc	ttcctacaga	agtgccacta	ccatcatggc	gccaacccgc	5400
tctattccaa	acccaagatg	ccgctgcctg	agttcaccat	caagcactat	gcaggcaagg	5460
tcacctacca	ggtgcacaag	ttcctggaca	agaaccacga	ccaagtgcgc	caggatgtgc	5520
tggacctgtt	cgtacggagc	cggacacggg	tgggggcaca	cctcttctcc	agccatgccc	5580
cacaggctgc	ccctcagcgc	ctgggcaaga	gcagctccgt	cactcggctc	tacaaggcgc	5640
acactgtggc	cgccaagttc	cagcagtcac	tcttggatct	ggtggaaaag	atggagaggt	5700

N3027PCT\_sequ. list.txt

gcaacccct t	gt t cat gcgt	t gcct gaagc	ccaaccacaa	gaaggagcca	ggt ct ct t t g	5760
agccagat gt	ggt aat ggca	caat t acgct	at t caggggt	gct ggagacc	gt gaggat cc	5820
gcaaggagg	at t t ccagt g	cgcct gcct t	t ccaggggt t	cat cgacagg	t act gct gt c	5880
t agt ggccct	caagcat gac	ct gccggct a	at ggggacat	gt gt gt gt ca	gt gct gagt c	5940
gcct gt gcaa	agt cat gcc	aacat gt acc	gt gt t ggggt	cagcaagct g	t t cct t aagg	6000
aacacct at a	ccagct gct g	gagagt at gc	gagagcat gt	cct gaat ct g	gcagccct ca	6060
ct ct gcagcg	ct gcct ccgt	ggct t ct t ca	t t aagcggcg	at t ccgct ct	ct gcgccaca	6120
agat cat cct	gct gcaaagc	cggggcccg t g	gct acct t gc	caggcaacgc	t at cagcaga	6180
t gaggaggag	t ct ggt gaag	t t ccggt ccc	t ggt acacgc	at acgt gagc	cgccgacgct	6240
at ct caagct	gagggcagag	t ggaggt gcc	aggt ggaggg	ggcgct gct g	t gggagcagg	6300
aggagct gag	caagcgggag	gt agt cgct g	t ggggcacct	ggaggt accg	gct gagct gg	6360
ct gggct ct t	gcaagcagt g	gcaggcct cg	ggct ggccca	ggt gcct cag	gt ggcccct g	6420
t gaggact cc	t cgact ccag	gct gagcccc	gt gt cacact	gcccct ggac	at caacaact	6480
at cct at ggc	caagt t t gt c	cagt gccact	t caaggaacc	t gcct t t ggg	at gct gacag	6540
t gcccct gag	gacacccct c	acgcagct gc	cagccgagca	ccat gcagaa	gccgt gagca	6600
t ct t caagct	gat cct gcgc	t t cat gggcg	acccccacct	gcat ggt gcc	cgggagaaca	6660
t ct t cgggaa	ct acat cgt g	cagaaggggc	t ggcggt gcc	t gagct gcgg	gat gagat cc	6720
t ggcacagct	ggccaat cag	gt gt ggcaca	at cacaat gc	ccacaat gct	gagcggggct	6780
ggct gct gct	ggccgcct gc	ct cagt ggct	t t gcacct t c	cccgt gct t c	aacaagt acc	6840
t t ct caagt t	t gt gt ct gat	t at gggcgga	at ggct t cca	ggct gt gt gt	cagcaccgcc	6900
t cat gcaggc	cat gggccgg	gccaacagc	agggct cggg	ggct gcccg	acct t acccc	6960
cgaccagct	cgagt ggaca	gcgacct at g	agaaggccag	cat ggcgct g	gacgt gggct	7020
gct t caat gg	t gaccagt t c	t cct gcccg	t gcact cct g	gagt acgggg	gaagaggt gg	7080
ct ggagacat	t ct gaggcac	agggggct gg	cagat ggct g	gcgcggct gg	accgt ggcca	7140
t gaagaat gg	t gt ccagt gg	gcagagct gg	ct ggccacga	ct acgt gt t a	gacct ggt gt	7200
cggacct gga	gct gct cagg	gact t ccct c	gacagaagt c	ct act t cat t	gt gggcacag	7260
aggggcct gc	agccagcagg	ggaggcccca	aagt ggt gt t	t gggaacagc	t gggact cgg	7320
at gaggacat	gt ccact aga	ccccagcccc	aggagcat	gccc aaagt a	ct t gact ct g	7380
at gggat acag	cagccacaat	caggacggt a	caaat gggga	gact gaggcc	caaagaggga	7440
cagcaaccca	ccaagagt ca	gacagt ct t g	gagagcct gc	t gt gccccac	aaggggct gg	7500
act gct acct	ggat agcct c	t t cgaccct g	t gct gt cct a	cggggat gcg	gacct ggaga	7560
agccaacagc	cat t gcct ac	cgcat gaaag	ggggaggcca	gcccgggt gga	ggcagcagt a	7620
gt ggt act ga	agacaccccc	aggagacccc	cagagccaaa	gccaat ccca	ggcct ggat g	7680
cct ccacat t	ggct ct gcag	caagcct t ca	t ccacaaaca	ggccgt gct g	ct ggcccggg	7740
ggat gaccct	gcaggccacg	gcact ccagc	agcaacccct	gagt gct gcc	ct gagat cct	7800

N3027PCT\_sequ. list . . txt

t gcccgcaga	gaaacccccca	gcaccagagg	cacagccgac	gt ct gt gggc	accggt cccc	7860
ct gccaaacc	cgt gct cct g	cgt gccact c	caaagccct t	ggccccagcc	cct ct ggcca	7920
aggct ccaag	gct ccccat c	aagcct gt gg	ct gcccct gt	t ct agct cag	gat caggct t	7980
ct ccagaaac	cact t cacc	t cccagagc	t ggt ccggt a	ct ct acgct c	aact ct gagg	8040
act t cccaca	gcccacacag	cagat caaga	at at t gt cag	gcagt accag	cagccgt t cc	8100
ggggaggccg	gcct gaggcc	ct caggaagg	at ggcgggaa	agt gt t cat g	aagcggccag	8160
accct cat ga	ggaggccct g	at gat cct ga	aagggcagat	gaccacct g	gcagct gcac	8220
ct ggcacca	gggt gt ccaga	gaggccgt gg	ccct ggt gaa	gccggt gacc	agt gcaccaa	8280
ggccat ccat	ggcaccact	t cagct ct gc	cct cgcgat c	gct ggagccc	cct gaggaac	8340
t cacgcagac	gcggct gcac	cgcct cat ca	at cccaact t	ct acggct at	caggacgccc	8400
cct ggaagat	ct t cct gcgc	aaagaggt gt	t t t accccaa	ggacagct ac	agccat cct g	8460
t gcagct t ga	cct cct gt t c	cggcagat cc	t gcacgacac	gct ct ccgag	gcct gcct t c	8520
gcat ct ct ga	ggat gagagg	ct caggat ga	aggcct t gt t	t gcccagaac	cagct ggaca	8580
cacagaagcc	t ct ggt aacg	gaaagcgt ga	agcgggcccgt	gggt cagcact	gcacgagaca	8640
cct gggaggt	ct act t ct cc	cgcct ct t cc	ccgccacggg	cagcgt gggc	act ggt gt gc	8700
agct cct agc	t gt gt cccac	gt gggcat ca	aact cct gag	gat ggt caag	gggt ggccagg	8760
aggccggcgg	gcagct gcgg	gt cct gcgt g	cat acagct t	t gcagat at c	ct gt t t gt ga	8820
ccat gccct c	ccagaacat g	ct ggagt t ca	acct ggccag	t gagaaggt c	at cct ct t ct	8880
cagcccagac	gcaccaggt c	aagaccct gg	t agat gact t	cat ct t ggag	ct gaagaagg	8940
act ct gact a	cgt ggt cgct	gt gaggaact	t cct gcct ga	ggaccct gcg	ct gct ggct t	9000
t ccacaaggg	t gacat cat a	cacct gcagc	ccct agagcc	acct cgagt g	ggct acagt g	9060
ct ggct gcgt	gggt t cgcagg	aaggt ggt gt	acct ggagga	gct gcgacgt	agaggccccc	9120
act t t ggct g	gaggt t cggg	accat ccacg	ggcgcgt ggg	ccgct t ccct	t cggagct gg	9180
t gcagcccgc	t gct gcccc	gact t cct gc	agct gccaac	ggagccaggc	cgcggccgag	9240
cagccgcccgt	ggccgct gct	gt ggcct ct g	cagccgct gc	acaggaggt g	ggccgcagga	9300
gagaggggt cc	cccagt cagg	gcccgt ct g	ct gaccat gg	ggaggacgcc	ct ggcgt cc	9360
caccct acac	aat gct cgag	t t t gccaga	agt at t t ccg	agaccct cag	aggagacccc	9420
aggat ggcct	caggct gaaa	t ccaaggagc	ct cgggagt c	cagaacct t g	gaggacat gc	9480
t t t gct t cac	caagact ccc	ct ccaggaat	ccct cat cga	act cagcgac	agcagcct ca	9540
gcaagat ggc	caccgacat g	t t cct agct g	t aat gaggt t	cat gggggat	gccccact ga	9600
agggccagag	t gacct ggac	gt gct t t gt a	acct cct gaa	gct gt gcggg	gaccat gagg	9660
t cat gcggga	t gaat gt t ac	t gccaaagt t g	t gaagcagat	cacagacaat	accagct cca	9720
agcaggacag	ct gccagcga	ggct ggaggc	t gct gt at at	cgt gaccgcc	t accacagct	9780
gct ct gaggt	cct ccacca	cacct cact c	gct t cct cca	agacgt gagc	cggaccccag	9840

N3027PCT\_sequ. list.txt

gcct gccct t t caggggat c gccaaggcct gcgagcagaa cct gcagaaa acct t gcgct	9900
t cggagggt cg t ct ggagct c cccagcagca t agagct t cg ggccat gt t g gcaggccgca	9960
gt t ccaagag gcaact ct t t ct t ct t cct g gaggcct t ga acgcat ct c aaaat caaaa	10020
cat gcaact gt ggccct ggac gt ggt ggaag agat at gt gc t gagat ggct ct gacacgcc	10080
ct gaggcct t caat gaat at gt t at ct t cg t t gt caccaa ccgt ggccag cat gt gt gcc	10140
cact cagt cg ccgt gct t ac at cct ggat g t ggcct caga gat ggagcag gt ggacggcg	10200
gct acat gct ct ggt t ccgg cgt gt gct ct gggat cagcc act caagt t c gagaat gagc	10260
t at at gt gac cat gcaact ac aaccagggt cc t gcct gact a cct gaaggga ct ct t cagca	10320
gt gt gccggc cagccggccc agcgagcagc t gct gcagca ggt gt ccaag ct ggct t cac	10380
t gcagcat cg cgccaaggac cact t ct acc t gccgagcgt gcggaagt c caggagt aca	10440
t cccagccca gct ct accgt acaacggcag gct cgacct g gct caacct g gt cagccagc	10500
accggcagca gacacaggcg ct cagccccc accaggcccg t gccagt t t ct gggcct cc	10560
t cagcgcct t acct at gt t c ggct cct cct t ct t ct t cat ccagagct gc agcaacat t g	10620
ct gt gccagc ccct t gcat c ct t gccat ca accacaat gg cct caact t t ct cagcacag	10680
agact cat ga at t gat ggt g aagt t ccccc t gaaggagat ccagt cgacg cggacccagc	10740
ggccacggc caact ccagc t acccct at g t ggagat t gc gct gggggac gt ggcggccc	10800
agcgcacct t gcagct gcag ct ggagcagg gact ggaact gt gt cgt gt g gt ggccgt gc	10860
acgt ggagaa cct gct cagt gccat gaga agcggct cac at t gcccccc agcgagat ca	10920
ccct gct ct g acccagcccc cagccct cca gt acct t ct g ccagaagact cact gt gt gg	10980
cct cagagaa at cact gaac ct ct caggat caat gacccc t gt aaggggc cagagcct t g	11040
gaggacact a agaggaggca ggaggagcaa ct caaat ccc caagaacaca agaagaccca	11100
t cct gaact g ggat ggaat g gcagcat gca aact t ggat c agat agcagg aggaact t t c	11160
aaaagt ct gg cccact gt gc agt ggagcag aaggcaggac cat gaggcct cct gccat gt	11220
acccat t gca gaccct gccc ct aact cct g cct at gacac agaagcccca caccagt t gc	11280
ccagat gaac t ggcct ct gc ct t t ggt t t a ct cagggt ct gat gt t ggaa t ct gct ccaa	11340
ct ccacaccc t agccct t ac at gt cct cct aaggggcccc t cct t gt gct gccagt cagc	11400
ct ggat t t ct ggt ct t t ggt t at t t ct gt g caaacaaaag gt gt gcct gg cagccat t t c	11460
t ccat ggagt t gct aagt gg ccggaacaca ggcct gaggg aggaggcagg agt t ggagt t	11520
acct t aggcc cct gat t cac t ggct at gaa cagacat cc cccact cct t gggt at cccc	11580
aaccccagac ccccat cact t gat gggcca cacaagt t t g agagt ggt ac aagggagaag	11640
t t t gggaaaa gcct t ct t gg aaaat gggac at t agcat t g agt t t t gaaa gat gagt agg	11700
agt t t gct aa gaat agat gg aagacagcag gat aaacat t ccagagaaaa t cat gt t t at	11760
t ccct gct gt at ct t ccaga acct aggagg at gcct aaca gagagt aagc act t aaaaaa	11820
t at t t gt cat at gaat gaaa aaat aaacga gt gaat gt t g at aaaaaaaaa aaaaaa	11876

<210> 90  
 <211> 3530  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(3530)  
 <223> unconventional myosin-15

<400> 90

Met Ala Lys Glu Glu Asp Glu Glu Lys Lys Ala Lys Lys Gly Lys Lys  
 1 5 10 15

Gly Lys Lys Ala Pro Glu Pro Glu Lys Pro Lys Arg Ser Leu Lys Gly  
 20 25 30

Thr Ser Arg Leu Phe Met Gly Phe Arg Asp Arg Thr Pro Lys Ile Ser  
 35 40 45

Lys Lys Gly Glu Phe Arg Ser Ala Ser Ala Phe Phe Trp Gly Leu His  
 50 55 60

Thr Gly Pro Glu Lys Thr Lys Arg Lys Arg Lys Ala Arg Thr Val Leu  
 65 70 75 80

Lys Ser Thr Ser Lys Leu Met Thr Glu Met Arg Met Gly Lys Lys Lys  
 85 90 95

Arg Ala Met Lys Gly Lys Lys Pro Ser Phe Met Val Ile Arg Phe Pro  
 100 105 110

Gly Arg Arg Gly Tyr Gly Arg Leu Arg Pro Arg Ala Arg Ser Leu Ser  
 115 120 125

Lys Ala Ser Thr Ala Ile Asn Trp Leu Thr Lys Lys Phe Leu Leu Lys  
 130 135 140

Lys Ala Glu Glu Ser Gly Ser Glu Glu Ala Thr Val Asp Ala Trp Leu  
 145 150 155 160

Glu Arg Ser Ser Ser Arg Met Gly Ser Arg Lys Leu Pro Phe Pro Ser  
 165 170 175

Gly Ala Glu Ile Leu Arg Pro Gly Gly Arg Leu Arg Arg Phe Pro Arg  
 180 185 190

Ser Arg Ser Ile Tyr Ala Ser Gly Glu Pro Leu Gly Phe Leu Pro Phe  
 195 200 205

Glu Asp Glu Ala Pro Phe His His Ser Gly Ser Arg Lys Ser Leu Tyr  
 210 215 220

N3027PCT\_sequ.list.txt

Gly 225 Leu Gu Gly Phe 230 Gln Asp Leu Gly Gu Tyr 235 Tyr Asp Tyr His Arg 240  
 Asp Gly Asp Asp Tyr 245 Tyr Asp Arg Gln Ser 250 Leu His Arg Tyr Glu 255 Gu  
 Gln Gu Pro Tyr 260 Leu Ala Gly Leu Gly 265 Pro Tyr Ser Pro Ala 270 Trp Pro  
 Pro Tyr Gly 275 Asp His Tyr Tyr Gly 280 Tyr Pro Pro Gu Asp 285 Pro Tyr Asp  
 Tyr Tyr 290 His Pro Asp Tyr Tyr 295 Gly Gly Pro Phe Asp 300 Pro Gly Tyr Thr  
 Tyr 305 Gly Tyr Gly Tyr Asp 310 Asp Tyr Gu Pro Pro 315 Tyr Ala Pro Pro Ser 320  
 Gly Tyr Ser Ser Pro 325 Tyr Ser Tyr His Asp 330 Gly Tyr Gu Gly 335 Glu Ala  
 His Pro Tyr Gly 340 Tyr Tyr Leu Asp Pro 345 Tyr Ala Pro Tyr Asp 350 Ala Pro  
 Tyr Pro Pro 355 Tyr Asp Leu Pro Tyr 360 His Thr Pro Tyr Asp 365 Val Pro Tyr  
 Phe Asp 370 Pro Tyr Gly Val His 375 Tyr Thr Val Pro Tyr 380 Ala Gu Gly Val  
 Tyr 385 Gly Gly Gly Asp Gu 390 Ala Ile Tyr Pro Pro 395 Gu Val Pro Tyr Phe 400  
 Tyr Pro Gu Gu Ser 405 Ala Ser Ala Phe Val 410 Tyr Pro Trp Val Pro 415 Pro  
 Pro Ile Pro Ser 420 Pro His Asn Pro Tyr 425 Ala His Ala Met Asp 430 Asp Ile  
 Ala Gu Leu 435 Gu Gu Pro Gu Asp 440 Ala Gly Val Gu Arg 445 Gln Gly Thr  
 Ser Phe 450 Arg Leu Pro Ser Ala 455 Ala Phe Phe Gu 460 Gln Gln Gly Met Asp  
 Lys 465 Pro Ala Arg Ser Lys 470 Leu Ser Leu Ile Arg 475 Lys Phe Arg Leu Phe 480  
 Pro Arg Pro Gln Val 485 Lys Leu Phe Gly Lys 490 Gu Lys Leu Gu Val 495 Pro  
 Leu Pro Pro Ser Leu Asp Ile Pro Leu Pro Leu Gly Asp Ala Asp Gu  
 Page 443

500

505

510

G u G u Asp G u G u G u Leu Pro Pro Val Ser Ala Val Pro Tyr Gly  
 515 520 525  
 Hi s Pro Phe Trp Gly Phe Leu Thr Pro Arg G n Arg Asn Leu G n Arg  
 530 535 540  
 Ala Leu Ser Ala Phe Gly Ala Hi s Arg Gly Leu Gly Phe Gly Pro Gu  
 545 550 555 560  
 Phe Gly Arg Pro Val Pro Arg Pro Ala Thr Ser Leu Ala Arg Phe Leu  
 565 570 575  
 Lys Lys Thr Leu Ser Gu Lys Lys Pro Ile Ala Arg Leu Arg Gly Ser  
 580 585 590  
 G n Lys Thr Arg Ala Gly Gly Pro Ala Val Arg Gu Ala Ala Tyr Lys  
 595 600 605  
 Arg Phe Gly Tyr Lys Leu Ala Gly Met Asp Pro Gu Lys Pro Gly Thr  
 610 615 620  
 Pro Ile Val Leu Arg Arg Ala G n Pro Arg Ala Arg Ser Ser Asn Asp  
 625 630 635 640  
 Ala Arg Arg Pro Pro Ala Pro G n Pro Ala Pro Arg Thr Leu Ser Hi s  
 645 650 655  
 Trp Ser Ala Leu Leu Ser Pro Pro Val Pro Pro Arg Pro Pro Ser Ser  
 660 665 670  
 Gly Pro Pro Pro Ala Pro Pro Leu Ser Pro Ala Leu Ser Gly Leu Pro  
 675 680 685  
 Arg Pro Ala Ser Pro Tyr Gly Ser Leu Arg Arg Hi s Pro Pro Pro Trp  
 690 695 700  
 Ala Ala Pro Ala Hi s Val Pro Pro Ala Pro G n Ala Ser Gly Trp Ala  
 705 710 715 720  
 Phe Val Gu Pro Pro Ala Val Ser Pro Gu Val Pro Pro Asp Leu Leu  
 725 730 735  
 Ala Phe Pro Gly Pro Arg Pro Ser Phe Arg Gly Ser Arg Arg Arg Gly  
 740 745 750  
 Ala Ala Phe Gly Phe Pro Gly Ala Ser Pro Arg Ala Ser Arg Arg Arg  
 755 760 765  
 Ala Trp Ser Pro Leu Ala Ser Pro G n Pro Ser Leu Arg Ser Ser Pro  
 770 775 780

N3027PCT\_sequ.list.txt

Gly Leu Gly Tyr Cys Ser Pro Leu Ala Pro Pro Ser Pro Gln Leu Ser  
 785 790 795 800  
 Leu Arg Thr Gly Pro Phe Gln Pro Pro Phe Leu Pro Pro Ala Arg Arg  
 805 810 815  
 Pro Arg Ser Leu Gln Glu Ser Pro Ala Pro Arg Arg Ala Ala Gly Arg  
 820 825 830  
 Leu Gly Pro Pro Gly Ser Pro Leu Pro Gly Ser Pro Arg Pro Pro Ser  
 835 840 845  
 Pro Pro Leu Gly Leu Cys His Ser Pro Arg Arg Ser Ser Leu Asn Leu  
 850 855 860  
 Pro Ser Arg Leu Pro His Thr Trp Arg Arg Leu Ser Glu Pro Pro Thr  
 865 870 875 880  
 Arg Ala Val Lys Pro Gln Val Arg Leu Pro Phe His Arg Pro Pro Arg  
 885 890 895  
 Ala Gly Ala Trp Arg Ala Pro Leu Glu His Arg Glu Ser Pro Arg Glu  
 900 905 910  
 Pro Glu Asp Ser Glu Thr Pro Trp Thr Val Pro Pro Leu Ala Pro Ser  
 915 920 925  
 Trp Asp Val Asp Met Pro Pro Thr Gln Arg Pro Pro Ser Pro Trp Pro  
 930 935 940  
 Gly Gly Ala Gly Ser Arg Arg Gly Phe Ser Arg Pro Pro Pro Val Pro  
 945 950 955 960  
 Glu Asn Pro Phe Leu Gln Leu Leu Gly Pro Val Pro Ser Pro Thr Leu  
 965 970 975  
 Gln Pro Glu Asp Pro Ala Ala Asp Met Thr Arg Val Phe Leu Gly Arg  
 980 985 990  
 His His Glu Pro Gly Pro Gly Gln Leu Thr Lys Ser Ala Gly Pro Thr  
 995 1000 1005  
 Pro Glu Lys Pro Glu Glu Glu Ala Thr Leu Gly Asp Pro Gln Leu  
 1010 1015 1020  
 Pro Ala Glu Thr Lys Pro Pro Thr Pro Ala Pro Pro Lys Asp Val  
 1025 1030 1035  
 Thr Pro Pro Lys Asp Ile Thr Pro Pro Lys Asp Val Leu Pro Glu  
 1040 1045 1050

N3027PCT\_sequ.list.txt

Gln	Lys	Thr	Leu	Arg	Pro	Ser	Leu	Ser	Tyr	Pro	Leu	Ala	Ala	Cys
	1055					1060					1065			
Asp	Gln	Thr	Arg	Ala	Thr	Trp	Pro	Pro	Trp	His	Arg	Trp	Gly	Thr
	1070					1075					1080			
Leu	Pro	Gln	Ala	Ala	Ala	Pro	Leu	Ala	Pro	Ile	Arg	Ala	Pro	Glu
	1085					1090					1095			
Pro	Leu	Pro	Lys	Gly	Gly	Glu	Arg	Arg	Gln	Ala	Ala	Pro	Gly	Arg
	1100					1105					1110			
Phe	Ala	Val	Val	Met	Pro	Arg	Val	Gln	Lys	Leu	Ser	Ser	Phe	Gln
	1115					1120					1125			
Arg	Val	Gly	Pro	Ala	Thr	Leu	Lys	Pro	Gln	Val	Gln	Pro	Ile	Gln
	1130					1135					1140			
Asp	Pro	Lys	Pro	Arg	Ala	Cys	Ser	Leu	Arg	Trp	Ser	Cys	Leu	Trp
	1145					1150					1155			
Leu	Arg	Ala	Asp	Ala	Tyr	Gly	Pro	Trp	Pro	Arg	Val	His	Thr	His
	1160					1165					1170			
Pro	Gln	Ser	Cys	His	Leu	Gly	Pro	Gly	Ala	Ala	Cys	Leu	Ser	Leu
	1175					1180					1185			
Arg	Gly	Ser	Trp	Glu	Glu	Val	Gly	Pro	Pro	Ser	Trp	Arg	Asn	Lys
	1190					1195					1200			
Met	His	Ser	Ile	Arg	Asn	Leu	Pro	Ser	Met	Arg	Phe	Arg	Glu	Gln
	1205					1210					1215			
His	Gly	Glu	Asp	Gly	Val	Glu	Asp	Met	Thr	Gln	Leu	Glu	Asp	Leu
	1220					1225					1230			
Gln	Glu	Thr	Thr	Val	Leu	Ser	Asn	Leu	Lys	Ile	Arg	Phe	Glu	Arg
	1235					1240					1245			
Asn	Leu	Ile	Tyr	Thr	Tyr	Ile	Gly	Ser	Ile	Leu	Val	Ser	Val	Asn
	1250					1255					1260			
Pro	Tyr	Gln	Met	Phe	Gly	Ile	Tyr	Gly	Pro	Glu	Gln	Val	Gln	Gln
	1265					1270					1275			
Tyr	Asn	Gly	Arg	Ala	Leu	Gly	Glu	Asn	Pro	Pro	His	Leu	Phe	Ala
	1280					1285					1290			
Val	Ala	Asn	Leu	Ala	Phe	Ala	Lys	Met	Leu	Asp	Ala	Lys	Gln	Asn
	1295					1300					1305			

G n Oys Ile Ile Ile Ser Gly Gu Ser Gly Ser Gly Lys Thr Gu  
 1310 1315 1320  
 Ala Thr Lys Leu Ile Leu Arg Tyr Leu Ala Ala Met Asn G n Lys  
 1325 1330 1335  
 Arg Gu Val Met G n G n Ile Lys Ile Leu Gu Ala Thr Pro Leu  
 1340 1345 1350  
 Leu Gu Ser Phe Gly Asn Ala Lys Thr Val Arg Asn Asp Asn Ser  
 1355 1360 1365  
 Ser Arg Phe Gly Lys Phe Val Gu Ile Phe Leu Gu Gly Gly Val  
 1370 1375 1380  
 Ile Ser Gly Ala Ile Thr Ser G n Tyr Leu Leu Gu Lys Ser Arg  
 1385 1390 1395  
 Ile Val Phe G n Ala Lys Asn Gu Arg Asn Tyr His Ile Phe Tyr  
 1400 1405 1410  
 Gu Leu Leu Ala Gly Leu Pro Ala G n Leu Arg G n Ala Phe Ser  
 1415 1420 1425  
 Leu G n Gu Ala Gu Thr Tyr Tyr Tyr Leu Asn G n Gly Gly Asn  
 1430 1435 1440  
 Oys Gu Ile Ala Gly Lys Ser Asp Ala Asp Asp Phe Arg Arg Leu  
 1445 1450 1455  
 Leu Ala Ala Met Gu Val Leu Gly Phe Ser Ser Gu Asp G n Asp  
 1460 1465 1470  
 Ser Ile Phe Arg Ile Leu Ala Ser Ile Leu His Leu Gly Asn Val  
 1475 1480 1485  
 Tyr Phe Gu Lys Tyr Gu Thr Asp Ala G n Gu Val Ala Ser Val  
 1490 1495 1500  
 Val Ser Ala Arg Gu Ile G n Ala Val Ala Gu Leu Leu G n Ile  
 1505 1510 1515  
 Ser Pro Gu Gly Leu G n Lys Ala Ile Thr Phe Lys Val Thr Gu  
 1520 1525 1530  
 Thr Met Arg Gu Lys Ile Phe Thr Pro Leu Thr Val Gu Ser Ala  
 1535 1540 1545  
 Val Asp Ala Arg Asp Ala Ile Ala Lys Val Leu Tyr Ala Leu Leu  
 1550 1555 1560  
 Phe Ser Trp Leu Ile Thr Arg Val Asn Ala Leu Val Ser Pro Arg

1565														
Gln	Asp	Thr	Leu	Ser	Ile	Ala	Ile	Leu	Asp	Ile	Tyr	Gly	Phe	Glu
1580						1585					1590			
Asp	Leu	Ser	Phe	Asn	Ser	Phe	Glu	Gln	Leu	Cys	Ile	Asn	Tyr	Ala
1595						1600					1605			
Asn	Glu	Asn	Leu	Gln	Tyr	Leu	Phe	Asn	Lys	Ile	Val	Phe	Gln	Glu
1610						1615					1620			
Glu	Gln	Glu	Glu	Tyr	Ile	Arg	Glu	Gln	Ile	Asp	Trp	Gln	Glu	Ile
1625						1630					1635			
Thr	Phe	Ala	Asp	Asn	Gln	Pro	Arg	Ile	Asn	Leu	Ile	Ser	Leu	Lys
1640						1645					1650			
Pro	Tyr	Gly	Ile	Leu	Arg	Ile	Leu	Asp	Asp	Gln	Cys	Cys	Phe	Pro
1655						1660					1665			
Gln	Ala	Thr	Asp	His	Thr	Phe	Leu	Gln	Lys	Cys	His	Tyr	His	His
1670						1675					1680			
Gly	Ala	Asn	Pro	Leu	Tyr	Ser	Lys	Pro	Lys	Met	Pro	Leu	Pro	Glu
1685						1690					1695			
Phe	Thr	Ile	Lys	His	Tyr	Ala	Gly	Lys	Val	Thr	Tyr	Gln	Val	His
1700						1705					1710			
Lys	Phe	Leu	Asp	Lys	Asn	His	Asp	Gln	Val	Arg	Gln	Asp	Val	Leu
1715						1720					1725			
Asp	Leu	Phe	Val	Arg	Ser	Arg	Thr	Arg	Val	Val	Ala	His	Leu	Phe
1730						1735					1740			
Ser	Ser	His	Ala	Pro	Gln	Ala	Ala	Pro	Gln	Arg	Leu	Gly	Lys	Ser
1745						1750					1755			
Ser	Ser	Val	Thr	Arg	Leu	Tyr	Lys	Ala	His	Thr	Val	Ala	Ala	Lys
1760						1765					1770			
Phe	Gln	Gln	Ser	Leu	Leu	Asp	Leu	Val	Glu	Lys	Met	Glu	Arg	Cys
1775						1780					1785			
Asn	Pro	Leu	Phe	Met	Arg	Cys	Leu	Lys	Pro	Asn	His	Lys	Lys	Glu
1790						1795					1800			
Pro	Gly	Leu	Phe	Glu	Pro	Asp	Val	Val	Met	Ala	Gln	Leu	Arg	Tyr
1805						1810					1815			
Ser	Gly	Val	Leu	Glu	Thr	Val	Arg	Ile	Arg	Lys	Glu	Gly	Phe	Pro
1820						1825					1830			

N3027PCT\_sequ.list.txt

Val	Arg	Leu	Pro	Phe	Gln	Gly	Phe	Ile	Asp	Arg	Tyr	Cys	Cys	Leu
	1835					1840					1845			
Val	Ala	Leu	Lys	His	Asp	Leu	Pro	Ala	Asn	Gly	Asp	Met	Cys	Val
	1850					1855					1860			
Ser	Val	Leu	Ser	Arg	Leu	Cys	Lys	Val	Met	Pro	Asn	Met	Tyr	Arg
	1865					1870					1875			
Val	Gly	Val	Ser	Lys	Leu	Phe	Leu	Lys	Glu	His	Leu	Tyr	Gln	Leu
	1880					1885					1890			
Leu	Glu	Ser	Met	Arg	Glu	His	Val	Leu	Asn	Leu	Ala	Ala	Leu	Thr
	1895					1900					1905			
Leu	Gln	Arg	Cys	Leu	Arg	Gly	Phe	Phe	Ile	Lys	Arg	Arg	Phe	Arg
	1910					1915					1920			
Ser	Leu	Arg	His	Lys	Ile	Ile	Leu	Leu	Gln	Ser	Arg	Ala	Arg	Gly
	1925					1930					1935			
Tyr	Leu	Ala	Arg	Gln	Arg	Tyr	Gln	Gln	Met	Arg	Arg	Ser	Leu	Val
	1940					1945					1950			
Lys	Phe	Arg	Ser	Leu	Val	His	Ala	Tyr	Val	Ser	Arg	Arg	Arg	Tyr
	1955					1960					1965			
Leu	Lys	Leu	Arg	Ala	Glu	Trp	Arg	Cys	Gln	Val	Glu	Gly	Ala	Leu
	1970					1975					1980			
Leu	Trp	Glu	Gln	Glu	Glu	Leu	Ser	Lys	Arg	Glu	Val	Val	Ala	Val
	1985					1990					1995			
Gly	His	Leu	Glu	Val	Pro	Ala	Glu	Leu	Ala	Gly	Leu	Leu	Gln	Ala
	2000					2005					2010			
Val	Ala	Gly	Leu	Gly	Leu	Ala	Gln	Val	Pro	Gln	Val	Ala	Pro	Val
	2015					2020					2025			
Arg	Thr	Pro	Arg	Leu	Gln	Ala	Glu	Pro	Arg	Val	Thr	Leu	Pro	Leu
	2030					2035					2040			
Asp	Ile	Asn	Asn	Tyr	Pro	Met	Ala	Lys	Phe	Val	Gln	Cys	His	Phe
	2045					2050					2055			
Lys	Glu	Pro	Ala	Phe	Gly	Met	Leu	Thr	Val	Pro	Leu	Arg	Thr	Pro
	2060					2065					2070			
Leu	Thr	Gln	Leu	Pro	Ala	Glu	His	His	Ala	Glu	Ala	Val	Ser	Ile
	2075					2080					2085			

N3027PCT\_sequ.list.txt

Phe	Lys	Leu	Ile	Leu	Arg	Phe	Met	Gly	Asp	Pro	His	Leu	His	Gly
	2090					2095					2100			
Ala	Arg	Glu	Asn	Ile	Phe	Gly	Asn	Tyr	Ile	Val	Gln	Lys	Gly	Leu
	2105					2110					2115			
Ala	Val	Pro	Glu	Leu	Arg	Asp	Glu	Ile	Leu	Ala	Gln	Leu	Ala	Asn
	2120					2125					2130			
Gln	Val	Trp	His	Asn	His	Asn	Ala	His	Asn	Ala	Glu	Arg	Gly	Trp
	2135					2140					2145			
Leu	Leu	Leu	Ala	Ala	Cys	Leu	Ser	Gly	Phe	Ala	Pro	Ser	Pro	Cys
	2150					2155					2160			
Phe	Asn	Lys	Tyr	Leu	Leu	Lys	Phe	Val	Ser	Asp	Tyr	Gly	Arg	Asn
	2165					2170					2175			
Gly	Phe	Gln	Ala	Val	Cys	Gln	His	Arg	Leu	Met	Gln	Ala	Met	Gly
	2180					2185					2190			
Arg	Ala	Gln	Gln	Gln	Gly	Ser	Gly	Ala	Ala	Arg	Thr	Leu	Pro	Pro
	2195					2200					2205			
Thr	Gln	Leu	Glu	Trp	Thr	Ala	Thr	Tyr	Glu	Lys	Ala	Ser	Met	Ala
	2210					2215					2220			
Leu	Asp	Val	Gly	Cys	Phe	Asn	Gly	Asp	Gln	Phe	Ser	Cys	Pro	Val
	2225					2230					2235			
His	Ser	Trp	Ser	Thr	Gly	Glu	Glu	Val	Ala	Gly	Asp	Ile	Leu	Arg
	2240					2245					2250			
His	Arg	Gly	Leu	Ala	Asp	Gly	Trp	Arg	Gly	Trp	Thr	Val	Ala	Met
	2255					2260					2265			
Lys	Asn	Gly	Val	Gln	Trp	Ala	Glu	Leu	Ala	Gly	His	Asp	Tyr	Val
	2270					2275					2280			
Leu	Asp	Leu	Val	Ser	Asp	Leu	Glu	Leu	Leu	Arg	Asp	Phe	Pro	Arg
	2285					2290					2295			
Gln	Lys	Ser	Tyr	Phe	Ile	Val	Gly	Thr	Glu	Gly	Pro	Ala	Ala	Ser
	2300					2305					2310			
Arg	Gly	Gly	Pro	Lys	Val	Val	Phe	Gly	Asn	Ser	Trp	Asp	Ser	Asp
	2315					2320					2325			
Glu	Asp	Met	Ser	Thr	Arg	Pro	Gln	Pro	Gln	Glu	His	Met	Pro	Lys
	2330					2335					2340			

Val Leu Asp Ser Asp Gly Tyr Ser Ser His Asn Gln Asp Gly Thr  
 2345 2350 2355  
 Asn Gly Gu Thr Gu Ala Gln Arg Gly Thr Ala Thr His Gln Gu  
 2360 2365 2370  
 Ser Asp Ser Leu Gly Gu Pro Ala Val Pro His Lys Gly Leu Asp  
 2375 2380 2385  
 Cys Tyr Leu Asp Ser Leu Phe Asp Pro Val Leu Ser Tyr Gly Asp  
 2390 2395 2400  
 Ala Asp Leu Gu Lys Pro Thr Ala Ile Ala Tyr Arg Met Lys Gly  
 2405 2410 2415  
 Gly Gly Gln Pro Gly Gly Gly Ser Ser Ser Gly Thr Gu Asp Thr  
 2420 2425 2430  
 Pro Arg Arg Pro Pro Gu Pro Lys Pro Ile Pro Gly Leu Asp Ala  
 2435 2440 2445  
 Ser Thr Leu Ala Leu Gln Gln Ala Phe Ile His Lys Gln Ala Val  
 2450 2455 2460  
 Leu Leu Ala Arg Gly Met Thr Leu Gln Ala Thr Ala Leu Gln Gln  
 2465 2470 2475  
 Gln Pro Leu Ser Ala Ala Leu Arg Ser Leu Pro Ala Gu Lys Pro  
 2480 2485 2490  
 Pro Ala Pro Gu Ala Gln Pro Thr Ser Val Gly Thr Gly Pro Pro  
 2495 2500 2505  
 Ala Lys Pro Val Leu Leu Arg Ala Thr Pro Lys Pro Leu Ala Pro  
 2510 2515 2520  
 Ala Pro Leu Ala Lys Ala Pro Arg Leu Pro Ile Lys Pro Val Ala  
 2525 2530 2535  
 Ala Pro Val Leu Ala Gln Asp Gln Ala Ser Pro Gu Thr Thr Ser  
 2540 2545 2550  
 Pro Ser Pro Gu Leu Val Arg Tyr Ser Thr Leu Asn Ser Gu His  
 2555 2560 2565  
 Phe Pro Gln Pro Thr Gln Gln Ile Lys Asn Ile Val Arg Gln Tyr  
 2570 2575 2580  
 Gln Gln Pro Phe Arg Gly Gly Arg Pro Gu Ala Leu Arg Lys Asp  
 2585 2590 2595  
 Gly Gly Lys Val Phe Met Lys Arg Pro Asp Pro His Gu Gu Ala  
 Page 451

2600															
Leu	Met	Ile	Leu	Lys	Gly	Gln	Met	Thr	His	Leu	Ala	Ala	Ala	Pro	
2615						2620					2625				
Gly	Thr	Gln	Val	Ser	Arg	Glu	Ala	Val	Ala	Leu	Val	Lys	Pro	Val	
2630						2635					2640				
Thr	Ser	Ala	Pro	Arg	Pro	Ser	Met	Ala	Pro	Thr	Ser	Ala	Leu	Pro	
2645						2650					2655				
Ser	Arg	Ser	Leu	Glu	Pro	Pro	Glu	Glu	Leu	Thr	Gln	Thr	Arg	Leu	
2660						2665					2670				
His	Arg	Leu	Ile	Asn	Pro	Asn	Phe	Tyr	Gly	Tyr	Gln	Asp	Ala	Pro	
2675						2680					2685				
Trp	Lys	Ile	Phe	Leu	Arg	Lys	Glu	Val	Phe	Tyr	Pro	Lys	Asp	Ser	
2690						2695					2700				
Tyr	Ser	His	Pro	Val	Gln	Leu	Asp	Leu	Leu	Phe	Arg	Gln	Ile	Leu	
2705						2710					2715				
His	Asp	Thr	Leu	Ser	Glu	Ala	Cys	Leu	Arg	Ile	Ser	Glu	Asp	Glu	
2720						2725					2730				
Arg	Leu	Arg	Met	Lys	Ala	Leu	Phe	Ala	Gln	Asn	Gln	Leu	Asp	Thr	
2735						2740					2745				
Gln	Lys	Pro	Leu	Val	Thr	Glu	Ser	Val	Lys	Arg	Ala	Val	Val	Ser	
2750						2755					2760				
Thr	Ala	Arg	Asp	Thr	Trp	Glu	Val	Tyr	Phe	Ser	Arg	Ile	Phe	Pro	
2765						2770					2775				
Ala	Thr	Gly	Ser	Val	Gly	Thr	Gly	Val	Gln	Leu	Leu	Ala	Val	Ser	
2780						2785					2790				
His	Val	Gly	Ile	Lys	Leu	Leu	Arg	Met	Val	Lys	Gly	Gly	Gln	Glu	
2795						2800					2805				
Ala	Gly	Gly	Gln	Leu	Arg	Val	Leu	Arg	Ala	Tyr	Ser	Phe	Ala	Asp	
2810						2815					2820				
Ile	Leu	Phe	Val	Thr	Met	Pro	Ser	Gln	Asn	Met	Leu	Glu	Phe	Asn	
2825						2830					2835				
Leu	Ala	Ser	Glu	Lys	Val	Ile	Leu	Phe	Ser	Ala	Arg	Ala	His	Gln	
2840						2845					2850				
Val	Lys	Thr	Leu	Val	Asp	Asp	Phe	Ile	Leu	Glu	Leu	Lys	Lys	Asp	
2855						2860					2865				

N3027PCT\_sequ.list.txt

Ser	Asp 2870	Tyr	Val	Val	Ala	Val 2875	Arg	Asn	Phe	Leu	Pro 2880	Glu	Asp	Pro
Ala	Leu 2885	Leu	Ala	Phe	His	Lys 2890	Gly	Asp	Ile	Ile	His 2895	Leu	Gln	Pro
Leu	Glu 2900	Pro	Pro	Arg	Val	Gly 2905	Tyr	Ser	Ala	Gly	Cys 2910	Val	Val	Arg
Arg	Lys 2915	Val	Val	Tyr	Leu	Glu 2920	Glu	Leu	Arg	Arg	Arg 2925	Gly	Pro	Asp
Phe	Gly 2930	Trp	Arg	Phe	Gly	Thr 2935	Ile	His	Gly	Arg	Val 2940	Gly	Arg	Phe
Pro	Ser 2945	Glu	Leu	Val	Gln	Pro 2950	Ala	Ala	Ala	Pro	Asp 2955	Phe	Leu	Gln
Leu	Pro 2960	Thr	Glu	Pro	Gly	Arg 2965	Gly	Arg	Ala	Ala	Ala 2970	Val	Ala	Ala
Ala	Val 2975	Ala	Ser	Ala	Ala	Ala 2980	Ala	Gln	Glu	Val	Gly 2985	Arg	Arg	Arg
Glu	Gly 2990	Pro	Pro	Val	Arg	Ala 2995	Arg	Ser	Ala	Asp	His 3000	Gly	Glu	Asp
Ala	Leu 3005	Ala	Leu	Pro	Pro	Tyr 3010	Thr	Met	Leu	Glu	Phe 3015	Ala	Gln	Lys
Tyr	Phe 3020	Arg	Asp	Pro	Gln	Arg 3025	Arg	Pro	Gln	Asp	Gly 3030	Leu	Arg	Leu
Lys	Ser 3035	Lys	Glu	Pro	Arg	Glu 3040	Ser	Arg	Thr	Leu	Glu 3045	Asp	Met	Leu
Cys	Phe 3050	Thr	Lys	Thr	Pro	Leu 3055	Gln	Glu	Ser	Leu	Ile 3060	Glu	Leu	Ser
Asp	Ser 3065	Ser	Leu	Ser	Lys	Met 3070	Ala	Thr	Asp	Met	Phe 3075	Leu	Ala	Val
Met	Arg 3080	Phe	Met	Gly	Asp	Ala 3085	Pro	Leu	Lys	Gly	Gln 3090	Ser	Asp	Leu
Asp	Val 3095	Leu	Cys	Asn	Leu	Leu 3100	Lys	Leu	Cys	Gly	Asp 3105	His	Glu	Val
Met	Arg 3110	Asp	Glu	Cys	Tyr	Cys 3115	Gln	Val	Val	Lys	Gln 3120	Ile	Thr	Asp

N3027PCT\_sequ.list.txt

Asn	Thr	Ser	Ser	Lys	Gln	Asp	Ser	Cys	Gln	Arg	Gly	Trp	Arg	Leu
3125						3130					3135			
Leu	Tyr	Ile	Val	Thr	Ala	Tyr	His	Ser	Cys	Ser	Glu	Val	Leu	His
3140						3145					3150			
Pro	His	Leu	Thr	Arg	Phe	Leu	Gln	Asp	Val	Ser	Arg	Thr	Pro	Gly
3155						3160					3165			
Leu	Pro	Phe	Gln	Gly	Ile	Ala	Lys	Ala	Cys	Glu	Gln	Asn	Leu	Gln
3170						3175					3180			
Lys	Thr	Leu	Arg	Phe	Gly	Gly	Arg	Leu	Glu	Leu	Pro	Ser	Ser	Ile
3185						3190					3195			
Glu	Leu	Arg	Ala	Met	Leu	Ala	Gly	Arg	Ser	Ser	Lys	Arg	Gln	Leu
3200						3205					3210			
Phe	Leu	Leu	Pro	Gly	Gly	Leu	Glu	Arg	His	Leu	Lys	Ile	Lys	Thr
3215						3220					3225			
Cys	Thr	Val	Ala	Leu	Asp	Val	Val	Glu	Glu	Ile	Cys	Ala	Glu	Met
3230						3235					3240			
Ala	Leu	Thr	Arg	Pro	Glu	Ala	Phe	Asn	Glu	Tyr	Val	Ile	Phe	Val
3245						3250					3255			
Val	Thr	Asn	Arg	Gly	Gln	His	Val	Cys	Pro	Leu	Ser	Arg	Arg	Ala
3260						3265					3270			
Tyr	Ile	Leu	Asp	Val	Ala	Ser	Glu	Met	Glu	Gln	Val	Asp	Gly	Gly
3275						3280					3285			
Tyr	Met	Leu	Trp	Phe	Arg	Arg	Val	Leu	Trp	Asp	Gln	Pro	Leu	Lys
3290						3295					3300			
Phe	Glu	Asn	Glu	Leu	Tyr	Val	Thr	Met	His	Tyr	Asn	Gln	Val	Leu
3305						3310					3315			
Pro	Asp	Tyr	Leu	Lys	Gly	Leu	Phe	Ser	Ser	Val	Pro	Ala	Ser	Arg
3320						3325					3330			
Pro	Ser	Glu	Gln	Leu	Leu	Gln	Gln	Val	Ser	Lys	Leu	Ala	Ser	Leu
3335						3340					3345			
Gln	His	Arg	Ala	Lys	Asp	His	Phe	Tyr	Leu	Pro	Ser	Val	Arg	Glu
3350						3355					3360			
Val	Gln	Glu	Tyr	Ile	Pro	Ala	Gln	Leu	Tyr	Arg	Thr	Thr	Ala	Gly
3365						3370					3375			

Ser Thr Trp Leu Asn Leu Val Ser Gln His Arg Gln Gln Thr Gln  
 3380 3385 3390  
 Ala Leu Ser Pro His Gln Ala Arg Ala Gln Phe Leu Gly Leu Leu  
 3395 3400 3405  
 Ser Ala Leu Pro Met Phe Gly Ser Ser Phe Phe Phe Ile Gln Ser  
 3410 3415 3420  
 Cys Ser Asn Ile Ala Val Pro Ala Pro Cys Ile Leu Ala Ile Asn  
 3425 3430 3435  
 His Asn Gly Leu Asn Phe Leu Ser Thr Glu Thr His Glu Leu Met  
 3440 3445 3450  
 Val Lys Phe Pro Leu Lys Glu Ile Gln Ser Thr Arg Thr Gln Arg  
 3455 3460 3465  
 Pro Thr Ala Asn Ser Ser Tyr Pro Tyr Val Glu Ile Ala Leu Gly  
 3470 3475 3480  
 Asp Val Ala Ala Gln Arg Thr Leu Gln Leu Gln Leu Glu Gln Gly  
 3485 3490 3495  
 Leu Glu Leu Cys Arg Val Val Ala Val His Val Glu Asn Leu Leu  
 3500 3505 3510  
 Ser Ala His Glu Lys Arg Leu Thr Leu Pro Pro Ser Glu Ile Thr  
 3515 3520 3525  
 Leu Leu  
 3530

<210> 91  
 <211> 3652  
 <212> DNA  
 <213> Toxoplasma gondii

<220>  
 <221> misc\_feature  
 <222> (1)..(3652)  
 <223> MyoA

<400> 91  
 ttccggcacga ggaaaaaaga agttttctct ccttcgttgt acctctttcc tcgtgttatc 60  
 tctctctgaa gcaaaatggc gagcaagacc acgtctgagg agctgaaaac ggccacggcg 120  
 ctgaagaaga ggtcgtccga tgtccacgcg gtcgaccact ccggcaatgt gtacaaagga 180  
 tttcaaatct ggacggactt ggcgccgtcg gtgaaggagg agccggacct gatgtttgcc 240  
 aagtgcacgt tgcaggcggg gacagacaag gggaacttga cctgcgtcca gatcgatcca 300  
 ccgggcttcg acgaaccgtt cgaagtcctg caggcgaatg cgtggaacgt aaacagcctg 360  
 atcgacccca tgacgtacgg agacatcggc atgttgctc acacgaacat tccttcgctc 420

N3027PCT\_sequ. list . . txt

ct cgact t cc t caaggt gcg	ct t cat gaag aat caaat ct	acacgact gc ggacccgct c	480
gt cgt cgcca t caat ccct t	ccgcgacct c gggaacacca	cgct cgact g gat t gt t cga	540
t acagagaca ct t t cgacct	ct ccaaact c gcgccccat g	t t t t ct acac cgccccgacgc	600
gcgct cgaca acct ccacgc	cgt caacaag t cgcaaacga	t cat cgt gt c cggt gagt ct	660
ggcgcgggca agacggaggc	gacgaagcag at t at gaggt	at t t t gcggc ggccaagacg	720
gggt cgat gg at t t gcggat	t cagaacgcg at cat ggcg	cgaat ccagt gct t gaggca	780
t t t ggaaat g cgaagacgat	t cgcaacaac aact cgt cgc	gt t t cgacg ct t cat gcag	840
ct ggat gt gg gt cggaagg	aggcat caag t t t ggct ccg	t cgt cgcct t t ct cct ggaa	900
aagt cgcgt g t t ct cagca	ggacgaacag gagcggcgt	accacat ct t ct accaaat g	960
t gcaaggggg cgacgcggc	gat gaaggag cgct t ccat a	t cct gccgct ct cggagt ac	1020
aagt acat ca at ccgt t gt g	cct ggacgcg ccagggat cg	acgacgt cgc ggagt t ccac	1080
gaagt ct gcg agt cgt t ccg	gt cgat gaat ct gacggagg	acgaagt cgc gagcgt gt gg	1140
agcat cgt ga gt ggagt gct	gct gct t ggc aacgt cgagg	t gacagcgac gaaggat ggg	1200
gggat cgacg acgccgcggc	gat cgagggg aagaact t gg	aggt t t t caa aaaggcct gc	1260
gggct gct ct t cct cgacgc	ggagcgcat t cgccaagagc	t gacggg gaa ggt t t cgt at	1320
gcgggggaat c aggagat ccg	cggccgggt gg aagcaggaag	acggagacat gct caagt cg	1380
t cgct cgca aggcgat gt a	cgacaagt t g t t cat gt gga	t cat t gccgt gt t gaaccgc	1440
agcat caagc ct ccgggcgg	ct t caagat c t t cat gggca	t gct cgacat ct t cggct t c	1500
gaagt ct t ca agaacaact c	gct ggagcag t t ct t cat ca	acat cacgaa cgaaat gct g	1560
cagaagaact t cgt cgacat	cgt ct t cgac cgcgagagca	agct gt at cg t gacgaggg	1620
gt ct cct cca aggagt t gat	t t t cacct cg aacgcagaag	t gat caagat ct t gacggcg	1680
aagaacaact cgggt gct cgc	t gcgct cgag gaccagt gcc	t cgcccct gg aggcagcgac	1740
gaaaagt t cc t ct cgacct g	caagaacgcg ct gaaaggaa	ccaccaagt t caagcct gcg	1800
aaggt ct ct c cgaacat caa	t t t cct cat c t cgcacact g	t cggcgacat ccagt acaac	1860
gccgaaggct t cct ct t caa	aaacaaagat gt cct gcgag	cagaaat cat ggaaat cgt g	1920
cagcaaagca agaaccctgt	t gt cgcgcaa ct ct t cgct g	gcat cgt cat ggagaagggg	1980
aagat ggcca agggacaact	gat t ggggt cg cagt t cct ct	cgcagct gca gagcct cat g	2040
gaact t at ca acagcaccga	gcct cact t c at t cgct gca	t caagccgaa cgacacgaag	2100
aagcccct cg act ggggt gcc	gt cgaaaat g ct cat t cagc	t gcacgcgct ct ccgt cct c	2160
gaggct ct t c agct ccgt ca	act cggct ac t ct t acagac	gt ccgt t caa ggagt t cct c	2220
t t ccagt t ca agt t t at cga	cct ct cggct t ct gaaaat c	caaat ct gga ccccaaagaa	2280
gct gcgct ga gact cct caa	aagcagcaaa ct gccacgcg	aagaat acca gct cgggaag	2340
acaat ggt t t t cct caagca	gacgggcgcg aaagaact ga	cgcagat t ca gagagaat gc	2400
ct t t ct t ct t gggagcct ct	cgt ct cagt g ct cgaggcgt	act acgct gg cagacgccac	2460

N3027PCT\_sequ.list.txt

aagaagcagc t gct gaaaaa gaccccccttc at cattcgcg cccaggct ca cat ccgcaga 2520  
cacct ggt gg acaacaacgt cagccccgcg act gtt cagc cggcgt t ct a gacacgt t cg 2580  
ttt gcct ttt gaact ct t ct cat ccatt t g t t g t t t t c t c t c t t c g c c g t t t c c t t c g a g 2640  
t g t c g t t c g t g t g g g t t t t g t a t g t g g a a c t g c t t t c g a c g a g a g c c g t t t g t g c g c t t c 2700  
t t t g t g t a g a g g a c g c g g a t c a a a g g c g g a a c t g a t g g t g t c a g t c c g t g g c t c t t t t t g 2760  
c c t t c t t t c t t t g t c c a g c a a g t c t g t g t t t c g a a g c a a g a g g a g a c g c a c a c a a g c a 2820  
a g g g c g a g g a a a g t t t a t g t t t g c a a a c t t g t c t a c g c t c g c g a g c g t g t g a a c a g c t t c 2880  
c c c t c t c a a g g c g c a g a a a g t c g c g c t g c a c g a c g t t c g t g t t t g g c t a c g g g g a c g c g 2940  
t a g g t c g a c g c g c t c c a t t c g c t g c t g t g t g g t t t g c g t c t c g a c g a g g a t g t a g t g t g 3000  
t t t g c t t t a g g g a c g t c t c t c t g g g c a g a c g c g a c t g c c g t c g t g c g t t g t t t t t c g c t 3060  
g g t t c c g t t c g a a g g c g c a c a g g c g a c g c c a g a g t t c g c g t t c g c g c t t c t t c a a g t 3120  
g a a a a c t g t g t g g c t c g c g c a t g c g t c g c t c t c g a g g c g c a g g a a a a a c g g g t c g a a g t g 3180  
a g c g t c t c t g a g a c g c g c a t c g c a c c g c g a a a a c c g c a g g g a a c a t g c a a a g a c a g 3240  
a g a a g c a t g t g g c g g t t t t c g t g t g c g g c g a a a t c t a g g a g a g a g c c t a g a a c g g g t g a 3300  
a g c a g g a a a g a a g t c g c a a c t g a a c a a g g g a t a t c t t c t t t t t c t t c t g c a t g t c t t c c 3360  
t g c g a g a g a a g c a a a t g t c g t g g a c g t c g c c g t g a g c g t c g c a g c t g t t t t c t c g c c g a a 3420  
g c a g t c a c c g t g g a a g c c g a g g g a a g g c a c a g a c c a g t g t g c g c g c a c a t a g a g g g c g g 3480  
g t t t g t g t t g c g c c a g a a a g t g g a c g c a c t g a g c a t c c g t g g a a g a a c g a a a a a c a g c a 3540  
a g t c a a a a a c c g t a g a a a a c g c g a g g a a a t c c a g a a t g c g t c g c c t g c a t g t t g t g t g c g 3600  
c c t g a c a t t t c a t a a a a a t c g g a t a t c t g t c t c t a a a a a a a a a a a a a a a a a a 3652

<210> 92  
<211> 831  
<212> PRT  
<213> Toxoplasma gondii

<220>  
<221> MSC\_FEATURE  
<222> (1)..(831)  
<223> MyoA

<400> 92

Met Ala Ser Lys Thr Thr Ser Glu Glu Leu Lys Thr Ala Thr Ala Leu  
1 5 10 15

Lys Lys Arg Ser Ser Asp Val His Ala Val Asp His Ser Gly Asn Val  
20 25 30

Tyr Lys Gly Phe Gln Ile Trp Thr Asp Leu Ala Pro Ser Val Lys Glu  
35 40 45

Glu Pro Asp Leu Met Phe Ala Lys Cys Ile Val Gln Ala Gly Thr Asp  
50 55 60

N3027PCT\_sequ.list.txt

Lys Gly Asn Leu Thr Cys Val Gln Ile Asp Pro Pro Gly Phe Asp Glu  
 65 70 75 80  
 Pro Phe Glu Val Pro Gln Ala Asn Ala Trp Asn Val Asn Ser Leu Ile  
 85 90 95  
 Asp Pro Met Thr Tyr Gly Asp Ile Gly Met Leu Pro His Thr Asn Ile  
 100 105 110  
 Pro Cys Val Leu Asp Phe Leu Lys Val Arg Phe Met Lys Asn Gln Ile  
 115 120 125  
 Tyr Thr Thr Ala Asp Pro Leu Val Val Ala Ile Asn Pro Phe Arg Asp  
 130 135 140  
 Leu Gly Asn Thr Thr Leu Asp Trp Ile Val Arg Tyr Arg Asp Thr Phe  
 145 150 155 160  
 Asp Leu Ser Lys Leu Ala Pro His Val Phe Tyr Thr Ala Arg Arg Ala  
 165 170 175  
 Leu Asp Asn Leu His Ala Val Asn Lys Ser Gln Thr Ile Ile Val Ser  
 180 185 190  
 Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Gln Ile Met Arg  
 195 200 205  
 Tyr Phe Ala Ala Ala Lys Thr Gly Ser Met Asp Leu Arg Ile Gln Asn  
 210 215 220  
 Ala Ile Met Ala Ala Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys  
 225 230 235 240  
 Thr Ile Arg Asn Asn Asn Ser Ser Arg Phe Gly Arg Phe Met Gln Leu  
 245 250 255  
 Asp Val Gly Arg Glu Gly Gly Ile Lys Phe Gly Ser Val Val Ala Phe  
 260 265 270  
 Leu Leu Glu Lys Ser Arg Val Leu Thr Gln Asp Glu Gln Glu Arg Ser  
 275 280 285  
 Tyr His Ile Phe Tyr Gln Met Cys Lys Gly Ala Asp Ala Ala Met Lys  
 290 295 300  
 Glu Arg Phe His Ile Leu Pro Leu Ser Glu Tyr Lys Tyr Ile Asn Pro  
 305 310 315 320  
 Leu Cys Leu Asp Ala Pro Gly Ile Asp Asp Val Ala Glu Phe His Glu  
 325 330 335

Val Oys Glu Ser Phe Arg Ser Met Asn Leu Thr Glu Asp Glu Val Ala  
 340 345 350  
 Ser Val Trp Ser Ile Val Ser Gly Val Leu Leu Leu Gly Asn Val Glu  
 355 360 365  
 Val Thr Ala Thr Lys Asp Gly Gly Ile Asp Asp Ala Ala Ala Ile Glu  
 370 375 380  
 Gly Lys Asn Leu Glu Val Phe Lys Lys Ala Cys Gly Leu Leu Phe Leu  
 385 390 395 400  
 Asp Ala Glu Arg Ile Arg Glu Glu Leu Thr Val Lys Val Ser Tyr Ala  
 405 410 415  
 Gly Asn Gln Glu Ile Arg Gly Arg Trp Lys Gln Glu Asp Gly Asp Met  
 420 425 430  
 Leu Lys Ser Ser Leu Ala Lys Ala Met Tyr Asp Lys Leu Phe Met Trp  
 435 440 445  
 Ile Ile Ala Val Leu Asn Arg Ser Ile Lys Pro Pro Gly Gly Phe Lys  
 450 455 460  
 Ile Phe Met Gly Met Leu Asp Ile Phe Gly Phe Glu Val Phe Lys Asn  
 465 470 475 480  
 Asn Ser Leu Glu Gln Phe Phe Ile Asn Ile Thr Asn Glu Met Leu Gln  
 485 490 495  
 Lys Asn Phe Val Asp Ile Val Phe Asp Arg Glu Ser Lys Leu Tyr Arg  
 500 505 510  
 Asp Glu Gly Val Ser Ser Lys Glu Leu Ile Phe Thr Ser Asn Ala Glu  
 515 520 525  
 Val Ile Lys Ile Leu Thr Ala Lys Asn Asn Ser Val Leu Ala Ala Leu  
 530 535 540  
 Glu Asp Gln Cys Leu Ala Pro Gly Gly Ser Asp Glu Lys Phe Leu Ser  
 545 550 555 560  
 Thr Oys Lys Asn Ala Leu Lys Gly Thr Thr Lys Phe Lys Pro Ala Lys  
 565 570 575  
 Val Ser Pro Asn Ile Asn Phe Leu Ile Ser His Thr Val Gly Asp Ile  
 580 585 590  
 Gln Tyr Asn Ala Glu Gly Phe Leu Phe Lys Asn Lys Asp Val Leu Arg  
 595 600 605  
 Ala Glu Ile Met Glu Ile Val Gln Gln Ser Lys Asn Pro Val Val Ala  
 Page 459

610

615

620

Gln Leu Phe Ala Gly Ile Val Met Glu Lys Gly Lys Met Ala Lys Gly  
625 630 635 640

Gln Leu Ile Gly Ser Gln Phe Leu Ser Gln Leu Gln Ser Leu Met Glu  
645 650 655

Leu Ile Asn Ser Thr Glu Pro His Phe Ile Arg Cys Ile Lys Pro Asn  
660 665 670

Asp Thr Lys Lys Pro Leu Asp Trp Val Pro Ser Lys Met Leu Ile Gln  
675 680 685

Leu His Ala Leu Ser Val Leu Glu Ala Leu Gln Leu Arg Gln Leu Gly  
690 695 700

Tyr Ser Tyr Arg Arg Pro Phe Lys Glu Phe Leu Phe Gln Phe Lys Phe  
705 710 715 720

Ile Asp Leu Ser Ala Ser Glu Asn Pro Asn Leu Asp Pro Lys Glu Ala  
725 730 735

Ala Leu Arg Leu Leu Lys Ser Ser Lys Leu Pro Ser Glu Glu Tyr Gln  
740 745 750

Leu Gly Lys Thr Met Val Phe Leu Lys Gln Thr Gly Ala Lys Glu Leu  
755 760 765

Thr Gln Ile Gln Arg Glu Cys Leu Ser Ser Trp Glu Pro Leu Val Ser  
770 775 780

Val Leu Glu Ala Tyr Tyr Ala Gly Arg Arg His Lys Lys Gln Leu Leu  
785 790 795 800

Lys Lys Thr Pro Phe Ile Ile Arg Ala Gln Ala His Ile Arg Arg His  
805 810 815

Leu Val Asp Asn Asn Val Ser Pro Ala Thr Val Gln Pro Ala Phe  
820 825 830

<210> 93  
<211> 3225  
<212> DNA  
<213> Toxoplasma gondii

<220>  
<221> misc\_feature  
<222> (1)..(3225)  
<223> MyoB

<400> 93  
atggagcgca aacaaaccca gatgat actg gggcggagac tggcgaaaga ct caccggag

60

N3027PCT\_sequ. list.txt

gt gaagcat t t t caaagaaa at cgagt gt c gt t cct t t cg gccgt gat gg acgcgct gcc	120
acgaact t t a cct gct ggac t gct gat t gc cccgcagt ga aagct gaccc caccct cgt t	180
t t t gccaat gcat agt cgt cggagggt cc at ggacacgc agct ggaact cgagcaagt c	240
gacccgccag cacgcgggac gt t t acggt t gcgcct acag at gt gt t caa cgcaaacgag	300
t t gat t gaac cggagacggt cgacgat at c ggct at ct t c ct cacacgaa t gt agcgt gt	360
gt ct t ggat g t t ct aaaaag ccgat t t t t g agaagcat ca t t t at acaac agct gagcca	420
ct t ct ggt ag ct at caaccc ct t caaggac ct ggggaaca ccacagat gc at ggat at cg	480
acat at cgga acgccagt aa gcct gagat g ct t ccaccac at gt ct t caa aacggcccg	540
gccgcgct t g aggacct t ga aggct acaag aaaaaccaat cgat cat t gt gt cgggcgaa	600
t ct ggagcag gaaagact ga agct acaaaa cagat cat gc ggt t t t t t gc gt cggcgt cc	660
t ct gaggt gc gcacgact at ccaagacacc at t at ggcag gcaat cccat cct t gaggcc	720
t t cggaaat g ccaaaacaat ccgt aat aat aact ccagcc gat t t ggacg at t cat gat g	780
ct cgat gt ct cgt ct cat cg gggcat t cag cacgggagt a t at ccaact t cct cct cgaa	840
aaagt gcgt g t ggt gt ccca ggaagcgaac gaacgat cct accat at t t t ct accagct g	900
ct caaaggcg cgacgagcga aat gcgt gca aagt accact t gcgcagt t t aaaggagt ac	960
gcgt at ct ga at ggt aaaaa cgggt ggat gc t acgat gt cc cgggcat cga t gacaaggcc	1020
gat t t cgagg aggt gct t ca at cgt t ggat gccat gcaga t cacgggt t c gaaacggcat	1080
t cgggt gt t t t caat t ct ct c cggcct t ct g ct t at t ggca at gt aagcat agaaggaaaa	1140
gacgcacagg gt gt cccgga t gcagcgt at at t t cgccgc agagcgagga aat cct ggag	1200
gaagct t gcc agct cct t ag cgt t gat gac gcagcact ca agaaggaaat t ct cgt gaag	1260
t cgacgaagg t t ggacct ca ggt cat cgaa ggt gt gcgt a caaaggat ga ggccaagacg	1320
t ct gt gt t gt cgct gt ct aa aaat gt gt at gacaagct ct t t gact ggct t gt t cgccag	1380
ct t aacagct t gat t gacgc t ccagat ggc at gcccaat t t cat t ggaat t ct t gat at t	1440
t t t ggct t t g aagt cct cga agt aaact cg ct t gagcagg t cct gat t aa cat t accaat	1500
gagt at ct gc aaaaacact t cat cgat gt t gt ct t cgat a t ggaaacgaa gct t t accaa	1560
gccgaagggt g t t ccgact ga ggccct cgag t acacggat a acct t gcact t gt cggcgt	1620
ct ct gt ggaa agaacgat t c gt t t t t cgct ct gct cgaag at gcct gct t aggcat cagg	1680
t caact gacg aggggt t t ct g cgggacgat c ct gcgccgcc t ggagccct c gggat t ct t t	1740
t t ggagt ct c gcagagacaa aaggct gaaa t t t at aat cc ggcacacgat t gccgat at c	1800
gagt at acat gt gaagggat gt t ggaaaag aacaaggact t t ct t cgt aa ggagggt gat g	1860
gat gt cat ga aggcgt caac t gaccct gt c acaaaggcgc t ct t cgaagg aat t gaaat c	1920
gaggcaggaa aaat cggcaa gggaacact a at cgcat cca gat t cct gaa gaact t ggag	1980
gagat gat cg gaat t gt agc gcaaacggag gcgcact t ca t ccgt t gcct gaagccgaac	2040
gaggagaaga agccccct ggg at ggaat ggg t cgaagggt gc t gaat cagct t t t ct cgct t	2100
t cgat ct t gg aggcaact t ca act ccgccaa gt cggat acg cgt at cggcg caact t cagc	2160

N3027PCT\_sequ. list . . txt

gaat t ct gca gt cat t t ccg at ggct cgat ct aggt ct t g t gaat t ct ga t cgcgacagg 2220  
aaggaggt cg cgcagct gct t ct cgaacaa t caggaat t c cggagt cgt c gt gggg gat c 2280  
ggaaaaacga t ggt gt t cgt gaagcct gac gcggcgaagg agt t gt cgat ct t gcagcgc 2340  
gagaagt t ga t gt gt t t cca gcct ct gat c ggct cct gg gcccgat gt g gaggaaggt t 2400  
ct cct ccgaa agaagat ggc aagggt t at c cact t cct ca cgagact gga at caaacgcg 2460  
cgcagacat c t ggagccgga cagcat t aac at ct ct cct g aagaacgaga agcgt t gt t g 2520  
t cgggaat gg agcgt cct cg aaat ccct gt gt cgt cgt t a agaaacgcgt t gaaccagag 2580  
cgagcgccgc caacgaaggt gct cagcct a t ct cgcgct a ggct t t cgct ct ct aaagaa 2640  
ct gcct cgaa att acgcagc gagcaacgaa gccct ggat g t t gat gat ac cat gt ct gt a 2700  
gacaccgat g cct t ct t acg t ct caaaat g aagcggc gc ccaacgagaa ct at ct ccgc 2760  
cagacagct t t ggcccgct gaaagagcgg cggccgt cgc acgt ct gcat ggaggaggcg 2820  
t at cacgt gt ggaggt cggg ggaact act a t t cagagagc ct ct gagt ga caagagact t 2880  
cagaacat t t gcact gt aat ccgaaacgat at ggaccagc att acggct t t t t ct ggcaa 2940  
gt aat cat ca at cgcact cc caact t cggc at ggct gcga ct cat at t ca cgggt ccct t 3000  
cacgt cgt t g aacaggaagg cat gt accga gacggccgac aat t cct ct t ccacct cat c 3060  
at gt at aaaa cccggaaacc ccgcaaggaa gagat t cgac t ccat gaaag ggccggcggag 3120  
aaaacgt at g gcat ct gt cg aaagagggat t t ct caggt a at gct ccaac acaggaat t t 3180  
gt t at t t t ct cact gacat g gaaacat aat caaaaacat a gct ag 3225

<210> 94  
<211> 1946  
<212> PRT  
<213> Toxoplasma gondii

<220>  
<221> MSC\_FEATURE  
<222> (1) . . (1946)  
<223> MyoB

<400> 94

Met Val Glu Ser Cys Leu Leu Thr Phe Arg Ala Phe Phe Trp Trp Ile  
1 5 10 15

Ala Leu Ile Lys Met Asp Leu Ser Asp Leu Gly Glu Ala Ala Ala Phe  
20 25 30

Leu Arg Arg Ser Glu Ala Glu Leu Leu Leu Leu Gln Ala Thr Ala Leu  
35 40 45

Asp Gly Lys Lys Lys Cys Trp Ile Pro Asp Gly Glu Asn Ala Tyr Ile  
50 55 60

Glu Ala Glu Val Lys Gly Ser Glu Asp Asp Gly Thr Val Ile Val Glu  
65 70 75 80

N3027PCT\_sequ.list.txt

Thr Ala Asp Gly Glu Ser Leu Ser Ile Lys Glu Asp Lys Ile Glu Glu  
85 90 95

Met Asn Pro Pro Glu Phe Glu Met Ile Glu Asp Met Ala Met Leu Thr  
100 105 110

His Leu Asn Glu Ala Ser Val Leu His Thr Leu Lys Arg Arg Tyr Gly  
115 120 125

Glu Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Ile Asn  
130 135 140

Pro Tyr Lys Trp Leu Pro Val Tyr Glu Lys Glu Val Met Ala Ala Tyr  
145 150 155 160

Lys Gly Lys Arg Arg Ser Glu Ala Pro Pro His Ile Phe Ala Val Ala  
165 170 175

Asn Asn Ala Phe Glu Asp Met Leu His Asn Arg Glu Asn Glu Ser Ile  
180 185 190

Leu Phe Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Ser Lys His  
195 200 205

Ile Ile Glu Tyr Phe Ala Thr Ile Ala Ala Met Ile Glu Ser Arg Lys  
210 215 220

Lys Glu Glu Ala Leu Glu Asp Glu Ile Met Glu Ala Asn Thr Ile Leu  
225 230 235 240

Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg  
245 250 255

Phe Gly Lys Phe Ile Arg Met His Phe Gly Ala Arg Gly Met Leu Ser  
260 265 270

Ser Val Asp Ile Asp Ile Tyr Leu Leu Glu Lys Ser Arg Val Ile Phe  
275 280 285

Glu Glu Ala Gly Glu Arg Asn Tyr His Ile Phe Tyr Glu Ile Leu Ser  
290 295 300

Gly Glu Lys Glu Leu His Asp Leu Leu Leu Val Ser Ala Asn Pro Ser  
305 310 315 320

Asp Phe His Phe Cys Ser Cys Gly Ala Val Thr Val Glu Ser Leu Asp  
325 330 335

Asp Ala Glu Glu Leu Leu Ala Thr Glu Glu Ala Met Asp Ile Leu Gly  
340 345 350

N3027PCT\_sequ.list.txt

Phe Leu Pro Asp Glu Lys Tyr Gly Cys Tyr Lys Leu Thr Gly Ala Ile  
 355 360 365  
 Met His Phe Gly Asn Met Lys Phe Lys Gln Lys Pro Arg Glu Glu Gln  
 370 375 380  
 Leu Glu Ala Asp Gly Thr Glu Asn Ala Asp Lys Ala Ala Phe Leu Met  
 385 390 395 400  
 Gly Ile Asn Ser Ser Glu Leu Val Lys Cys Leu Ile His Pro Arg Ile  
 405 410 415  
 Lys Val Gly Asn Glu Tyr Val Thr Arg Gly Gln Thr Ile Glu Gln Val  
 420 425 430  
 Thr Cys Ala Val Gly Ala Leu Ser Lys Ser Met Tyr Glu Arg Met Phe  
 435 440 445  
 Lys Trp Leu Val Ala Arg Ile Asn Arg Ala Leu Asp Ala Lys Leu Ser  
 450 455 460  
 Arg Gln Phe Phe Ile Gly Ile Leu Asp Ile Thr Gly Phe Glu Ile Leu  
 465 470 475 480  
 Glu Tyr Asn Ser Leu Glu Gln Leu Cys Ile Asn Phe Thr Asn Glu Lys  
 485 490 495  
 Leu Gln Gln Phe Phe Asn Trp Tyr Met Phe Val Leu Glu Gln Glu Glu  
 500 505 510  
 Tyr Lys Lys Glu Ser Ile Glu Trp Val Ser Ile Gly Phe Gly Leu Asp  
 515 520 525  
 Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met Gly Ile Leu Ser  
 530 535 540  
 Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr Asp Leu Thr Phe  
 545 550 555 560  
 Lys Thr Lys Leu Phe Asp Asn His Phe Gly Lys Ser Val His Leu Gln  
 565 570 575  
 Lys Pro Lys Pro Asp Lys Lys Lys Phe Glu Ala His Phe Glu Leu Val  
 580 585 590  
 His Tyr Ala Gly Val Val Pro Tyr Asn Ile Ser Gly Trp Leu Glu Lys  
 595 600 605  
 Asn Lys Asp Leu Leu Asn Glu Thr Val Val Ala Val Phe Gln Lys Ser  
 610 615 620

Ser 625 Asn Arg Leu Leu Ala 630 Ser Leu Phe Gu Asn 635 Tyr Met Ser Thr Asp 640  
 Ser Ala Ile Pro Phe 645 Gly Gu Lys Lys Arg 650 Lys Lys Gly Ala Ser 655 Phe  
 Gln Thr Val Ala 660 Ser Leu His Lys 665 Gu Asn Leu Asn Lys Leu 670 Met Thr  
 Asn Leu Lys 675 Ser Thr Ala Pro His 680 Phe Val Arg Cys Ile 685 Asn Pro Asn  
 Val Asn 690 Lys Ile Pro Gly Ile 695 Leu Asp Pro Tyr Leu 700 Val Leu Gln Gln  
 Leu 705 Arg Cys Asn Gly Val 710 Leu Gu Gly Thr Arg 715 Ile Cys Arg Gu Gly 720  
 Phe Pro Asn Arg Leu 725 Gln Tyr Ala Asp Phe 730 Lys Gln Arg Tyr Cys Ile 735  
 Leu Asn Pro Arg 740 Thr Phe Pro Lys Ser 745 Lys Phe Val Ser 750 Ser Arg Lys  
 Ala Ala Gu 755 Gu Leu Leu Gly Ser 760 Leu Gu Ile Asp His 765 Thr Gln Tyr  
 Arg Phe 770 Gly Ile Thr Lys Val 775 Phe Phe Lys Ala Gly 780 Phe Leu Gly Gln  
 Leu 785 Gu Ala Ile Arg Asp 790 Gu Arg Leu Ser Lys 795 Val Phe Thr Leu Phe 800  
 Gln Ala Arg Ala 805 Gln Gly Lys Leu Met Arg 810 Ile Lys Phe Gln Lys 815 Ile  
 Leu Gu Gu Arg 820 Asp Ala Leu Ile Leu 825 Ile Gln Trp Asn Ile 830 Arg Ala  
 Phe Met Ala 835 Val Lys Asn Trp Pro 840 Trp Met Arg Leu Phe 845 Phe Lys Ile  
 Lys Pro 850 Leu Val Lys Ser Ser 855 Gu Val Gly Gu 860 Gu Val Ala Gly Leu  
 Lys 865 Gu Gu Cys Ala Gln 870 Leu Gln Lys Ala Leu 875 Gu Lys Ser Gu Phe 880  
 Gln Arg Gu Gu Leu 885 Lys Ala Lys Gln Val 890 Ser Leu Thr Gln Gu 895 Lys  
 Asn Asp Leu Ile Leu Gln Leu Gln Ala Gu Gln Gu Thr Leu Ala Asn

900

905

910

Val Glu Glu Gln Cys Glu Trp Leu Ile Lys Ser Lys Ile Gln Leu Glu  
 915 920 925

Ala Arg Val Lys Glu Leu Ser Glu Arg Val Glu Glu Glu Glu Ile  
 930 935 940

Asn Ser Glu Leu Thr Ala Arg Gly Arg Lys Leu Glu Asp Glu Cys Phe  
 945 950 955 960

Glu Leu Lys Lys Glu Ile Asp Asp Leu Glu Thr Met Leu Val Lys Ser  
 965 970 975

Glu Lys Glu Lys Arg Thr Thr Glu His Lys Val Lys Asn Leu Thr Glu  
 980 985 990

Glu Val Glu Phe Leu Asn Glu Asp Ile Ser Lys Leu Asn Arg Ala Ala  
 995 1000 1005

Lys Val Val Gln Glu Ala His Gln Gln Thr Leu Asp Asp Leu His  
 1010 1015 1020

Met Glu Glu Glu Lys Leu Ser Ser Leu Ser Lys Ala Asn Leu Lys  
 1025 1030 1035

Leu Glu Gln Gln Val Asp Glu Leu Glu Gly Ala Leu Glu Gln Glu  
 1040 1045 1050

Arg Lys Ala Arg Met Asn Cys Glu Arg Glu Leu His Lys Leu Glu  
 1055 1060 1065

Gly Asn Leu Lys Leu Asn Arg Glu Ser Met Glu Asn Leu Glu Ser  
 1070 1075 1080

Ser Gln Arg His Leu Ala Glu Glu Leu Arg Lys Lys Glu Leu Glu  
 1085 1090 1095

Leu Ser Gln Met Asn Ser Lys Val Glu Asn Glu Lys Gly Leu Val  
 1100 1105 1110

Ala Gln Leu Gln Lys Thr Val Lys Glu Leu Gln Thr Gln Ile Lys  
 1115 1120 1125

Asp Leu Lys Glu Lys Leu Glu Ala Glu Arg Thr Thr Arg Ala Lys  
 1130 1135 1140

Met Glu Arg Glu Arg Ala Asp Leu Thr Gln Asp Leu Ala Asp Leu  
 1145 1150 1155

Asn Glu Arg Leu Glu Glu Val Gly Gly Ser Ser Leu Ala Gln Leu  
 1160 1165 1170

N3027PCT\_sequ.list.txt

G u	I l e	Thr	Lys	Lys	G n	G u	Thr	Lys	I l e	G n	Lys	Leu	H i s	Arg
	1175					1180					1185			
Asp	Met	G u	G u	Al a	Thr	Leu	H i s	Phe	G u	Thr	Thr	Ser	Al a	Ser
	1190					1195					1200			
Leu	Lys	Lys	Arg	H i s	Al a	Asp	Ser	Leu	Al a	G u	Leu	G u	G y	G n
	1205					1210					1215			
Val	G u	Asn	Leu	G n	G n	Val	Lys	G n	Lys	Leu	G u	Lys	Asp	Lys
	1220					1225					1230			
Ser	Asp	Leu	G n	Leu	G u	Val	Asp	Asp	Leu	Leu	Thr	Arg	Val	G u
	1235					1240					1245			
G n	Met	Thr	Arg	Al a	Lys	Al a	Asn	Al a	G u	Lys	Leu	Cys	Thr	Leu
	1250					1255					1260			
Tyr	G u	G u	Arg	Leu	H i s	G u	Al a	Thr	Al a	Lys	Leu	Asp	Lys	Val
	1265					1270					1275			
Thr	G n	Leu	Al a	Asn	Asp	Leu	Al a	Al a	G n	Lys	Thr	Lys	Leu	Trp
	1280					1285					1290			
Ser	G u	Ser	G y	G u	Phe	Leu	Arg	Arg	Leu	G u	G u	Lys	G u	Al a
	1295					1300					1305			
Leu	I l e	Asn	G n	Leu	Ser	Arg	G u	Lys	Ser	Asn	Phe	Thr	Arg	G n
	1310					1315					1320			
I l e	G u	Asp	Leu	Arg	G y	G n	Leu	G u	Lys	G u	Thr	Lys	Ser	G n
	1325					1330					1335			
Ser	Al a	Leu	Al a	H i s	Al a	Leu	G n	Lys	Al a	G n	Arg	Asp	Cys	Asp
	1340					1345					1350			
Leu	Leu	Arg	G u	G n	Tyr	G u	G u	G u	G n	G u	Val	Lys	Al a	G u
	1355					1360					1365			
Leu	H i s	Arg	Thr	Leu	Ser	Lys	Val	Asn	Al a	G u	Met	Val	G n	Trp
	1370					1375					1380			
Arg	Met	Lys	Tyr	G u	Asn	Asn	Val	I l e	G n	Arg	Thr	G u	Asp	Leu
	1385					1390					1395			
G u	Asp	Al a	Lys	Lys	G u	Leu	Al a	I l e	Arg	Leu	G n	G u	Al a	Al a
	1400					1405					1410			
G u	Al a	Met	G y	Val	Al a	Asn	Al a	Arg	Asn	Al a	Ser	Leu	G u	Arg
	1415					1420					1425			

N3027PCT\_sequ.list.txt

Ala	Arg	His	Gln	Leu	Gln	Leu	Glu	Leu	Gly	Asp	Ala	Leu	Ser	Asp
1430						1435					1440			
Leu	Gly	Lys	Val	Arg	Ser	Ala	Ala	Ala	Arg	Leu	Asp	Gln	Lys	Gln
1445						1450					1455			
Leu	Gln	Ser	Gly	Lys	Ala	Leu	Ala	Asp	Trp	Lys	Gln	Lys	His	Glu
1460						1465					1470			
Glu	Ser	Gln	Ala	Leu	Leu	Asp	Ala	Ser	Gln	Lys	Glu	Val	Gln	Ala
1475						1480					1485			
Leu	Ser	Thr	Glu	Leu	Leu	Lys	Leu	Lys	Asn	Thr	Tyr	Glu	Glu	Ser
1490						1495					1500			
Ile	Val	Gly	Gln	Glu	Thr	Leu	Arg	Arg	Glu	Asn	Lys	Asn	Leu	Gln
1505						1510					1515			
Glu	Glu	Ile	Ser	Asn	Leu	Thr	Asn	Gln	Val	Arg	Glu	Gly	Thr	Lys
1520						1525					1530			
Asn	Leu	Thr	Glu	Met	Glu	Lys	Val	Lys	Lys	Leu	Ile	Glu	Glu	Glu
1535						1540					1545			
Lys	Thr	Glu	Val	Gln	Val	Thr	Leu	Glu	Glu	Thr	Glu	Gly	Ala	Leu
1550						1555					1560			
Glu	Arg	Asn	Glu	Ser	Lys	Ile	Leu	His	Phe	Gln	Leu	Glu	Leu	Leu
1565						1570					1575			
Glu	Ala	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Leu	Ser	Glu	Lys	Asp	Glu
1580						1585					1590			
Glu	Ile	Glu	Asn	Phe	Arg	Arg	Lys	Gln	Gln	Cys	Thr	Ile	Asp	Ser
1595						1600					1605			
Leu	Gln	Ser	Ser	Leu	Asp	Ser	Glu	Ala	Lys	Ser	Arg	Ile	Glu	Val
1610						1615					1620			
Thr	Arg	Leu	Lys	Lys	Lys	Met	Glu	Glu	Asp	Leu	Asn	Glu	Met	Glu
1625						1630					1635			
Leu	Gln	Leu	Ser	Cys	Ala	Asn	Arg	Gln	Val	Ser	Glu	Ala	Thr	Lys
1640						1645					1650			
Ser	Leu	Gly	Gln	Leu	Gln	Ile	Gln	Ile	Lys	Asp	Leu	Gln	Met	Gln
1655						1660					1665			
Leu	Asp	Asp	Ser	Thr	Gln	Leu	Asn	Ser	Asp	Leu	Lys	Glu	Gln	Val
1670						1675					1680			

Ala Val 1685 Ala Glu Arg Arg Asn 1690 Ser Leu Leu Glu Ser 1695 Glu Leu Glu  
 Asp Leu 1700 Arg Ser Leu Glu Glu 1705 Glu Thr Glu Arg Gly 1710 Arg Arg Leu  
 Ser Glu 1715 Glu Glu Leu Leu Glu 1720 Ala Thr Glu Arg Ile 1725 Asn Leu Phe  
 Tyr Thr 1730 Glu Asn Thr Ser Leu 1735 Leu Ser Glu Lys Lys 1740 Lys Leu Glu  
 Ala Asp 1745 Val Ala Arg Met Glu 1750 Lys Glu Ala Glu Glu 1755 Val Val Glu  
 Glu Cys 1760 Glu Asn Ala Glu Glu 1765 Lys Ala Lys Lys Ala 1770 Ala Ile Glu  
 Ala Ala 1775 Asn Leu Ser Glu Glu 1780 Leu Lys Lys Lys Glu 1785 Asp Thr Ile  
 Ala His 1790 Leu Glu Arg Thr Arg 1795 Glu Asn Met Glu Glu 1800 Thr Ile Thr  
 Asp Leu 1805 Glu Lys Arg Leu Ala 1810 Glu Ala Glu Glu Met 1815 Ala Leu Met  
 Gly Ser 1820 Arg Lys Glu Ile Glu 1825 Lys Leu Glu Ser Arg 1830 Val Arg Glu  
 Leu Glu 1835 Gly Glu Leu Glu Gly 1840 Glu Ile Arg Arg Ser 1845 Ala Glu Ala  
 Glu Arg 1850 Gly Ala Arg Arg Leu 1855 Glu Arg Cys Ile Lys 1860 Glu Leu Thr  
 Tyr Glu 1865 Ala Glu Glu Asp Lys 1870 Lys Asn Leu Ser Arg 1875 Met Glu Thr  
 Glu Met 1880 Asp Lys Leu Glu Leu 1885 Lys Val Glu Asn Tyr 1890 Lys Glu Glu  
 Val Glu 1895 Val Ala Glu Thr Glu 1900 Ala Asn Glu Tyr Leu 1905 Ser Lys Tyr  
 Lys Lys 1910 Glu Glu His Glu Leu 1915 Asn Glu Val Lys Glu 1920 Arg Ala Glu  
 Val Ala 1925 Glu Ser Glu Val Asn 1930 Lys Leu Lys Ile Lys 1935 Ala Arg Glu  
 Phe Gly Lys Lys Val Glu Glu Glu

1940

<210> 95  
<211> 3516  
<212> DNA  
<213> Toxoplasma gondii

<220>  
<221> misc\_feature  
<222> (1) .. (3516)  
<223> MyoC

```

<400> 95
at ggagcgca aacaaaccca gat gat act g gggcggagac tggcgaaaga ct caccggag      60
gt gaagcatt t t caaagaaa at cgagt gt c gt t cct t t cg gccgt gat gg acgcgct gcc      120
acgaact t t a cct gct ggac t gct gat t gc cccgcagt ga aagct gaccc caccct cgt t      180
t t t gccaaagt gcat agt cgt cggaggggt cc at ggacacgc agct ggaact cgagcaagt c      240
gacccgccag cacgcgggac gt t t acggt t gcgcct acag at gt gt t caa cgcaaacgag      300
t t gat t gaac cggagacggt cgacgat at c ggct at ct t c ct cacacgaa t gt agcgt gt      360
gt ct t ggat g t t ct aaaaag ccgat t t t t g agaagcat ca t t t at acaac agct gagcca      420
ct t ct ggt ag ct at caaccc ct t caaggac ct ggggaaca ccacagat gc at ggat at cg      480
acat at cgga acgccagt aa gcct gagat g ct t ccaccac at gt ct t caa aacggcccgc      540
gccgcgct t g aggacct t ga aggct acaag aaaaaccaat cgat cat t gt gt cgggcgaa      600
t ct ggagcag gaaagact ga agct acaaaa cagat cat gc ggt t t t t t gc gt cggcgt cc      660
t ct gaggt gc gcacgact at ccaagacacc at t at ggcag gcaat cccat cct t gaggcc      720
t t cggaaat g ccaaaacaat ccgt aat aat aact ccagcc gat t t ggacg at t cat gat g      780
ct cgat gt ct cgt ct cat cg gggcat t cag cacgggagt a t at ccaact t cct cct cgaa      840
aaagt gcgt g t ggt gt ccca ggaagcgaac gaacgat cct accat at t t t ct accagct g      900
ct caaaggcg cgacgagcga aat gcgt gca aagt accact t gcgcagt t t aaaggagt ac      960
gcgt at ct ga at ggt aaaaa cggg ggat gc t acgat gt cc cgggcat cga t gacaaggcc      1020
gat t t cgagg aggt gct t ca at cgt t ggat gccat gcaga t cacgggt t c gaaacggcat      1080
t cgggt gt t t t caat t ct ct c cggcct t ct g ct t at t ggca at gt aagcat agaaggaaaa      1140
gacgcacagg gt gt cccgga t gcagcgt at at t t cgccgc agagcgagga aat cct ggag      1200
gaagct t gcc agct cct t ag cgt t gat gac gcagcact ca agaaggaaat t ct cgt gaag      1260
t cgacgaagg t t ggacct ca ggt cat cgaa ggt gt gcgt a caaaggat ga ggccaagacg      1320
t ct gt gt t gt cgct gt ct aa aaat gt gt at gacaagct ct t t gact ggct t gt t cgccag      1380
ct t aacagct t gat t gacgc t ccagat ggc at gcccaat t t cat t ggaat t ct t gat at t      1440
t t t ggct t t g aagt cct cga agt aaact cg ct t gagcagg t cct gat t aa cat t accaat      1500
gagt at ct gc aaaaacact t cat cgat gt t gt ct t cgat a t ggaaacgaa gct t t accaa      1560
gccgaagggt g t t ccgact ga ggccct cgag t acacggat a acct t gcact t gt cggcgt      1620

```

N3027PCT\_sequ. list . . txt

ct ct gt ggaa agaacgat t c g t t t t t cgct ct gct cgaag at gcct gct t aggc at cagg	1680
t caact gacg aggg t t t ct g cgggacgat c ct gcgcgcgc t ggagccct c gggat t ct t t	1740
t t ggagt ct c gcagagacaa aaggct gaaa t t t at aat cc ggcacacgat t gccgat at c	1800
gagt at acat gt gaagggat gt t ggaaaag aacaaggact t t ct t cgt aa ggaggt gat g	1860
gat gt cat ga aggcgt caac t gaccct gt c acaaaggcgc t ct t cgaagg aat t gaaat c	1920
gaggcaggaa aaat cggcaa gggaacact a at cgc at cca gat t cct gaa gaact t ggag	1980
gagat gat cg gaat t gt agc gcaaacggag gcgcact t ca t ccgt t gcct gaagccgaac	2040
gaggagaaga agcccct ggg at ggaat ggg t cgaaggt gc t gaat cagct t t t ct cgct t	2100
t cgat ct t gg aggcact t ca act ccgcaa gt cggat acg cgt at cggcg caact t cagc	2160
gaat t ct gca gt cat t t ccg at ggct cgat ct aggt ct t g t gaat t ct ga t cgcgacagg	2220
aaggaggt cg cgcagct gct t ct cgaacaa t caggaat t c cggagt cgt c gt gggat gat c	2280
ggaaaaacga t ggt gt t cgt gaagcct gac gcggcgaagg agt t gt cgat ct t gcagcgc	2340
gagaagt t ga t gt gt t t cca gcct ct gat c ggct cct gg gcccgat gt g gaggaaggt t	2400
ct cct ccgaa agaagat ggc aagggt t at c cact t cct ca cgagact gga at caaacgcg	2460
cgcagacat c t ggagccgga cagcat t aac at ct ct cct g aagaacgaga agcgt t gt t g	2520
t cgggaat gg agcgt cct cg aaat ccct gt gt cgt cgt t a agaaacgcgt t gaaccagag	2580
cgaagcgcgc caacgaaggt gct cagcct a t ct cgcgct a ggct t t cgct ct ct aaagaa	2640
ct gcct cgaa at t acgcagc gagcaacgaa gccct ggat g t t gat gat ac cat gt ct gt a	2700
gacaccgat g cct t ct t acg t ct caaaat g aagcggcgc ccaacgagaa ct at ct ccgc	2760
cagacagct t t ggcccgcct gaaagagcgg cggccgt cgc acgt ct gcat ggaggaggcg	2820
t at cacgt gt ggaggt cggg ggaact act a t t cagagagc ct ct gagt ga caagagact t	2880
cagaacat t t gcact gt aat ccgaaacgat at ggaccagc at t acggct t t t t ct ggcaa	2940
gt aat cat ca at cgcact cc caact t cggc at ggct gcga ct cat at t ca cgggt ccct t	3000
cacgt cgt t g aacaggaagg cat gt accga gacggccgac aat t cct ct t ccacct cat c	3060
at gt at aaaa cccggaaacc ccgcaaggaa gagat t cgac t ccat gaaag ggccggcgag	3120
aaaacgt at g gcat ct gt cg aaagagggat t t ct caggca t t gt gcgcgt cat gaat agc	3180
aaagt gccgc cgt acat gca gaaggacgt c t cgt act t ga t t ggcat gct ct t t cagcga	3240
t accagt aca ct agagact g gacgaat t t t gccacct gca t t cagt cgt a cct gat t ggc	3300
cgt t acagcg aaccgt t cgg aggagct t gg aacgt ggt ag cacaggaagg cgcgt t t t t c	3360
t t gagt cgcc t gt ggaccaa acat agt cga t t cct gcgcg t ggaaat t ga ct t ccct gct	3420
ct agcagaac aggcgagt ag t gaacct t gt ccaggct gt c ct accccagt cct t act gt c	3480
gt gt gct t cg aggcct gt gc gccggat aga ccgt ga	3516

<210> 96  
 <211> 1171  
 <212> PRT  
 <213> Toxoplasma gondii

&lt;220&gt;

&lt;221&gt; M SC\_FEATURE

&lt;222&gt; (1)..(1171)

&lt;223&gt; MyoC

&lt;400&gt; 96

Met Glu Arg Lys Gln Thr Gln Met Ile Leu Gly Arg Arg Leu Ala Lys  
1 5 10 15

Asp Ser Pro Glu Val Lys His Phe Gln Arg Lys Ser Ser Val Val Pro  
20 25 30

Phe Gly Arg Asp Gly Arg Ala Ala Thr Asn Phe Thr Cys Trp Thr Ala  
35 40 45

Asp Cys Pro Ala Val Lys Ala Asp Pro Thr Leu Val Phe Ala Lys Cys  
50 55 60

Ile Val Val Gly Gly Ser Met Asp Thr Gln Leu Glu Leu Glu Gln Val  
65 70 75 80

Asp Pro Pro Ala Arg Gly Thr Phe Thr Val Ala Pro Thr Asp Val Phe  
85 90 95

Asn Ala Asn Glu Leu Ile Glu Pro Glu Thr Val Asp Asp Ile Gly Tyr  
100 105 110

Leu Pro His Thr Asn Val Ala Cys Val Leu Asp Val Leu Lys Ser Arg  
115 120 125

Phe Leu Arg Ser Ile Ile Tyr Thr Thr Ala Glu Pro Leu Leu Val Ala  
130 135 140

Ile Asn Pro Phe Lys Asp Leu Gly Asn Thr Thr Asp Ala Trp Ile Ser  
145 150 155 160

Thr Tyr Arg Asn Ala Ser Lys Pro Glu Met Leu Pro Pro His Val Phe  
165 170 175

Lys Thr Ala Arg Ala Ala Leu Glu Asp Leu Glu Gly Tyr Lys Lys Asn  
180 185 190

Gln Ser Ile Ile Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala  
195 200 205

Thr Lys Gln Ile Met Arg Phe Phe Ala Ser Ala Ser Ser Glu Val Arg  
210 215 220

Thr Thr Ile Gln Asp Thr Ile Met Ala Gly Asn Pro Ile Leu Glu Ala  
225 230 235 240

Phe Gly Asn Ala Lys Thr Ile Arg Asn Asn Asn Ser Ser Arg Phe Gly  
245 250 255

Arg Phe Met Met Leu Asp Val Ser Ser His Arg Gly Ile Gln His Gly  
260 265 270

Ser Ile Ser Asn Phe Leu Leu Gu Lys Val Arg Val Val Ser Gln Gu  
275 280 285

Ala Asn Gu Arg Ser Tyr His Ile Phe Tyr Gln Leu Leu Lys Gly Ala  
290 295 300

Thr Ser Gu Met Arg Ala Lys Tyr His Leu Arg Ser Leu Lys Gu Tyr  
305 310 315 320

Ala Tyr Leu Asn Gly Lys Asn Gly Gly Cys Tyr Asp Val Pro Gly Ile  
325 330 335

Asp Asp Lys Ala Asp Phe Gu Gu Val Leu Gln Ser Leu Asp Ala Met  
340 345 350

Gln Ile Thr Gly Ser Lys Arg His Ser Val Phe Ser Ile Leu Ser Gly  
355 360 365

Leu Leu Leu Ile Gly Asn Val Ser Ile Gu Gly Lys Asp Ala Gln Gly  
370 375 380

Val Pro Asp Ala Ala Tyr Ile Ser Pro Gln Ser Gu Gu Ile Leu Gu  
385 390 395 400

Gu Ala Cys Gln Leu Leu Ser Val Asp Asp Ala Ala Leu Lys Lys Gu  
405 410 415

Ile Leu Val Lys Ser Thr Lys Val Gly Pro Gln Val Ile Gu Gly Val  
420 425 430

Arg Thr Lys Asp Gu Ala Lys Thr Ser Val Leu Ser Leu Ser Lys Asn  
435 440 445

Val Tyr Asp Lys Leu Phe Asp Trp Leu Val Arg Gln Leu Asn Ser Leu  
450 455 460

Ile Asp Ala Pro Asp Gly Met Pro Asn Phe Ile Gly Ile Leu Asp Ile  
465 470 475 480

Phe Gly Phe Gu Val Leu Gu Val Asn Ser Leu Gu Gln Val Leu Ile  
485 490 495

Asn Ile Thr Asn Gu Tyr Leu Gln Lys His Phe Ile Asp Val Val Phe  
500 505 510

Asp Met Gu Thr Lys Leu Tyr Gln Ala Gu Gly Val Pro Thr Gu Ala  
Page 473

515

Leu Glu Tyr Thr Asp Asn Leu Ala Leu Val Gly Ala Leu Cys Gly Lys  
530 535 540

Asn Asp Ser Phe Phe Ala Leu Leu Glu Asp Ala Cys Leu Gly Ile Arg  
545 550 555 560

Ser Thr Asp Glu Gly Phe Cys Gly Thr Ile Leu Arg Arg Leu Glu Pro  
565 570 575

Ser Gly Phe Phe Leu Glu Ser Arg Arg Asp Lys Arg Leu Lys Phe Ile  
580 585 590

Ile Arg His Thr Ile Ala Asp Ile Glu Tyr Thr Cys Glu Gly Met Leu  
595 600 605

Glu Lys Asn Lys Asp Phe Leu Arg Lys Glu Val Met Asp Val Met Lys  
610 615 620

Ala Ser Thr Asp Pro Val Thr Lys Ala Leu Phe Glu Gly Ile Glu Ile  
625 630 635 640

Glu Ala Gly Lys Ile Gly Lys Gly Thr Leu Ile Ala Ser Arg Phe Leu  
645 650 655

Lys Asn Leu Glu Glu Met Ile Gly Ile Val Ala Glu Thr Glu Ala His  
660 665 670

Phe Ile Arg Cys Leu Lys Pro Asn Glu Glu Lys Lys Pro Leu Gly Trp  
675 680 685

Asn Gly Ser Lys Val Leu Asn Glu Leu Phe Ser Leu Ser Ile Leu Glu  
690 695 700

Ala Leu Glu Leu Arg Glu Val Gly Tyr Ala Tyr Arg Arg Asn Phe Ser  
705 710 715 720

Glu Phe Cys Ser His Phe Arg Trp Leu Asp Leu Gly Leu Val Asn Ser  
725 730 735

Asp Arg Asp Arg Lys Glu Val Ala Glu Leu Leu Leu Glu Glu Ser Gly  
740 745 750

Ile Pro Glu Ser Ser Trp Val Ile Gly Lys Thr Met Val Phe Val Lys  
755 760 765

Pro Asp Ala Ala Lys Glu Leu Ser Ile Leu Glu Arg Glu Lys Leu Met  
770 775 780

Cys Phe Glu Pro Leu Ile Gly Val Leu Gly Pro Met Trp Arg Lys Val  
785 790 795 800

N3027PCT\_sequ.list.txt

Leu Leu Arg Lys Lys Met Ala Arg Val Ile His Phe Leu Thr Arg Leu  
 805 810 815  
 Glu Ser Asn Ala Arg Arg His Leu Glu Pro Asp Ser Ile Asn Ile Ser  
 820 825 830  
 Pro Glu Glu Arg Glu Ala Leu Leu Ser Gly Met Glu Arg Pro Arg Asn  
 835 840 845  
 Pro Cys Val Val Val Lys Lys Arg Val Glu Pro Glu Arg Ala Pro Pro  
 850 855 860  
 Thr Lys Val Leu Ser Leu Ser Arg Ala Arg Leu Ser Leu Ser Lys Glu  
 865 870 875 880  
 Leu Pro Arg Asn Tyr Ala Ala Ser Asn Glu Ala Leu Asp Val Asp Asp  
 885 890 895  
 Thr Met Ser Val Asp Thr Asp Ala Phe Leu Arg Leu Lys Met Lys Arg  
 900 905 910  
 Ser Pro Asn Glu Asn Tyr Leu Arg Gln Thr Ala Leu Ala Arg Leu Lys  
 915 920 925  
 Glu Arg Arg Pro Ser His Val Cys Met Glu Glu Ala Tyr His Val Trp  
 930 935 940  
 Arg Ser Val Glu Leu Leu Phe Arg Glu Pro Leu Ser Asp Lys Arg Leu  
 945 950 955 960  
 Gln Asn Ile Cys Thr Val Ile Arg Asn Asp Met Asp Gln His Tyr Gly  
 965 970 975  
 Phe Phe Trp Gln Val Ile Ile Asn Arg Thr Pro Asn Phe Gly Met Ala  
 980 985 990  
 Ala Thr His Ile His Gly Ser Leu His Val Val Glu Gln Glu Gly Met  
 995 1000 1005  
 Tyr Arg Asp Gly Arg Gln Phe Leu Phe His Leu Ile Met Tyr Lys  
 1010 1015 1020  
 Thr Arg Lys Pro Arg Lys Glu Glu Ile Arg Leu His Glu Arg Ala  
 1025 1030 1035  
 Ala Glu Lys Thr Tyr Gly Ile Cys Arg Lys Arg Asp Phe Ser Gly  
 1040 1045 1050  
 Ile Val Arg Val Met Asn Ser Lys Val Pro Pro Tyr Met Gln Lys  
 1055 1060 1065

N3027PCT\_sequ.list.txt

Asp Val Ser Tyr Leu Ile Gly Met Leu Phe Gln Arg Tyr Gln Tyr  
1070 1075 1080

Thr Arg Asp Trp Thr Asn Phe Ala Thr Cys Ile Gln Ser Tyr Leu  
1085 1090 1095

Ile Gly Arg Tyr Ser Glu Pro Phe Gly Gly Ala Trp Asn Val Val  
1100 1105 1110

Ala Gln Glu Gly Ala Phe Phe Leu Ser Arg Leu Trp Thr Lys His  
1115 1120 1125

Ser Arg Phe Leu Arg Val Glu Ile Asp Phe Pro Ala Leu Ala Glu  
1130 1135 1140

Gln Ala Ser Ser Glu Pro Cys Pro Gly Cys Pro Thr Pro Val Leu  
1145 1150 1155

Thr Val Val Cys Phe Glu Ala Cys Ala Pro Asp Arg Pro  
1160 1165 1170

<210> 97  
<211> 2469  
<212> DNA  
<213> Toxoplasma gondii

<220>  
<221> misc\_feature  
<222> (1)..(2469)  
<223> MyoD

<400> 97  
atggcggcaa aaccggagca ggactgcaag acagcggcgg ctctcat t cg ggcggggg t cg 60  
ttgatagaag gcgttgaatc agcaggcaaa gactttttag tctggacgac acagggcccc 120  
gctgtaaaaa aagatccaga tctcctcttc agtctctgtc gagtgttgcc tggcagcaca 180  
cagcagacgc tgaaactcca gcaggtcgaa ccgactgcgg actcacagga actgaccgtc 240  
caagccaagg aagtttggca ggcgaaacccc ggcatcgacc ccctgactta cggcgacatc 300  
ggcggggtgc cgcacacgaa cgagccatgc gtgctggtt t tctggcgcg acgctaccag 360  
agcaaagtga tctacacgac tgcagagccg ctgattgtcg cagtgaatcc gtttcaggac 420  
ctgaaaaatg cgggcccgga cacgattgcg ctctacagag acgccccga tgtggacaag 480  
ctcccgccgc acgtcttcta cgccagtcga cgcgccatga cgaacatgca ccagctgaag 540  
aagccgcaga cgatcat t gt cagtggcgag agtggcgctg gaaagactga gacgactaag 600  
atgctcatga agtacctggc aaccagcgcc ggtgggaacc tggacctgaa gatccagact 660  
gcgatcatgg cggcgaaaccc tgtgctcgag gcgtttggaa acgcaaagac agttcgcaac 720  
aacaacagca gtcgcttcgg cagattcatg ctctcgatg tgcgcagaga gggcggcatt 780  
caacacggca aggttgtcgc ctctctgttg gaaaaagcc gaatcgtctg ccaagacaaa 840

N3027PCT\_sequ. list . . txt

gacgaacgca act accacat ct t ct accag t t ct t gaagg gcgct cct gg ccat at gcgc	900
cagcggg t aca t gct gcagcc cct ggaggca t acacct t ca t caacccgca ct gcct cgat	960
gcaccaggg t cgt cgacac ggaggact t t gagcaaacgg t caaat cat t agagt caat g	1020
aacat gacgg agacggagac at gcaccat c t ggt caat cg t ct caggt gt t ct gct cat g	1080
ggaaat gcc a gcct act gg aaaaaccgag gct ggt gt cg agaacgccgc at gct t cgt c	1140
ggcgagt cag aagccgct ct gcggaat gca t gcagt ct gc t ct t cct cga ct acccgagc	1200
at t ct acat g aact aacggt gaagacaact t at gccggaa gcaacaagat cgagagt cgg	1260
t ggaccgt cc cagact ccga gat gct gcgt gcat ct ct gg cgaagggcat gt t cgaacag	1320
t t gt t t ct gt ggat t at t cg caagct gaac gcagacat t g agccgaaggg aggat cgt t c	1380
gat gt ct t t a t ggggt ct gct ggat at ct t c ggt t t t gaag t t t t ccaaaa caact ccct c	1440
gagcagt t gt t cat t aacat t accaacgaa gt gct t caga gaaact t t ac ggacat t gt c	1500
t t cgagaaaag aact gcagct ct acagcaaa gaaggcat ct cat cgaagaa aat t gaat ac	1560
accacgaat g aaaagct gat t gagaccct t ct gggaaaag gaact t cgggt t t t ggct gcc	1620
t t ggaggat c agt gcat ct c gcct agcggg act gacgaga aat t t gt ct c gagt t t ggcg	1680
agcaagt t gg cggggaacaa gt gct t cat t ccct cgaaaa acaccaagag t ct ggagt t c	1740
accgt t gt t c acaccat cgg gaaagt cat c t acaacgccg at ggct t t gc t t t caaaaac	1800
aaagacgt t c t gcgcccggg aat cat cgaa at cacgcggg cgt cgacgaa cgacgt t gt t	1860
cgcggt t at t t gagggcgt caaagt t gag aaggggaaga t ggcaaaagg cat gt t gat c	1920
ggaagt cagt t t at gacgca gct caagggg ct gat ggaag t gat t cagaa aacggaat ct	1980
cact t cat t c gt t gcat caa accgaacgac gacaaggt gc ct ct caagt g ggt gaacagc	2040
aaggt cct ca t t cagct gca t gcact ct cg at t t t ggagg ct ct t cacct ccgccaaact c	2100
gcct t ct cct accgaagaac ct t cgaggag t t cgct gcgc agt t t cgct t cat caat ct g	2160
ggcgt t t caa acaagccagg cgccgacgcg aagaccat ct gt gt ggagt t gt t gaagagc	2220
acaagcat t t ct gcagacga gt acgcact c ggcaagacga t ggt at t t ct caagccgcaa	2280
gcagcaaaga t gt t ggt gcg gct gcagcgc gaagcgt t gt cagct t ggga gcct ct cgt c	2340
ggt gt gt t cg aggggat gac t gt t ct gaaa agggcaaagc agct gt cgac t ggccggggcg	2400
gt cccggcga ct cgcat t t g cgcgaaat gt t cgccgaaaac t cgt ccaagc gggcat caag	2460
gt t t gct ag	2469

<210> 98  
 <211> 822  
 <212> PRT  
 <213> Toxoplasma gondii

<220>  
 <221> MSC\_FEATURE  
 <222> (1) . . (822)  
 <223> MyoD

<400> 98

N3027PCT\_sequ.list.txt

```

Met Ala Ala Lys Pro Glu Gln Asp Cys Lys Thr Ala Ala Ala Leu Ile
1      5      10

Arg Ala Gly Ser Leu Ile Glu Gly Val Glu Ser Ala Gly Lys Asp Phe
20     25     30

Leu Val Trp Thr Thr Gln Gly Pro Ala Val Lys Lys Asp Pro Asp Leu
35     40     45

Leu Phe Ser Leu Cys Arg Val Leu Pro Gly Ser Thr Gln Gln Thr Leu
50     55     60

Lys Leu Gln Gln Val Glu Pro Thr Ala Asp Ser Gln Glu Leu Thr Val
65     70     75     80

Gln Ala Lys Glu Val Trp Gln Ala Asn Pro Gly Ile Asp Pro Leu Thr
85     90     95

Tyr Gly Asp Ile Gly Gly Leu Pro His Thr Asn Glu Pro Cys Val Leu
100    105    110

Asp Phe Leu Ala Arg Arg Tyr Gln Ser Lys Val Ile Tyr Thr Thr Ala
115    120    125

Glu Pro Leu Ile Val Ala Val Asn Pro Phe Gln Asp Leu Lys Asn Ala
130    135    140

Gly Pro Asp Thr Ile Ala Leu Tyr Arg Asp Ala Pro Asp Val Asp Lys
145    150    155    160

Leu Pro Pro His Val Phe Tyr Ala Ser Arg Arg Ala Met Thr Asn Met
165    170    175

His Gln Leu Lys Lys Pro Gln Thr Ile Ile Val Ser Gly Glu Ser Gly
180    185    190

Ala Gly Lys Thr Glu Thr Thr Lys Met Leu Met Lys Tyr Leu Ala Thr
195    200    205

Ser Ala Gly Gly Asn Leu Asp Leu Lys Ile Gln Thr Ala Ile Met Ala
210    215    220

Ala Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn
225    230    235    240

Asn Asn Ser Ser Arg Phe Gly Arg Phe Met Leu Leu Asp Val Ala Arg
245    250    255

Glu Gly Gly Ile Gln His Gly Lys Val Val Ala Phe Leu Leu Glu Lys
260    265    270

```

Ser Arg Ile Val Cys Gln Asp Lys Asp Glu Arg Asn Tyr His Ile Phe  
275 280 285

Tyr Gln Phe Leu Lys Gly Ala Pro Gly His Met Arg Gln Arg Tyr Met  
290 295 300

Leu Gln Pro Leu Glu Ala Tyr Thr Phe Ile Asn Pro His Cys Leu Asp  
305 310 315 320

Ala Pro Gly Ile Val Asp Thr Glu Asp Phe Glu Gln Thr Val Lys Ser  
325 330 335

Leu Glu Ser Met Asn Met Thr Glu Thr Glu Thr Cys Thr Ile Trp Ser  
340 345 350

Ile Val Ser Gly Val Leu Leu Met Gly Asn Ala Lys Pro Thr Gly Lys  
355 360 365

Thr Glu Ala Gly Val Glu Asn Ala Ala Cys Phe Val Gly Glu Ser Glu  
370 375 380

Ala Ala Leu Arg Asn Ala Cys Ser Leu Leu Phe Leu Asp Tyr Pro Ser  
385 390 395 400

Ile Leu His Glu Leu Thr Val Lys Thr Thr Tyr Ala Gly Ser Asn Lys  
405 410 415

Ile Glu Ser Arg Trp Thr Val Pro Asp Ser Glu Met Leu Arg Ala Ser  
420 425 430

Leu Ala Lys Gly Met Phe Glu Gln Leu Phe Leu Trp Ile Ile Arg Lys  
435 440 445

Leu Asn Ala Asp Ile Glu Pro Lys Gly Gly Ser Phe Asp Val Phe Met  
450 455 460

Gly Leu Leu Asp Ile Phe Gly Phe Glu Val Phe Gln Asn Asn Ser Leu  
465 470 475 480

Glu Gln Leu Phe Ile Asn Ile Thr Asn Glu Val Leu Gln Arg Asn Phe  
485 490 495

Thr Asp Ile Val Phe Glu Lys Glu Leu Gln Leu Tyr Ser Lys Glu Gly  
500 505 510

Ile Ser Ser Lys Lys Ile Glu Tyr Thr Thr Asn Glu Lys Leu Ile Glu  
515 520 525

Thr Leu Leu Gly Lys Gly Thr Ser Val Leu Ala Ala Leu Glu Asp Gln  
530 535 540

Cys Ile Ser Pro Ser Gly Thr Asp Glu Lys Phe Val Ser Ser Leu Ala  
Page 479

Page 480

N3027PCT\_sequ. list . . txt

<210> 99  
 <211> 2493  
 <212> DNA  
 <213> Toxoplasma gondii

<220>  
 <221> misc\_feature  
 <222> (1)..(2493)  
 <223> MyoE

<400> 99  
 at gaacgctt tctccatatt caggaggggc atgcgcgggg ggcccgcgag tgcacatgga 60  
 gacaagcttc gtcgaggag aacagaagtc gatccaaagg cggat acgct gcagggcattg 120  
 aaaat atgga caaacaacgc gccagccgtg cagcgaacg ctgatgagt gcttgcgctc 180  
 tgccttattc tttcccgagt c gagt gaaact gt tctccatc tgaagcagat tgaccctccc 240  
 cctgacacca cagaagcgga gtcat t cag atcgatccag aggatgcat t caacgcgaac 300  
 atcggcatcg aagtggaaca gt tccctgac atcgggtttgc tccctcaca aaat tgcgcg 360  
 gcagt tctgg atttctt aaa gcaacgat at cctcctggatc tcat t tat ac cactgcagat 420  
 cccctcctga tgcctatcaa tccattcaaa gatcttaaca acacgactcc agagt ggtta 480  
 cagctctacc gggatgcccc cgacgccgag atactcgctc cgcatgtctt t cggctggca 540  
 cgcacggtac tttgagagatt gtctgccttt atggccagtc aaaccatcat cgtcagcggc 600  
 gagt caggag cagggaaaac ggaagccaca aagcagatca tgtcttactt t gccgctggg 660  
 aagcgaggag aggtatctca ccaacgcattc caaatgccg tcat tgcggc aaatcctgtt 720  
 ct cgaagcct t cggcaatgc gaagactgtc cggaacaaca actccagt cg ct t cggcgc 780  
 t tcatgcagc t tcaactggg ggagaaggga ggcatcgaat acggctccat ccgcaacttt 840  
 t tgttggaga aagtcgcgt gaccagt cag gagcaacatg agagatccta ccacat tttt 900  
 tatcaactag tgaagggcgc t gacgacgca aaacgaaggc agctgcatct gcttaatctc 960  
 gaagactaca cctacctctc aaagaacggt ggctgctacg actgtcccgg aatcgacgac 1020  
 gtcaaagatt tcaaagaaat gaataagagt t tgcgctcca taggtctcaa cctggatgac 1080  
 gttgaaagcc tttggtcgat tatcgcaggc gtcttcttc tgggaaacgt gcacttggaa 1140  
 agtcgggaga cagacggtca gcctaatgca gctgccctca cccagacgg agaggcgacc 1200  
 ctgcagaagt gctgtgact tttgtttgtc gatgaggagg cagt gaaaaa ggagattctc 1260  
 taaaagtca aaacaattgg tgaccaacaa atagagtccc caaacagctt gt cggatgct 1320  
 ttgatgaatc gggactcctt agcgaaggcc gtgtacgaga agt tgt t cga t t gggcgtt 1380  
 cgtcgtgtca acgcaacaat cgaacctcct caaggttttg gaatcttcat gggaatgctg 1440  
 gacatctttg gt ttcgaaat gt t t gagaac aat tccctgg aacagcttct catcaat atc 1500  
 accaatgagc agctgcagaa aaactttatc caaatcgttt t t gctcgtga aacgaagt t g 1560  
 tactacgaag aaggaatcgg aaatgtgaaa at t acgtgga cagacaacga gaacgtgatc 1620  
 aaagctttgt gcgggaaatc gtctcctcagtc ct t gccat ac t caggacaa gagtctt gct 1680

N3027PCT\_sequ.list.txt

ccgggaggca ct gat gaagc aat cgt cacg t ccat gaacc aggct ct aaa gt cct ct gat 1740  
gt gt ggaaac ccggggcagaa gaacccgcgt at tt gct ttt gcat ct gcca caccat t gcc 1800  
gat at t cagt acgat gcaac t ggct t cat c gagaagaaca aagacct t ct gaagcccag 1860  
ct ct gct cca t cgt acaggc t t ct t caaac aat gt ggcaa aggaat t at t t gaaggt gt c 1920  
gt cat gcaga agggcaagat t gccaaaggg caact cat t g ct t ct cagt t t at gcgct ct 1980  
ct t gat gct c t ct t gact ct gat ct cgagt acagaat cgc at t t t at t cg t t gct t gaaa 2040  
ccgaat gaga cgaagaat cc t cat gat t gg t caaacggaa aagt t ct cgc gcagct t t t c 2100  
t ccct gt cga t ct t ggaagc act ccaact c aagaat ct t t ct t t t cct a ccggcggccg 2160  
t acgcagact t ct t gaaaca gt t cgagcag ct agat ct cg aggt caccag gaagt ccgga 2220  
aat gcaaagg agaagacgaa gcagct t ct t act cgagcaa at gt accaca agccaaat gg 2280  
gcgct cggca acacaat ggt gt t t at gaaa ccagacgcag t t cgagagct gacacaaaaa 2340  
at gcgact ga t t gt ggt ggc gt gggaaccg ct cat t cgt g t t t t agaggc t t gccat t cc 2400  
cgt gct t t aa aaat gcgggc cat aaggggac agt gt gcaat gggg ggt t cg aat ccagt ca 2460  
cagat ccgga aggcgcgagt gat t at ggag t ag 2493

<210> 100  
<211> 830  
<212> PRT  
<213> Toxoplasma gondii

<220>  
<221> MSC\_FEATURE  
<222> (1) .. (830)  
<223> MyoE

<400> 100

Met Asn Ala Phe Ser Ile Phe Arg Arg Gly Met Arg Gly Gly Pro Ala  
1 5 10 15

Ser Ala His Gly Asp Lys Leu Arg Arg Gly Arg Thr Glu Val Asp Pro  
20 25 30

Lys Ala Asp Thr Leu Gln Gly Met Lys Ile Trp Thr Asn Asn Ala Pro  
35 40 45

Ala Val His Ala Asn Ala Asp Glu Cys Phe Ala Leu Cys Leu Ile Leu  
50 55 60

Pro Glu Ser Ser Glu Thr Val Leu His Leu Lys Gln Ile Asp Pro Pro  
65 70 75 80

Pro Asp Thr Thr Glu Ala Glu Ser Phe Thr Ile Asp Pro Glu Asp Ala  
85 90 95

Phe Asn Ala Asn Ile Gly Ile Glu Val Asp Lys Phe Pro Asp Ile Gly  
100 105 110

N3027PCT\_sequ.list.txt

Leu Leu Pro His Lys Asn Cys Ala Ala Val Leu Asp Phe Leu Lys Gln  
 115 120 125  
 Arg Tyr Leu Leu Asp Leu Ile Tyr Thr Thr Ala Asp Pro Leu Leu Ile  
 130 135 140  
 Ala Ile Asn Pro Phe Lys Asp Leu Asn Asn Thr Thr Pro Glu Trp Leu  
 145 150 155  
 Gln Leu Tyr Arg Asp Ala Pro Asp Ala Glu Ile Leu Ala Pro His Val  
 165 170 175  
 Phe Arg Leu Ala Arg Thr Val Leu Glu Arg Leu Ser Ala Phe Met Ala  
 180 185 190  
 Ser Gln Thr Ile Ile Val Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu  
 195 200 205  
 Ala Thr Lys Gln Ile Met Ser Tyr Phe Ala Ala Gly Lys Arg Gly Glu  
 210 215 220  
 Val Ser His Gln Arg Ile Gln Asn Ala Val Ile Ala Ala Asn Pro Val  
 225 230 235 240  
 Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asn Asn Ser Ser  
 245 250 255  
 Arg Phe Gly Arg Phe Met Gln Leu Gln Leu Gly Glu Lys Gly Gly Ile  
 260 265 270  
 Glu Tyr Gly Ser Ile Arg Asn Phe Leu Leu Glu Lys Val Arg Val Thr  
 275 280 285  
 Ser Gln Glu Gln His Glu Arg Ser Tyr His Ile Phe Tyr Gln Leu Val  
 290 295 300  
 Lys Gly Ala Asp Asp Ala Lys Arg Arg Gln Leu His Leu Leu Asn Leu  
 305 310 315 320  
 Glu Asp Tyr Thr Tyr Leu Ser Lys Asn Gly Gly Cys Tyr Asp Cys Pro  
 325 330 335  
 Gly Ile Asp Asp Val Lys Asp Phe Lys Glu Met Asn Lys Ser Leu Arg  
 340 345 350  
 Ser Ile Gly Leu Asn Leu Asp Asp Val Glu Ser Leu Trp Ser Ile Ile  
 355 360 365  
 Ala Gly Val Leu Leu Leu Gly Asn Val His Leu Glu Ser Arg Glu Thr  
 370 375 380

N3027PCT\_sequ.list.txt

Asp Gly Gln Pro Asn Ala Ala Ala Leu Thr Pro Asp Gly Glu Ala Thr  
 385 390 395 400  
 Leu Gln Lys Cys Cys Ala Leu Leu Phe Val Asp Glu Glu Ala Val Lys  
 405 410 415  
 Lys Glu Ile Leu Tyr Lys Val Lys Thr Ile Gly Asp Gln Gln Ile Glu  
 420 425 430  
 Ser Pro Asn Ser Leu Ser Asp Ala Leu Met Asn Arg Asp Ser Leu Ala  
 435 440 445  
 Lys Ala Val Tyr Glu Lys Leu Phe Asp Trp Val Val Arg Arg Val Asn  
 450 455 460  
 Ala Thr Ile Glu Pro Pro Gln Gly Phe Gly Ile Phe Met Gly Met Leu  
 465 470 475  
 Asp Ile Phe Gly Phe Glu Met Phe Glu Asn Asn Ser Leu Glu Gln Leu  
 485 490 495  
 Leu Ile Asn Ile Thr Asn Glu Gln Leu Gln Lys Asn Phe Ile Gln Ile  
 500 505 510  
 Val Phe Ala Arg Glu Thr Lys Leu Tyr Tyr Glu Glu Gly Ile Gly Asn  
 515 520 525  
 Val Lys Ile Thr Trp Thr Asp Asn Glu Asn Val Ile Lys Ala Leu Cys  
 530 535 540  
 Gly Lys Ser Ser Ser Val Leu Ala Ile Leu Glu Asp Lys Ser Leu Ala  
 545 550 555 560  
 Pro Gly Gly Thr Asp Glu Ala Ile Val Thr Ser Met Asn Gln Ala Leu  
 565 570 575  
 Lys Ser Ser Asp Val Trp Lys Pro Gly Gln Lys Asn Pro Arg Ile Cys  
 580 585 590  
 Phe Cys Ile Cys His Thr Ile Ala Asp Ile Gln Tyr Asp Ala Thr Gly  
 595 600 605  
 Phe Ile Glu Lys Asn Lys Asp Leu Leu Lys Pro Glu Leu Cys Ser Ile  
 610 615 620  
 Val Gln Ala Ser Ser Asn Asn Val Ala Lys Glu Leu Phe Glu Gly Val  
 625 630 635 640  
 Val Met Gln Lys Gly Lys Ile Ala Lys Gly Gln Leu Ile Ala Ser Gln  
 645 650 655

# N3027PCT\_sequ.list.txt

Phe Met Arg Ser Leu Asp Ala Leu Leu Thr Leu Ile Ser Ser Thr Glu  
660 665 670

Ser His Phe Ile Arg Cys Leu Lys Pro Asn Glu Thr Lys Asn Pro His  
675 680 685

Asp Trp Ser Asn Gly Lys Val Leu Ala Gln Leu Phe Ser Leu Ser Ile  
690 695 700

Leu Glu Ala Leu Gln Leu Lys Asn Leu Ser Phe Ser Tyr Arg Arg Pro  
705 710 715 720

Tyr Ala Asp Phe Leu Lys Gln Phe Glu Gln Leu Asp Leu Glu Val Thr  
725 730 735

Arg Lys Ser Gly Asn Ala Lys Glu Lys Thr Lys Gln Leu Leu Thr Arg  
740 745 750

Ala Asn Val Pro Gln Ala Lys Trp Ala Leu Gly Asn Thr Met Val Phe  
755 760 765

Met Lys Pro Asp Ala Val Arg Glu Leu Thr Gln Lys Met Arg Leu Ile  
770 775 780

Val Val Ala Trp Glu Pro Leu Ile Arg Val Leu Glu Ala Cys His Ser  
785 790 795 800

Arg Ala Leu Lys Met Arg Ala Ile Arg Asp Ser Val Gln Trp Val Val  
805 810 815

Arg Ile Gln Ser Gln Ile Arg Lys Ala Arg Val Ile Met Glu  
820 825 830

<210> 101  
<211> 5940  
<212> DNA  
<213> Toxoplasma gondii

<220>  
<221> misc\_feature  
<222> (1)..(5940)  
<223> MyoF

<400> 101  
atgacggcat ctctgcaga tggggcgtct gccccgggag gcggcgaccc gggagaggag 60  
gaggtccgct gcgccgttgg aaccaagatc tacgtccctg acgccgctga tgtttggaga 120  
acagcggaag tggatgaagat ccaagaggat ggcagctctca ccgccagagt cgatgcagac 180  
aatgaactgg tgcagctcaa aaaaaacgat atatggatc tgtgcaat ac cgatgtgtgg 240  
aacaccaccg gactgagtc gccgacagat ttgacgatgc tgacgcattt gcatgaggcg 300  
gccgtcctcg actctctcaa cctccgcttc gatatcgacg agatctacac tttcacgggt 360  
cccatctga ttgcggtcaa tccttttaaa cagatcacag gtctctacga catgaagcaa 420

N3027PCT\_sequ. list . . txt

t t ggt t cgg	acat cgcgag	t t cggagct g	ccgat gccc	gagt gcct t c	t t cct cgt cc	480
ggct ct t ct t	ccaacgcacc	cgt cgcgct g	ccgat at ct c	gacagcct ca	cgt ct t cgcc	540
t cgagcagcg	ccgcgt acca	gggcat gt gc	aacgagaagc	agagt cagac	gat t ct gat t	600
t ct ggggaga	gcggagcagg	caagacagaa	agcacgaaat	t cgt gat gaa	gt t cct cgcc	660
t gt gccggca	gcgaagact t	ggagcgccgg	t cgcaagt cg	aggcgcaagt	cct cgagagc	720
aat cct ct cc	t ggaagcat t	cggaaacgcc	cggacgct gc	gaaacgacaa	cagcagt cgc	780
t t cgggaagt	t cat t gaact	ccagt t ccaa	acaagcaaag	ccaagcggat	gt ct ggaaac	840
cgcggcaggc	t ct gt ggagc	t cgaat t caa	acgt at t t gc	t ggagaaggt	ccgcgt ct gc	900
gaccagcaag	agggagagag	gaact at cac	at ct t ct acc	aact t t gt gc	agct gcagaa	960
gct gcagct c	agacgggagg	cat ct at t ac	t t cct t t ccc	cgaaat t ccg	aaaagccgca	1020
gat gcaaagg	cacaagagat	ggat at gt ct	ct ct t cgagc	cgcgcgacaa	at t caagt at	1080
t t gaccaaga	gcagct gcc	ccagct gcag	ggcgt ggacg	act gcgagga	gt t cgagagc	1140
acgct ct t cg	cgat gcagac	gg t t ggcat c	t ccccgagg	agcaaat gag	cat t ct ct cg	1200
gt cgt gggcg	ccgt t ct t t g	t ct gggaaat	gt t t ct t t cg	agact ccgaa	ggccaat agc	1260
gaaggat cgc	aggt cgcagc	gagct gcact	gagt acgt ct	gcaaggcct g	ccgcct t ct g	1320
ggcgt ccaga	gggaggct ct	gcaagaggcg	at gt gct acc	gaacaat caa	gaccgcacac	1380
gagagct acc	ggaagccgt t	gaagacagac	gaagcat ggg	agat gaagga	cgcgct gt gt	1440
cgggcgct gt	acggt t gt ct	gt t t ct gcaa	gt t gt cgcga	agacgaacgc	gt ct at aggt	1500
t acct gaagg	aggt gcagag	t gcagacgat	t t gct t ct gt	t t t gcggagt	gct ggacat t	1560
t t cggct t cg	aat gt t t cca	gt t caact cg	t t cgagcagc	t gt gcat caa	ct t caccaac	1620
gagcgt ct gc	agaat t t ct t	caat acgt t c	gt ct t caagt	gcgaggaaga	gct ct accgc	1680
gccgaaggca	t ccagt ggaa	ccct ct ggac	t t cccggaca	acgcagact g	cgt cgcgct g	1740
ct gcaggaaa	agccgct cgg	t ct gt t ct cc	at gct cgacg	aagagt gcat	gt t ccccgca	1800
ggcaaagacc	gaggat t caa	caacaaagt c	t gccagaaac	acggcggt ca	caaacgt t t c	1860
ggcgt gat ca	aaacgaaacc	t aat t gct t c	gt ggt gcacc	act t t gccgg	cagcgt agag	1920
t act gct ccg	acggat t t ct	ggagaagaac	aaggaccagc	t gt ccgt gga	t ct gcaggag	1980
gcagt gaagg	ct t cgacgat	cccgt t cgt c	t ccaact t gt	t t t ct gcgt t	cct gaaccgc	2040
ggcacagcgg	aagacggat c	ggggaagaag	cgaaagt t cg	t gacggt gt c	gagcgagt t t	2100
cgcgagcaac	t cggcgcgct	gat ggagacc	gt cgacaaga	cggcaccgca	ct t cat t cgc	2160
t gcat caaac	ccaat ccgca	gaacct ccca	gacct ct t cg	accgcgcgac	agt gaacgag	2220
cagct ccgat	at ggaggcgt	cct gcaagcg	gt gcaggt ca	gccgt gcagg	gt accct gt g	2280
cgcct ct cgc	accgcgact g	ct t ct t cgac	t at agggcgc	t cgcagacgg	agcgct t gct	2340
gcgcagct gt	cgcagggcac	agagacgcc	gaggcct ggc	gcggccgcgc	t gaggct ct g	2400
ct ccgccacc	t ggacgagaa	gct gaagct c	gaccgccgga	aaaaagagac	agact ccccg	2460

N3027PCT\_sequ.l i st . . t x t

gaccgaacct	gggccgt cgg	gaagaccct c	t gct t c t t c a	aaaacgaagc	gt acgagat t	2520
ct t t cggcga	act t gat gag	cgt gagggg t	gct gcggcga	cggcgat t ga	ggcgaggt ac	2580
aagt gct t t g	t gcagaggcg	at t c t t cct g	at gt at cggc	agact gt cgt	t t t t c t gcag	2640
t c t cacat t c	gcat gt t t c t	t t gcaagt t g	gaggcccaga	gact gcgaga	gt cacgcgct	2700
gcgcggcgcg	t ggagaact t	cat gcgaggc	gccgt t gcgc	gt ct gcggg a	cct gcggact	2760
ct ggagaaca	t ccggcgaa t	t caggcggcc	t ggcgaggca	agcagacaag	gt cgcagct t	2820
cgcgat cgaa	agct cgagga	agccgccagt	aaaat ccagg	cgt t c t ggaa	gat gcacaag	2880
caacgcat gt	t c t acacgaa	t t t gaagaaa	gcct cgact a	t t gct caact	caagt ggaag	2940
agaat t c t gg	ct cggcgcat	gct gcggcga	ct gcgagagg	aggct cgcga	ggg ct caggc	3000
ct t c t gaaga	aggcgcaaga	t c t gcagcgc	gact t gt gcg	aagagaagaa	caagagaagc	3060
gacgcggaaa	gccat gt t c t	t cagt t gcag	gcgaaaaacg	aagat c t cct	caaagaaat c	3120
cagaaaact cc	agaggggaact	cgaacgcgcg	aaagaagat g	t cgct t c t c t	acaagcat ct	3180
aacgacgact	t t gct t caca	agt aaagcag	ct gaaggaga	gt t t gacggg	gggct c t t cg	3240
acgccaacga	cgcct cagat	gacat t cggg	accacaaga	gaagggt gt c	gaacaacgca	3300
gat gt ccccc	at t c t caaga	gaaggacaag	t t t ccgacag	acgaggagt t	gaaggct t t g	3360
cggacagagt	t ggagagacg	cgacgcggag	gct caacagc	agcaggcaga	gcacgaggct	3420
ct cat cgcgg	agct ccgagc	ggcgt t gaag	gacgct gaga	gt gcat gt ga	at acgagcga	3480
acgcaacgca	aagaagct ga	ggcgcggg ac	cgact ggt cc	t cgaagact c	gagcgcaagc	3540
agt act cacg	t ccgcgcgt c	gt ct gcct ca	aaggct gcgg	t cgcggact c	t gcgcccaca	3600
gct ct gt t ga	gagagaagt g	t at ggagagc	gacat ggcga	cagggcgacc	t ggagact cg	3660
ct cgcgt ct t	cggg cgcgt c	cgct gct cct	ct ct cgcct c	cggg cgcgt	ggagcct gaa	3720
ct t t gggagt	cggg gct gca	cgaccagcgg	t ggat cgact	t gct t c t gct	gggt cct gcc	3780
ggcgt gggca	agacaggt t t	gct ggagcaa	t t t c t t gt ga	agt t gggaga	cgaagt t cat	3840
ct ggagcagc	t ccgagt gag	ccgaaagat g	gaggaccaag	cgccct t cag	caagct gccg	3900
caacact acg	aact cgt ct a	ct ct cccgac	agccaggaag	gccgt gaacg	agaagaagct	3960
cgagt gaacg	t act cgact t	t ccaggcct c	t cgcgt acca	agcagaat cc	cgcgt gagg	4020
gt caagcagg	cct t cgt cgt	cgcggg cgt c	t t cgat ccca	ccagacct ga	aact t gt gca	4080
gaggcgct gc	aaat c t t gac	caacgt cgt g	ct gcct gct c	ggcccaaagt	ct ct gcacaa	4140
gaccctgt t gg	gcgcct gcat	cagcggcaga	gt t t acct cg	t t gaaaacgg	gt ggcgcgca	4200
gccgccaaaag	aagct gct gt	gcaagt cgac	act gcagct g	t cagagacaa	agct gcgggt	4260
ct ccgct gt c	act accgcga	at t ggt gcat	ct ggagt ct c	t ggt cgacga	aat t gt gcct	4320
ct gat gt cga	gct ggagaga	t c t gct t cag	cagcagagac	t t gccat gct	gcagcaccac	4380
gcgcgggct gc	agccgggt gg	gcct t c t ccg	cat gcgt ct c	cgt t c t ccct	gcct cgct cg	4440
cagacaggt c	gcggagct t c	gct ct t cgcc	act gcgt cgc	agt ct ggagc	t ct aggcgcc	4500
t ccgct gt cg	gaggacagga	gaacggagt t	gagaagt cgt	cgt cgggcgt	ct ct gct cac	4560

N3027PCT\_sequ.list.txt

```

agacagggag gcttgtctgc gaacttcttc gacagcattc gctctttcct ctcacagtcg 4620
tcgatgcgac ctgcggggaa cgttctggct tctggaaagc aggccgcgga cctgaagctg 4680
ctcagaccga gcatgaagcc tgggggcacc gcgatgatga agaaactgaa gacgcgaagt 4740
ctcgaccaac actcggctcgt ccctgtgcag gaactgcagg actcggactc tgcgatcacc 4800
tgcgtgggtgt ttggcaagga gaaagaaaac cgggactaca ttcttctcgc ggctgcgagc 4860
aaagacggca gcgtagt gat ctaccgggtgt taccgtctag aagctgaaag acaaatgttc 4920
gaccaggagc aagtttctct agtcactcct gcggcttcgc ggaccactga cagcaaggag 4980
cacatcgggc cttctgtctc cgtgcactcg cgactcgtgg ggcacagccg cgccgtcacc 5040
tgtctcttct tctcgctctt ggaagaccag ctgattacaa cttcaatcga caagtctgtg 5100
cgattttggc atgtcgat ac gggggacatg ctgaaagtct tccagactc ttctcctgcg 5160
ctggctgccg ccttctccc gtccaacccc acagcctttg tgcgtcgaa ctcaaactcc 5220
attcttcggc tggctcgcgc caccagt gga cgcgtgattc agaagctgaa agtggagagc 5280
gaagtgaggg cgctcaagt t cgacgacaca gggctcttct gt tttgctgg aacgaaggca 5340
ggagcagtc acgttctgga ggccagcgac acagtcaaca ttcgatttaa attcaagact 5400
tctttgggga agggcgctgt gacgtgcatc acctttgtgc cgagcacagg acctggacag 5460
tatccgcgcc tcctcatcaa ctgctgcgac tccagcgtcg ccgtcgtcga gtgtatctac 5520
ggcccgcctc cgggcgtcct caccaacttg ctcgttcgcc accgtgtgag aatcgccac 5580
agtctgcttc ctctaagatg ctggttctca aactttggag gagggtggct tatcaccggt 5640
agtgaggaca aggacgtgta ctgtttctct cttcaacaag gcgcgaactt caaggcaatc 5700
tcgctcaaac atcaccaggt aacgcctgaa ctgacagaga tcatgggtcc ctcatcgaat 5760
ttcagagaca gctgtttttt cttcttcaca cccttcatct tcagtctttg tcat t tctct 5820
cagtcggttt ttgtatctct gtctctcatc tgtatcggat tttctccccg tagctttccc 5880
tgtctgtact ctgttttcag cctctgtccg ctgcgctatg tgtgtgtgtg tctcttgtga 5940

```

<210> 102  
 <211> 1979  
 <212> PRT  
 <213> Toxoplasma gondii

<220>  
 <221> MSC\_FEATURE  
 <222> (1)..(1979)  
 <223> MyoF

<400> 102

Met Thr Ala Ser Ser Ala Asp Gly Ala Ser Ala Pro Gly Gly Gly Asp  
1 5 10 15

Pro Gly Glu Glu Glu Val Arg Cys Ala Val Gly Thr Lys Ile Tyr Val  
20 25 30

Pro Asp Ala Ala Asp Val Trp Arg Thr Ala Glu Val Val Lys Ile Gln  
 35 40 45  
 Glu Asp Gly Ser Leu Thr Ala Arg Val Asp Ala Asp Asn Glu Leu Val  
 50 55 60  
 Gln Leu Lys Lys Asn Asp Ile Trp Tyr Leu Cys Asn Thr Asp Val Trp  
 65 70 75 80  
 Asn Thr Thr Gly Leu Ser Ala Pro Thr Asp Leu Thr Met Leu Thr His  
 85 90 95  
 Leu His Glu Ala Ala Val Leu Asp Ser Leu Asn Leu Arg Phe Asp Ile  
 100 105 110  
 Asp Glu Ile Tyr Thr Phe Thr Gly Pro Ile Leu Ile Ala Val Asn Pro  
 115 120 125  
 Phe Lys Gln Ile Thr Gly Leu Tyr Asp Met Lys Gln Leu Val Arg Tyr  
 130 135 140  
 Ile Ala Ser Ser Glu Leu Pro Met Pro Gly Val Pro Ser Ser Ser Ser  
 145 150 155 160  
 Gly Ser Ser Ser Asn Ala Pro Val Ala Leu Pro Ile Ser Arg Gln Pro  
 165 170 175  
 His Val Phe Ala Ser Ser Ser Ala Ala Tyr Gln Gly Met Cys Asn Glu  
 180 185 190  
 Lys Gln Ser Gln Thr Ile Leu Ile Ser Gly Glu Ser Gly Ala Gly Lys  
 195 200 205  
 Thr Glu Ser Thr Lys Phe Val Met Lys Phe Leu Ala Cys Ala Gly Ser  
 210 215 220  
 Glu Asp Leu Glu Arg Arg Ser Gln Val Glu Ala Gln Val Leu Glu Ser  
 225 230 235 240  
 Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Arg Thr Leu Arg Asn Asp  
 245 250 255  
 Asn Ser Ser Arg Phe Gly Lys Phe Ile Glu Leu Gln Phe Gln Thr Ser  
 260 265 270  
 Lys Ala Lys Arg Met Ser Gly Asn Arg Gly Arg Leu Cys Gly Ala Arg  
 275 280 285  
 Ile Gln Thr Tyr Leu Leu Glu Lys Val Arg Val Cys Asp Gln Gln Glu  
 290 295 300  
 Gly Glu Arg Asn Tyr His Ile Phe Tyr Gln Leu Cys Ala Ala Ala Glu  
 Page 489

305                      310                      315                      320  
 Ala Ala Ala Gln Thr Gly Gly Ile Tyr Tyr Phe Pro Ser Pro Lys Phe  
                                  325                                   330                                   335  
 Arg Lys Ala Ala Asp Ala Lys Ala Gln Glu Met Asp Met Ser Leu Phe  
                                  340                                   345                                   350  
 Glu Pro Arg Asp Lys Phe Lys Tyr Leu Thr Lys Ser Ser Cys His Gln  
                                  355                                   360                                   365  
 Leu Gln Gly Val Asp Asp Cys Glu Glu Phe Glu Ser Thr Leu Phe Ala  
                                  370                                   375                                   380  
 Met Gln Thr Val Gly Ile Ser Pro Glu Glu Gln Met Ser Ile Leu Ser  
                                  385                                   390                                   395                                   400  
 Val Val Gly Ala Val Leu Cys Leu Gly Asn Val Ser Phe Glu Thr Pro  
                                  405                                   410                                   415  
 Lys Ala Asn Ser Glu Gly Ser Gln Val Ala Ala Ser Cys Thr Glu Tyr  
                                  420                                   425                                   430  
 Val Cys Lys Ala Cys Arg Leu Leu Gly Val Gln Arg Glu Ala Leu Gln  
                                  435                                   440                                   445  
 Glu Ala Met Cys Tyr Arg Thr Ile Lys Thr Ala His Glu Ser Tyr Arg  
                                  450                                   455                                   460  
 Lys Pro Leu Lys Thr Asp Glu Ala Trp Glu Met Lys Asp Ala Leu Cys  
                                  465                                   470                                   475                                   480  
 Arg Ala Leu Tyr Gly Cys Leu Phe Leu Gln Val Val Ala Lys Thr Asn  
                                  485                                   490                                   495  
 Ala Ser Ile Gly Tyr Leu Lys Glu Val Gln Ser Ala Asp Asp Leu Leu  
                                  500                                   505                                   510  
 Leu Phe Cys Gly Val Leu Asp Ile Phe Gly Phe Glu Cys Phe Gln Phe  
                                  515                                   520                                   525  
 Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe Thr Asn Glu Arg Leu Gln  
                                  530                                   535                                   540  
 Asn Phe Phe Asn Thr Phe Val Phe Lys Cys Glu Glu Glu Leu Tyr Arg  
                                  545                                   550                                   555                                   560  
 Ala Glu Gly Ile Gln Trp Asn Pro Leu Asp Phe Pro Asp Asn Ala Asp  
                                  565                                   570                                   575  
 Cys Val Ala Leu Leu Gln Glu Lys Pro Leu Gly Leu Phe Ser Met Leu  
                                  580                                   585                                   590

N3027PCT\_sequ.list.txt

Asp Gl u Gl u Cys Met Phe Pro Al a Gly Lys Asp Arg Gly Phe Asn Asn  
 595 600 605  
 Lys Val Cys G n Lys Hi s Gly Gly Hi s Lys Arg Phe Gly Val Ile Lys  
 610 615 620  
 Thr Lys Pro Asn Cys Phe Val Val Hi s Hi s Phe Al a Gly Ser Val Gl u  
 625 630 635  
 Tyr Cys Ser Asp Gly Phe Leu Gl u Lys Asn Lys Asp G n Leu Ser Val  
 645 650 655  
 Asp Leu G n Gl u Al a Val Lys Al a Ser Thr Ile Pro Phe Val Ser Asn  
 660 665 670  
 Leu Phe Ser Al a Phe Leu Asn Arg Gly Thr Al a Gl u Asp Gly Ser Gly  
 675 680 685  
 Lys Lys Arg Lys Phe Val Thr Val Ser Ser Gl u Phe Arg Gl u G n Leu  
 690 695 700  
 Gly Al a Leu Met Gl u Thr Val Asp Lys Thr Al a Pro Hi s Phe Ile Arg  
 705 710 715 720  
 Cys Ile Lys Pro Asn Pro G n Asn Leu Pro Asp Leu Phe Asp Arg Al a  
 725 730 735  
 Thr Val Asn Gl u G n Leu Arg Tyr Gly Gly Val Leu G n Al a Val G n  
 740 745 750  
 Val Ser Arg Al a Gly Tyr Pro Val Arg Leu Ser Hi s Arg Asp Cys Phe  
 755 760 765  
 Phe Asp Tyr Arg Al a Leu Al a Asp Gly Al a Leu Al a Al a G n Leu Ser  
 770 775 780  
 G n Gly Thr Gl u Thr Pro Gl u Al a Trp Arg Gly Arg Al a Gl u Al a Leu  
 785 790 795 800  
 Leu Arg Hi s Leu Asp Gl u Lys Leu Lys Leu Asp Arg Arg Lys Lys Gl u  
 805 810 815  
 Thr Asp Ser Pro Asp Arg Thr Trp Al a Val Gly Lys Thr Leu Cys Phe  
 820 825 830  
 Phe Lys Asn Gl u Al a Tyr Gl u Ile Leu Ser Al a Asn Leu Met Ser Val  
 835 840 845  
 Arg Val Al a Al a Al a Thr Al a Ile Gl u Al a Arg Tyr Lys Cys Phe Val  
 850 855 860

N3027PCT\_sequ.list.txt

Gln Arg Arg Phe Phe Leu Met Tyr Arg Gln Thr Val Val Phe Leu Gln  
 865 870 875 880  
 Ser His Ile Arg Met Phe Leu Cys Lys Leu Glu Ala Gln Arg Leu Arg  
 885 890 895  
 Glu Ser Arg Ala Ala Arg Arg Val Glu Asn Phe Met Arg Gly Ala Val  
 900 905 910  
 Ala Arg Leu Arg Tyr Leu Arg Thr Leu Glu Asn Ile Arg Arg Ile Gln  
 915 920 925  
 Ala Ala Trp Arg Gly Lys Gln Thr Arg Ser Gln Leu Arg Asp Arg Lys  
 930 935 940  
 Leu Glu Glu Ala Ala Ser Lys Ile Gln Ala Phe Trp Lys Met His Lys  
 945 950 955 960  
 Gln Arg Met Phe Tyr Thr Asn Leu Lys Lys Ala Ser Thr Ile Ala Gln  
 965 970 975  
 Leu Lys Trp Lys Arg Ile Leu Ala Arg Arg Met Leu Arg Arg Leu Arg  
 980 985 990  
 Glu Glu Ala Arg Glu Val Ser Gly Leu Leu Lys Lys Ala Gln Asp Leu  
 995 1000 1005  
 Gln Arg Asp Leu Cys Glu Glu Lys Asn Lys Arg Ser Asp Ala Glu  
 1010 1015 1020  
 Ser His Val Leu Gln Leu Gln Ala Lys Asn Glu Asp Leu Leu Lys  
 1025 1030 1035  
 Glu Ile Gln Lys Leu Gln Arg Glu Leu Glu Arg Ala Lys Glu Asp  
 1040 1045 1050  
 Val Ala Ser Leu Gln Ala Ser Asn Asp Asp Phe Ala Ser Gln Val  
 1055 1060 1065  
 Lys Gln Leu Lys Glu Ser Leu Thr Val Gly Ser Ser Thr Pro Thr  
 1070 1075 1080  
 Thr Pro Gln Met Thr Phe Gly Thr His Lys Arg Arg Val Ser Asn  
 1085 1090 1095  
 Asn Ala Asp Val Pro His Ser Gln Glu Lys Asp Lys Phe Pro Thr  
 1100 1105 1110  
 Asp Glu Glu Leu Lys Ala Leu Arg Thr Glu Leu Glu Arg Arg Asp  
 1115 1120 1125

Ala	Glu	Ala	Gln	Gln	Gln	Gln	Ala	Glu	His	Glu	Ala	Leu	Ile	Ala
1130						1135					1140			
Glu	Leu	Arg	Ala	Ala	Leu	Lys	Asp	Ala	Glu	Ser	Ala	Cys	Glu	Tyr
1145						1150					1155			
Glu	Arg	Thr	Gln	Arg	Lys	Glu	Ala	Glu	Ala	Arg	Tyr	Arg	Leu	Val
1160						1165					1170			
Leu	Glu	Asp	Ser	Ser	Ala	Ser	Ser	Thr	His	Val	Arg	Ala	Ser	Ser
1175						1180					1185			
Ala	Ser	Lys	Ala	Ala	Val	Ala	Asp	Ser	Ala	Pro	Thr	Ala	Leu	Leu
1190						1195					1200			
Arg	Glu	Lys	Cys	Met	Glu	Ser	Asp	Met	Ala	Thr	Gly	Arg	Pro	Gly
1205						1210					1215			
Asp	Ser	Leu	Ala	Ser	Ser	Val	Ala	Ser	Ala	Ala	Pro	Leu	Ser	Pro
1220						1225					1230			
Pro	Val	Ala	Leu	Glu	Pro	Glu	Leu	Trp	Glu	Ser	Val	Leu	His	Asp
1235						1240					1245			
Gln	Arg	Trp	Ile	Asp	Leu	Leu	Leu	Leu	Gly	Pro	Ala	Gly	Val	Gly
1250						1255					1260			
Lys	Thr	Gly	Leu	Leu	Glu	Gln	Phe	Leu	Val	Lys	Leu	Gly	Asp	Glu
1265						1270					1275			
Val	His	Leu	Glu	Gln	Leu	Arg	Val	Ser	Arg	Lys	Met	Glu	Asp	Gln
1280						1285					1290			
Ala	Pro	Phe	Ser	Lys	Leu	Pro	Gln	His	Tyr	Glu	Leu	Val	Tyr	Ser
1295						1300					1305			
Pro	Asp	Ser	Gln	Glu	Gly	Arg	Glu	Arg	Glu	Glu	Ala	Arg	Val	Asn
1310						1315					1320			
Val	Leu	Asp	Phe	Pro	Gly	Leu	Ser	Arg	Thr	Lys	Gln	Asn	Pro	Ala
1325						1330					1335			
Leu	Arg	Val	Lys	Gln	Ala	Phe	Val	Val	Ala	Val	Val	Phe	Asp	Pro
1340						1345					1350			
Thr	Arg	Pro	Glu	Thr	Cys	Ala	Glu	Ala	Leu	Gln	Ile	Leu	Thr	Asn
1355						1360					1365			
Val	Val	Leu	Pro	Ala	Arg	Pro	Lys	Val	Ser	Ala	Gln	Asp	Pro	Leu
1370						1375					1380			
Gly	Ala	Cys	Ile	Ser	Gly	Arg	Val	Tyr	Leu	Val	Glu	Asn	Gly	Trp

1385														
Arg	Ala	Ala	Ala	Lys	Glu	Ala	Ala	Val	Gln	Val	Asp	Thr	Ala	Ala
1400						1405					1410			
Val	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Arg	Cys	His	Tyr	Arg	Glu	Leu
1415						1420					1425			
Val	His	Leu	Glu	Ser	Leu	Val	Asp	Glu	Ile	Val	Pro	Leu	Met	Ser
1430						1435					1440			
Ser	Trp	Arg	Asp	Leu	Leu	Gln	Gln	Gln	Arg	Leu	Ala	Met	Leu	Gln
1445						1450					1455			
His	His	Ala	Arg	Leu	Gln	Pro	Gly	Gly	Pro	Ser	Pro	His	Ala	Ser
1460						1465					1470			
Pro	Phe	Ser	Leu	Pro	Arg	Ser	Gln	Thr	Gly	Arg	Gly	Ala	Ser	Leu
1475						1480					1485			
Phe	Ala	Thr	Ala	Ser	Gln	Ser	Gly	Ala	Leu	Gly	Ala	Ser	Ala	Val
1490						1495					1500			
Gly	Gly	Gln	Glu	Asn	Gly	Val	Glu	Lys	Ser	Ser	Ser	Gly	Val	Ser
1505						1510					1515			
Ala	His	Arg	Gln	Gly	Gly	Leu	Ser	Ala	Asn	Phe	Phe	Asp	Ser	Ile
1520						1525					1530			
Arg	Ser	Phe	Leu	Ser	Gln	Ser	Ser	Met	Arg	Pro	Ala	Gly	Asn	Val
1535						1540					1545			
Leu	Ala	Ser	Gly	Lys	Gln	Ala	Ala	Asp	Leu	Lys	Leu	Leu	Arg	Pro
1550						1555					1560			
Ser	Met	Lys	Pro	Gly	Gly	Thr	Ala	Met	Met	Lys	Lys	Leu	Lys	Thr
1565						1570					1575			
Arg	Ser	Leu	Asp	Gln	His	Ser	Val	Val	Pro	Val	Gln	Glu	Leu	Gln
1580						1585					1590			
Asp	Ser	Asp	Ser	Ala	Ile	Thr	Cys	Val	Val	Phe	Gly	Lys	Glu	Lys
1595						1600					1605			
Glu	Asn	Arg	Asp	Tyr	Ile	Leu	Leu	Ala	Ala	Ala	Ser	Lys	Asp	Gly
1610						1615					1620			
Ser	Val	Val	Ile	Tyr	Arg	Cys	Tyr	Arg	Leu	Glu	Ala	Glu	Arg	Gln
1625						1630					1635			
Met	Phe	Asp	Gln	Glu	Gln	Val	Ser	Leu	Val	Thr	Pro	Ala	Ala	Ser
1640						1645					1650			

N3027PCT\_sequ.list.txt

Arg	Thr	Thr	Asp	Ser	Lys	Glu	His	Ile	Gly	Pro	Ser	Val	Ser	Val
	1655					1660					1665			
His	Ser	Arg	Leu	Val	Gly	His	Ser	Arg	Ala	Val	Thr	Cys	Leu	Phe
	1670					1675					1680			
Phe	Ser	Leu	Leu	Glu	Asp	Gln	Leu	Ile	Thr	Thr	Ser	Ile	Asp	Lys
	1685					1690					1695			
Ser	Val	Arg	Phe	Trp	His	Val	Asp	Thr	Gly	Asp	Met	Leu	Lys	Val
	1700					1705					1710			
Phe	Thr	Asp	Ser	Ser	Pro	Ala	Leu	Ala	Ala	Ala	Phe	Leu	Pro	Phe
	1715					1720					1725			
Asn	Pro	Thr	Ala	Phe	Val	Ala	Ser	Asn	Ser	Asn	Ser	Ile	Leu	Arg
	1730					1735					1740			
Leu	Val	Cys	Ala	Thr	Ser	Gly	Arg	Val	Ile	Gln	Lys	Leu	Lys	Val
	1745					1750					1755			
Glu	Ser	Glu	Val	Arg	Ala	Leu	Lys	Phe	Asp	Asp	Thr	Gly	Leu	Phe
	1760					1765					1770			
Cys	Phe	Ala	Gly	Thr	Lys	Ala	Gly	Ala	Val	His	Val	Leu	Glu	Ala
	1775					1780					1785			
Ser	Asp	Thr	Val	Asn	Ile	Arg	Phe	Lys	Phe	Lys	Thr	Ser	Leu	Gly
	1790					1795					1800			
Lys	Gly	Ala	Val	Thr	Cys	Ile	Thr	Phe	Val	Pro	Ser	Thr	Gly	Pro
	1805					1810					1815			
Gly	Gln	Tyr	Pro	Arg	Leu	Leu	Ile	Asn	Cys	Cys	Asp	Ser	Ser	Val
	1820					1825					1830			
Ala	Val	Val	Glu	Cys	Ile	Tyr	Gly	Pro	Pro	Pro	Gly	Val	Leu	Thr
	1835					1840					1845			
Asn	Leu	Leu	Val	Arg	His	Arg	Val	Arg	Ile	Ala	His	Ser	Leu	Leu
	1850					1855					1860			
Pro	Leu	Arg	Cys	Trp	Phe	Ser	Asn	Phe	Gly	Gly	Gly	Trp	Leu	Ile
	1865					1870					1875			
Thr	Gly	Ser	Glu	Asp	Lys	Asp	Val	Tyr	Cys	Phe	Ser	Leu	Gln	Gln
	1880					1885					1890			
Gly	Ala	Asn	Phe	Lys	Ala	Ile	Ser	Leu	Lys	His	His	Gln	Val	Thr
	1895					1900					1905			

N3027PCT\_sequ.list.txt

Pro Glu Leu Thr Glu Ile Met Gly Pro Ser Ser Asn Phe Arg Asp  
 1910 1915 1920

Ser Cys Phe Phe Phe Phe Thr Pro Phe Ile Phe Ser Leu Cys His  
 1925 1930 1935

Phe Ser Gln Ser Val Phe Val Ser Leu Ser Leu Ile Cys Ile Gly  
 1940 1945 1950

Phe Ser Pro Arg Ser Phe Pro Cys Leu Tyr Ser Val Phe Ser Leu  
 1955 1960 1965

Cys Pro Leu Arg Tyr Val Cys Val Cys Leu Leu  
 1970 1975

<210> 103  
 <211> 6180  
 <212> DNA  
 <213> Toxoplasma gondii

<220>  
 <221> misc\_feature  
 <222> (1)..(6180)  
 <223> MyoG

<400> 103  
 atgacggaca ggtgctggat tctcatccc actgaggttt gggggatcgc agttccagcc 60  
 ggggcccccg gcacctgcac gtataaactt gtcgaggtca ccgatgatgg caccgacccg 120  
 cgcaaattgg aagtcacttt agccaagtca gctttgacac aagtcgcgcc tgttacagac 180  
 ccgcatccc ttgaaggcgt ccaaaatgta tgcgtcctgg gcgatgtgtc agaggcgtct 240  
 gttctccat a cagtcctgt tctgatcaa agagacgaaa tctacacaaa cgtagggcac 300  
 attgttctcg ccctcaatcc cttaaatat ctccagctgt atggtcccga cttcgttcgg 360  
 acttattttg aagacacgca tgtattcgac ctcccaccgc atctcttcca agtttctgcg 420  
 gccgcagtca aaggtctatc agaaagaggg aaacctcaga gcacgctgat cacaggcgaa 480  
 tccggcgtg gcaagacgga gtcgaccaag ttgattcttc agtttcttgc cgacgtcagt 540  
 gaggttatcct cgtcttcgtc gtcttcgttc aaagtttctt ctggcgacg cttagtggag 600  
 agagctgaaa ggaacagaag catcagtcag aaagaccggg ggtcttgcgg gactggagga 660  
 gacaacgctc tccaatcagg cgttggatct ggaagccaag ggcgcgaggc gacgtctctt 720  
 caacagagaa ttttagagat aagcccgtc ttggagagct tcggaaatgc atcgactagc 780  
 agaaaccca actccagtcg atttgggaag tggattgaag tctatttcgg ggacaaatt a 840  
 aaggtcctag gcgccagtat cacgtcgtac cttctcgagc ttccacgcgt gactcgccac 900  
 atcgcagggg agagaaacta ccatgtcttt taccaactag ttcacggttt gaatacatct 960  
 gatttagtcg gcgtggctga aacgtatcgc ctgggaaccg attcactggc cttctcctat 1020  
 ctcacacctc aagaacaaac cgtgaacacc aaaagtacaa aagcagacac agaggtttcg 1080

N3027PCT\_sequ. list.txt

t cgccggct c	ct gat at t ga	t gat ct cacc	ggct t ct cag	agct gaaacg	cgccct gct g	1140
gt cct ggggt t	t cagt cct t c	aaccagaaat	t ccat t t t ct	ct at t gt ggc	ggcgat t ct t	1200
cat ct t ggca	acgt cact t t	t gct cccgaa	gccggaggt g	aaaagt gct c	t gt ggt gagg	1260
aacagt cgcg	at cacct cac	agcagcgagc	gagct ct t gg	gcct cgat gt	gccgct ggt g	1320
gaaggagct c	t gacgagccg	t aagat gaag	acaggaaat g	agagcat t ct	gat t ccgct c	1380
aagaccgacc	aagccgat gc	cgcgcgcgac	agct t t gcaa	agct cgt t t a	cgggt at ct c	1440
t t caact ggc	t cat t gcgca	gaccaacgca	aat ct agcgc	ct t ct ggagg	aat ggat t t c	1500
gat t t gaat c	gct acgt ggg	gct gct ggac	at cgct ggt t	t cgagagct t	t cgct aaac	1560
ggat t t gagg	agct ct gcat	caat ct gt cg	aat gaagagt	t gcaacacca	t t t caat gca	1620
gat at t t t cc	t gaacgaagt	caaggact ac	gagaat gat g	gact gcaggg	gggt ct caat t	1680
acgt at gagg	acaacgccga	t gt gt t gt cg	ct gat t gcgg	gaaaaggcgg	cgt cat t gca	1740
act ct cgacg	aagaggt gt t	t gt cccaga	ggct ct gat c	aaggct t cct	caacaaat t g	1800
aacaaggccc	aaacgaacca	caaacgct ac	at t gagaaca	aaat aaaagg	gt cgat ggcc	1860
t t cggcatt c	aacact acgc	aggagat gt g	act t aact g	t caccggct g	gct cgt gaaa	1920
gacaaaaat g	cgccgcct ca	agaggcgaga	gact gcct ct	t aact t cgga	aaat ccagt t	1980
gt aaaggcca	t t at ggagac	agcgt ccagc	gacact caac	gacgaggccc	gggagggaag	2040
agt act gt ag	gct ct gt ct t	caagaagcaa	ct gagt gagg	t gat ggcgaa	gat aaat gga	2100
act gacagt c	act acat ccg	gt gcat caaa	ccgaaccccg	cacat aagcc	gagggt gat c	2160
cact cgagcc	agat t ct gaa	t caact cgt c	t gct caggcg	t cat ggaggc	aat t cgcat t	2220
cggaagt cgg	gggt t cgccct t	gcgt ct ct t a	cat caggact	t cgt ggaccg	ct accggct c	2280
gt gt t gggct	cgaaagccgc	ggcaggcct t	cggaccct t g	at gccgccag	t gcagcccag	2340
cagct ggt aa	cccagct ggt	t gcgaacaaa	t ggggt t t ccc	aggaggaat g	t ct cat cggc	2400
agaaccaagg	t at t cgccaa	at ccact gt t	caagact t cc	t t gaacgcgc	ccgagaggaa	2460
gct ct ggt cg	aaccct gat	t ct cat t caa	gct ct gt at c	gcggct accg	aaccgccag	2520
cagt gcagag	t t ct ct t t ga	gggt gt at gga	cagct gaagg	agt t t ct gga	cgcgggcggc	2580
gaggcgt cga	agcgcggggg	ct act t gaca	gat cccgt t t	t ccccgat gc	cagcaccct	2640
gagct gct t c	agaagaaagc	gaat t cgt t g	ggagat t t aa	t t t cacaact	cgagact ct t	2700
gat gcct ct c	t t caaccaag	gt gcct gt ca	act gt ct cca	agt accacgt	t cgaat gacc	2760
caggaagcgt	cgct t t ccct	ggagct caag	cgt cagct gg	aact cacaga	t ggagagggc	2820
gct gaggacg	agt gt gacgc	act ct caat g	ct acgcgcga	ct ct gcagaa	agcagaaagt	2880
aaaaaagt ct	caggacct t t	cgt t act gcg	gcgcgagagc	gggt gaat cg	act ggaggca	2940
gagaccagcc	t cggagact t	gct t gaccag	gct ct gcagg	ccaaagacaa	agat gat t t a	3000
gccacct cc	t aacagaggc	gaggcagct t	gagct ct cgt	ccacgccct c	t cgct t ct t c	3060
act t cct acc	t ct cct cgggt	cgt t gccgcg	gcagaggcgt	acct t gcgag	caacgcgaga	3120
gagaat gaac	gact t cagcg	agagagggaa	caggcagcag	agt cccggaa	ggcgct gaag	3180

N3027PCT\_sequ. list . . txt

gaaagacagc agcaagaggc cct gct gaag gat gcagt t g aagagcgcaa acgaagt gat	3240
cggt t gt ct c t t ct ct ct gt ggct t ccgat at caaaaagg ccaagaggaa ccacgaggct	3300
cat cgaggt g t acagacagc agaaacgt cc agcct gagga t cgagt acga cgaggaagca	3360
accgt gt cca cat ccgagt c agagt ggact gaaagcagcg aagcagaaaag cgaagagcct	3420
ct cagcgacc cct act ccac caaagat gaa gaaggcggcg aaggcct ggc gt ct gcgt at	3480
ct gcggaagt t cat gcagga ggt ggcgcgc gcgacccggg agt gcgaccc ggcgagct g	3540
acat t t t t t c t cgagcgggc gagagaagcg aat ct cggt a aaggcccgcg agagct gcag	3600
ct t gcgcgcg t gcagt t gga gaat t t aagc gat ccgt cgt t cct caacgc ggagt t gaag	3660
gaggcgacga t cggcgt cac gt ggggt gt t gcgacacagg aagact t cgt caagct gcgg	3720
aacct cgt t g agcaagcgaa ggcgat caga gcgaagcaga agggagaagc agagagat ct	3780
gacct ct gc gcct ccaaac cat t gacgag aaagt ct t gg cat cggcagc t gcaacgct t	3840
gagt ct ct ga ggagaacgga aggcagagaa cgcggt t cct ccgccaagt t t ggaggcacc	3900
t t cggt gaga ggggagacag aggaggt gga ct gacggcgt at ct t t t cga gaact acccc	3960
ct gct t ggca t caacat ccg gat t caggaa accaagagca t gcgaaagac ggagcaact t	4020
gt gct gcgcc gggaggaact gt t gagccat caaacggat c ct t t ggcaga gcct t t gct g	4080
cagct gcct g accat cacgc cgaggt ggt g gcgct gacgt gct t t cgct c t ct t t t ggga	4140
gt gat gggag agcgt t t ct g t gt agggcga agcgcgct ga gt gacgagat t t t ggcgt t g	4200
ggcagaaacg cagaagat ct t cgagacgag at t t act gt c aaat t ct caa gcagct gaga	4260
aacaat ccct cggcagggag caccgt t gcg ggact ccggc t t ct ccagt c ct gct gt cag	4320
acct t t ccgc ct t ccgagac t ct cgcgct t acct ccgct t cgcgat cca gagt t t ct t g	4380
t ct gggct ct ct gcgcct gg aggcgagagc acgggcgcca t caaat t t ca gcaagaagt g	4440
gagcaaat ct gt cgacaggc t ct acacgat ct cgagct ga cct gcggagc ct cgagagaa	4500
gaggaaggc ggccagggga cagcacgggc caaggcgct g t ct ccgccga acgagagaca	4560
cgcgt gt at g t t cagat acg act cgcagac ggat cacagc gacgcct cgc gct t gacggc	4620
gacct t ccag gcgat ct ct c t cggcgt ct g gt gaaggat c t gaat t t act cggt gcagac	4680
t ct t gggcca t t at ggaaca gct t t cccag t acgacct t a aaaagacaag cgcgcgagaa	4740
t ct ccaccag ccacat t t cg cct ct t acca cct gaggaac t t gt t cagga t t acct ct cc	4800
aaacgagat t ct caggt cca gt t at ggct t cgt cgt ccga t gct gagt ct ggaagat cct	4860
ct gt ct ct gc at cct gcgac ggcagcgct g at at at cgt c aggcagt ct c t cagt at caa	4920
cagcat gt ct t caat gagga t cccagt ct c ct agcat cga t aagt gccca t t t gct t caa	4980
gcggacggt c t cct agact c t t cgccgcct cgagt t ccac cct ggccgt c act cagct gg	5040
accat t cct c agcgt ct cca ct ggct t cgg agt gaagcag act ggacagc agccat t gcg	5100
gaagaggcga agcacat cga ccct gagga ggacacct t c t cgct at ggg ggct gcgt t c	5160
cgct cat gc agaagt t gcg aggc t t t gga ggct at gt t t ggct t gcaga cgcct t ccca	5220

N3027PCT\_sequ.list.txt

cttttttcgg cggacctgaa aggcgaggcg cgactgcatg cagtgttgaa gcagacaacg 5280  
cctgggtcgc gtgtttctct ctcgccgttg attgaaatga ggcgagtgcc gttggcgctt 5340  
cgtcgccggt ttttgcgcgt gttaggcgat gaagaagaca gggagtgat gcagcagctc 5400  
gcgctccttg cgcagaagca gcaaacgagg cgaagtcgaa aaacagatcc gacgcatacc 5460  
tcaagctcgt catcgaaggc agcgtggctc aacgaaggca gcgatgggca tgttctctct 5520  
acgaagatag cgaacttcaa gagacgcgtc tgcagagccc tgcgtgtgcag gacagatccg 5580  
tcgtcgcgca gtgcctcttg gggagctgtg agaggccgga aacgagaccc taagaaaacg 5640  
aaaaacgcgt tcaactcac tgggaagggtg tggattgccg tgagccaccg cggaatcgaa 5700  
atcgcgactg tcttcgattc agacggtctc gcggcggcgc ccgtgcctga ctccgaggca 5760  
gcactgttcg ctctctgagac tgaccgaagg accgaaaaaa gaccacagaa acggggaaaa 5820  
gcgtggaagg actcggacga agacgcagaa gatggagcca tgcaggaaga cgcggaacctc 5880  
gaaaaccaca gaagcacagc gagagaacac aacggagaca gcggcaggaa cagtgaat a 5940  
caacagggct cagaaaaagg cgtattcacc atttctccgg agaagctttg gctggttgct 6000  
gccgtgccgc ctgtgggga agcacctgac cgcctcat tt tgggctacga cgatcccagg 6060  
acaggaaaaa gaaggttggg ggcat ttgtc actcaagttg ctgcggacga cgtggttcgt 6120  
ctcgttcttt tattcttccc ctctgtgcc ctcgataatc aggcctctcc gacaggttaa 6180

<210> 104  
<211> 2059  
<212> PRT  
<213> Toxoplasma gondii

<220>  
<221> MSC\_FEATURE  
<222> (1)..(2059)  
<223> MyoG

<400> 104

Met Thr Asp Arg Cys Trp Ile Pro His Pro Thr Glu Val Trp Gly Ile  
1 5 10 15

Ala Val Pro Ala Gly Ala Pro Gly Thr Cys Thr Tyr Lys Leu Val Glu  
20 25 30

Val Thr Asp Asp Gly Thr Asp Pro Arg Lys Leu Glu Val Thr Leu Ala  
35 40 45

Lys Ser Ala Leu Thr Gln Val Ala Pro Val Thr Asp Pro Arg Ser Leu  
50 55 60

Glu Gly Val Gln Asn Val Cys Val Leu Gly Asp Val Ser Glu Ala Ser  
65 70 75 80

Val Leu His Thr Val Arg Leu Arg Tyr Gln Arg Asp Glu Ile Tyr Thr  
85 90 95

N3027PCT\_sequ.list.txt

Asn Val Gly His Ile Val Leu Ala Leu Asn Pro Phe Lys Tyr Leu Gln  
 100 105 110  
 Leu Tyr Gly Pro Asp Phe Val Arg Thr Tyr Phe Glu Asp Thr His Val  
 115 120 125  
 Phe Asp Leu Pro Pro His Leu Phe Gln Val Ser Ala Ala Ala Val Lys  
 130 135 140  
 Gly Leu Ser Glu Arg Gly Lys Pro Gln Ser Thr Leu Ile Thr Gly Glu  
 145 150 155 160  
 Ser Gly Ala Gly Lys Thr Glu Ser Thr Lys Leu Ile Leu Gln Phe Leu  
 165 170 175  
 Ala Asp Val Ser Glu Leu Ser Ser Ser Ser Ser Ser Phe Lys Val  
 180 185 190  
 Ser Ser Gly Ala Arg Leu Val Glu Arg Ala Glu Arg Asn Arg Ser Ile  
 195 200 205  
 Ser Gln Lys Asp Arg Gly Ser Cys Gly Thr Gly Gly Asp Asn Ala Leu  
 210 215 220  
 Gln Ser Gly Val Gly Ser Gly Ser Gln Gly Arg Glu Ala Thr Ser Leu  
 225 230 235 240  
 Gln Gln Arg Ile Leu Glu Ile Ser Pro Val Leu Glu Ser Phe Gly Asn  
 245 250 255  
 Ala Ser Thr Ser Arg Asn Pro Asn Ser Ser Arg Phe Gly Lys Trp Ile  
 260 265 270  
 Glu Val Tyr Phe Gly Asp Lys Leu Lys Val Leu Gly Ala Ser Ile Thr  
 275 280 285  
 Ser Tyr Leu Leu Glu Leu Pro Arg Val Thr Arg His Ile Ala Gly Glu  
 290 295 300  
 Arg Asn Tyr His Val Phe Tyr Gln Leu Val His Gly Leu Asn Thr Ser  
 305 310 315 320  
 Asp Leu Val Gly Val Ala Glu Thr Tyr Arg Leu Gly Thr Asp Ser Leu  
 325 330 335  
 Ala Phe Ser Tyr Leu Thr Pro Gln Glu Gln Thr Val Asn Thr Lys Ser  
 340 345 350  
 Thr Lys Ala Asp Thr Glu Val Ser Ser Pro Ala Pro Asp Ile Asp Asp  
 355 360 365

N3027PCT\_sequ.list.txt

Leu Thr Gly Phe Ser Gu Leu Lys Arg Ala Leu Leu Val Leu Gly Phe  
370 375 380

Ser Pro Ser Thr Gn Asn Ser Ile Phe Ser Ile Val Ala Ala Ile Leu  
385 390 395 400

His Leu Gly Asn Val Thr Phe Ala Pro Gu Ala Gly Gly Gu Lys Cys  
405 410 415

Ser Val Val Ser Asn Ser Arg Asp His Leu Thr Ala Ala Ser Gu Leu  
420 425 430

Leu Gly Leu Asp Val Pro Leu Val Gu Gly Ala Leu Thr Ser Arg Lys  
435 440 445

Met Lys Thr Gly Asn Gu Ser Ile Leu Ile Pro Leu Lys Thr Asp Gn  
450 455 460

Ala Asp Ala Ala Arg Asp Ser Phe Ala Lys Leu Val Tyr Gly Tyr Leu  
465 470 475 480

Phe Asn Trp Leu Ile Ala Gn Thr Asn Ala Asn Leu Ala Pro Ser Gly  
485 490 495

Gly Met Asp Phe Asp Leu Asn Arg Tyr Val Gly Leu Leu Asp Ile Ala  
500 505 510

Gly Phe Gu Ser Phe Arg Val Asn Gly Phe Gu Gn Leu Cys Ile Asn  
515 520 525

Leu Ser Asn Gu Gu Leu Gn His His Phe Asn Ala Asp Ile Phe Leu  
530 535 540

Asn Gu Val Lys Asp Tyr Gu Asn Asp Gly Leu Gn Gly Val Ser Ile  
545 550 555 560

Thr Tyr Gu Asp Asn Ala Asp Val Leu Ser Leu Ile Ala Gly Lys Gly  
565 570 575

Gly Val Ile Ala Thr Leu Asp Gu Gu Val Phe Val Pro Arg Gly Ser  
580 585 590

Asp Gn Gly Phe Leu Asn Lys Leu Asn Lys Ala Gn Thr Asn His Lys  
595 600 605

Arg Tyr Ile Gu Asn Lys Ile Lys Gly Ser Met Ala Phe Gly Ile Gn  
610 615 620

His Tyr Ala Gly Asp Val Thr Tyr Thr Val Thr Gly Trp Leu Val Lys  
625 630 635 640

Asp Gn Asn Ala Pro Pro Gn Gu Ala Arg Asp Cys Leu Leu Thr Ser

645

650

655

G u A s n P r o V a l V a l L y s A l a I l e M e t G u T h r A l a S e r S e r A s p T h r  
 660 665 670  
 G n A r g A r g G y P r o G y G y L y s S e r T h r V a l G y S e r V a l P h e L y s  
 675 680  
 L y s G n L e u S e r G u L e u M e t A l a L y s I l e A s n G y T h r A s p S e r H i s  
 690 695 700  
 T y r I l e A r g C y s I l e L y s P r o A s n P r o A l a H i s L y s P r o A r g V a l I l e  
 705 710 715 720  
 H i s S e r S e r G n I l e L e u A s n G n L e u V a l C y s S e r G y V a l M e t G u  
 725 730 735  
 A l a I l e A r g I l e A r g L y s S e r G y P h e A l a L e u A r g L e u L e u H i s G n  
 740 745 750  
 A s p P h e V a l A s p A r g T y r A r g L e u V a l L e u G y S e r L y s A l a A l a A l a  
 755 760 765  
 G y L e u A r g T h r L e u A s p A l a A l a S e r A l a A l a G n G n L e u V a l T h r  
 770 775 780  
 G n L e u V a l A l a A s n L y s T r p V a l S e r G n G u G u C y s L e u I l e G y  
 785 790 795 800  
 A r g T h r L y s V a l P h e A l a L y s S e r T h r V a l G n A s p P h e L e u G u A r g  
 805 810 815  
 A l a A r g G u G u A l a L e u V a l G u P r o V a l I l e L e u I l e G n A l a L e u  
 820 825 830  
 T y r A r g G y T y r A r g T h r A r g G n G n C y s A r g V a l L e u P h e G u V a l  
 835 840 845  
 T y r G y G n L e u L y s G u P h e L e u A s p A l a G y G y G u A l a S e r L y s  
 850 855 860  
 A r g G y G y T y r L e u T h r A s p P r o V a l P h e P r o A s p A l a S e r T h r P r o  
 865 870 875 880  
 G u L e u L e u G n L y s L y s A l a A s n S e r L e u G y A s p L e u I l e S e r G n  
 885 890 895  
 L e u G u T h r L e u A s p A l a S e r L e u G n P r o A r g C y s L e u S e r T h r V a l  
 900 905 910  
 S e r L y s T y r H i s V a l A r g M e t T h r G n G u A l a S e r L e u S e r L e u G u  
 915 920 925

N3027PCT\_sequ.list.txt

Leu Lys Arg Gln Leu Glu Leu Thr Asp Gly Glu Gly Ala Glu Asp Glu  
 930 935 940  
 Cys Asp Ala Leu Ser Met Leu Arg Ala Thr Leu Gln Lys Ala Glu Ser  
 945 950 955 960  
 Lys Lys Val Ser Gly Pro Phe Val Thr Ala Ala Arg Glu Arg Val Asn  
 965 970 975  
 Arg Leu Glu Ala Glu Thr Ser Leu Gly Asp Leu Leu Asp Gln Ala Leu  
 980 985 990  
 Gln Ala Lys Asp Lys Asp Asp Leu Ala His Leu Leu Thr Glu Ala Arg  
 995 1000 1005  
 Gln Leu Glu Leu Ser Ser Thr Pro Ser Arg Phe Phe Thr Ser Tyr  
 1010 1015 1020  
 Leu Ser Ser Val Val Ala Ala Ala Glu Ala Tyr Leu Ala Ser Asn  
 1025 1030 1035  
 Ala Arg Glu Asn Glu Arg Leu Gln Arg Glu Arg Glu Gln Ala Ala  
 1040 1045 1050  
 Glu Ser Arg Lys Ala Leu Lys Glu Arg Gln Gln Gln Glu Ala Leu  
 1055 1060 1065  
 Leu Lys Asp Ala Val Glu Glu Arg Lys Arg Ser Asp Arg Leu Ser  
 1070 1075 1080  
 Leu Leu Ser Val Ala Ser Asp Ile Lys Lys Ala Lys Arg Asn His  
 1085 1090 1095  
 Glu Ala His Arg Gly Val Gln Thr Ala Glu Thr Ser Ser Leu Arg  
 1100 1105 1110  
 Ile Glu Tyr Asp Glu Glu Ala Thr Val Ser Thr Ser Glu Ser Glu  
 1115 1120 1125  
 Trp Thr Glu Ser Ser Glu Ala Glu Ser Glu Glu Pro Leu Ser Asp  
 1130 1135 1140  
 Pro Tyr Ser Thr Lys Asp Glu Glu Gly Gly Glu Gly Leu Ala Ser  
 1145 1150 1155  
 Ala Tyr Leu Arg Lys Phe Met Gln Glu Val Ala Arg Ala Thr Arg  
 1160 1165 1170  
 Glu Cys Asp Pro Ala Gln Leu Thr Phe Phe Leu Glu Arg Ala Arg  
 1175 1180 1185

N3027PCT\_sequ.list.txt

Glu	Ala	Asn	Leu	Gly	Lys	Gly	Pro	Arg	Glu	Leu	Gln	Leu	Ala	Arg
	1190					1195					1200			
Val	Gln	Leu	Glu	Asn	Leu	Ser	Asp	Pro	Ser	Phe	Leu	Asn	Ala	Glu
	1205					1210					1215			
Leu	Lys	Glu	Ala	Thr	Ile	Gly	Val	Thr	Trp	Gly	Val	Ala	Thr	Gln
	1220					1225					1230			
Glu	Asp	Phe	Val	Lys	Leu	Arg	Asn	Leu	Val	Glu	Gln	Ala	Lys	Ala
	1235					1240					1245			
Ile	Arg	Ala	Lys	Gln	Lys	Gly	Glu	Ala	Glu	Arg	Ser	Asp	Pro	Leu
	1250					1255					1260			
Arg	Leu	Gln	Thr	Ile	Asp	Glu	Lys	Val	Leu	Ala	Ser	Ala	Ala	Ala
	1265					1270					1275			
Thr	Leu	Glu	Ser	Leu	Arg	Arg	Thr	Glu	Gly	Arg	Glu	Arg	Gly	Ser
	1280					1285					1290			
Ser	Ala	Lys	Phe	Gly	Gly	Thr	Phe	Gly	Glu	Arg	Gly	Asp	Arg	Gly
	1295					1300					1305			
Gly	Gly	Leu	Thr	Ala	Tyr	Leu	Phe	Glu	Asn	Tyr	Pro	Leu	Leu	Gly
	1310					1315					1320			
Ile	Asn	Ile	Arg	Ile	Gln	Glu	Thr	Lys	Ser	Met	Arg	Lys	Thr	Glu
	1325					1330					1335			
Gln	Leu	Val	Leu	Arg	Arg	Glu	Glu	Leu	Leu	Ser	His	Gln	Thr	Asp
	1340					1345					1350			
Pro	Leu	Ala	Glu	Pro	Leu	Leu	Gln	Leu	Pro	Asp	His	His	Ala	Glu
	1355					1360					1365			
Val	Val	Ala	Leu	Thr	Cys	Phe	Arg	Ser	Leu	Leu	Gly	Val	Met	Gly
	1370					1375					1380			
Glu	Arg	Phe	Cys	Val	Gly	Arg	Ser	Ala	Leu	Ser	Asp	Glu	Ile	Leu
	1385					1390					1395			
Ala	Leu	Gly	Arg	Asn	Ala	Glu	Asp	Leu	Arg	Asp	Glu	Ile	Tyr	Cys
	1400					1405					1410			
Gln	Ile	Leu	Lys	Gln	Leu	Arg	Asn	Asn	Pro	Ser	Ala	Gly	Ser	Thr
	1415					1420					1425			
Val	Ala	Gly	Leu	Arg	Leu	Leu	Gln	Ser	Cys	Cys	Gln	Thr	Phe	Pro
	1430					1435					1440			

Pro Ser Glu Thr Leu Ala Pro Tyr Leu Arg Phe Ala Ile Gln Ser  
 1445 1450 1455  
 Phe Leu Ser Gly Leu Ser Ala Pro Gly Gly Glu Ser Thr Gly Ala  
 1460 1465 1470  
 Ile Lys Phe Gln Gln Glu Val Glu Gln Ile Cys Arg Gln Ala Leu  
 1475 1480 1485  
 His Asp Leu Glu Leu Thr Cys Gly Ala Ser Arg Glu Glu Gly Arg  
 1490 1495 1500  
 Arg Pro Gly Asp Ser Thr Gly Gln Gly Ala Val Ser Ala Glu Arg  
 1505 1510 1515  
 Glu Thr Arg Met Tyr Val Gln Ile Arg Leu Ala Asp Gly Ser Gln  
 1520 1525 1530  
 Arg Arg Leu Ala Leu Asp Gly Asp Leu Pro Gly Asp Leu Ser Arg  
 1535 1540 1545  
 Arg Leu Val Lys Asp Leu Asn Leu Leu Gly Ala Asp Ser Trp Ala  
 1550 1555 1560  
 Ile Met Glu Gln Leu Ser Gln Tyr Asp Leu Lys Lys Thr Ser Ala  
 1565 1570 1575  
 Arg Glu Ser Pro Pro Ala Thr Phe Arg Leu Leu Pro Pro Glu Glu  
 1580 1585 1590  
 Leu Val Gln Asp Tyr Leu Ser Lys Arg Asp Ser Gln Val Gln Leu  
 1595 1600 1605  
 Trp Leu Arg Arg Pro Met Leu Ser Leu Glu Asp Pro Leu Ser Leu  
 1610 1615 1620  
 His Pro Ala Thr Ala Ala Leu Ile Tyr Arg Gln Ala Val Ser Gln  
 1625 1630 1635  
 Tyr Gln Gln His Val Phe Asn Glu Asp Pro Ser Leu Leu Ala Ser  
 1640 1645 1650  
 Ile Ser Ala His Leu Leu Gln Ala Asp Gly Leu Leu Asp Ser Ser  
 1655 1660 1665  
 Pro Pro Arg Val Pro Pro Trp Pro Ser Leu Ser Trp Thr Ile Pro  
 1670 1675 1680  
 Gln Arg Leu His Trp Leu Arg Ser Glu Ala Asp Trp Thr Ala Ala  
 1685 1690 1695  
 Ile Ala Glu Glu Ala Lys His Ile Asp Pro Glu Glu Gly Asp Leu



N3027PCT\_sequ.list.txt

Glu His Asn Gly Asp Ser Gly Arg Asn Ser Glu Ile Gln Gln Gly  
 1970 1975 1980  
 Ser Glu Lys Gly Val Phe Thr Ile Ser Pro Glu Lys Leu Trp Leu  
 1985 1990 1995  
 Val Ala Ala Val Pro Pro Arg Gly Glu Ala Pro Asp Arg Leu Ile  
 2000 2005 2010  
 Leu Gly Tyr Asp Asp Pro Arg Thr Gly Lys Arg Arg Leu Glu Ala  
 2015 2020 2025  
 Phe Val Thr Gln Val Ala Ala Asp Asp Val Val Arg Leu Val Leu  
 2030 2035 2040  
 Leu Phe Phe Pro Phe Cys Ala Leu Asp Asn Gln Ala Pro Pro Thr  
 2045 2050 2055

Gly

<210> 105  
 <211> 2457  
 <212> DNA  
 <213> Plasmodium falciparum

<220>  
 <221> misc\_feature  
 <222> (1)..(2457)  
 <223> MyoA

<400> 105  
 at ggct gtt a caaat gaaga aat aaaaacg gcaagt aaga ttgtt agaag agt t t caaat 60  
 gt agaagcat ttgacaaaag tgggttcagtt ttt aagggtt at caaat at g gact gat at a 120  
 t ct ccgacaa tagaaaat ga tccaaat at t atgtttgt aa aatgtgtt gt acaacaagga 180  
 t caaaaaaag aaaaattaac cgttgt acaa attgatccac ccggaacagg aactccat ac 240  
 gat at t gat c caactcacgc atggaactgc aactctcaag tagaccccat gtctttt ggt 300  
 gat at t ggt c tttt aaat ca caccaacat c ccatgtgttc ttgacttttt aaagcacaga 360  
 t at t t aaaaa at caaat at a caccactgct gttcccctta ttgttgcaat aaacccat ac 420  
 aaggatttag gaaacacaac taatgaatgg attcgt agat atcgt gat ac agct gat cat 480  
 act aagttgc caccacacgt gttcacatgt gctagggaag cttt gtctaa tctccat ggt 540  
 gt aaacaaga gccaaactat t at t gt at ct ggtgaatct g gtgcaggaaa aaccgaagca 600  
 acaaaacaaa tcatgagata ttttgcttct tct aagagt g gaaat at gga ttt acgt at t 660  
 cagacagcaa taatggctgc aaatccagtt cttgaagctt ttggtaatgc gaaaact at a 720  
 agaaat aaca at t cat ct cg tttt ggtcgt t t cat gcagt tggtt at at c ccat gaagga 780  
 ggt at aagat acggttccgt tgttgctttt ctgttggaat aatctagaat t at t acacaa 840

# N3027PCT\_sequ. list . . txt

gat gat aat g aaaggt cat a t cat at at t t t at caat t t c t t aagggg gc aaat agt acg	900
at gaaat ct a aat t t ggt t t aaaaggagt t act gaat aca aat t at t gaa cccaaat t ca	960
acagaggt aa gt ggagt aga t gat gt aaaa gat t t t gaag aggt aat t ga at cgt t gaaa	1020
aat at ggaat t aagt gaat c agat at t gaa gt aat at t t t caat agt agc t ggt at at t a	1080
acat t aggaa at gt aagat t aat t gagaag caagaagct g gat t aagt ga t gct gct gct	1140
at t at ggat g aggat at ggg t gt gt t t aat aaagct t gt g aat t gat gt a t t t agaccct	1200
gaat t aat aa aaaggggaaat at t aat t aag gt aact gt t g ct ggaggaac aaaaat t gaa	1260
ggg agat gga at aaaaat ga t gcagaagt g t t gaaat ct t cct t at gt aa agct at gt at	1320
gagaaat t gt t t t t at ggat aat aagacat t t gaat t caa gaat t gaacc agaaggagga	1380
t t t aaaacat t t at gggat at gt t agat at t t t t ggt t t t g aagt at t t aa aaat aat t ca	1440
t t ggaacaat t at t t at t aa cat t act aac gaaat gct t c agaaaaat t t t gt agat at t	1500
gt t t t t gaaa gagaat caaa at t at at aaa gacgaaggaa t at caacagc t gaat t aaag	1560
t acaccagt a at aaggaagt aat aaacgt a ct t t gt gaga agggg aaat c agt act t t ca	1620
t act t agagg accaat gt t t agcacct gga ggaaccgat g aaaagt t t gt aagt t cct gt	1680
gct acaaat t t aaaggaaaa t aat aagt t t accccagcaa aagt agcat c gaat aaaaat	1740
t t t at aat ac aacat act at aggaccaat t caat at t gt g ct gaaagct t t t t gct t aaa	1800
aacaaggat g t ct t aagagg t gat t t agt t gaagt aat t a aggat t cccc caat ccaat a	1860
gt acaacagt t at t t gaagg t caagt aat t gagaagggt a aaat agct aa aggt t cat t a	1920
at aggt t ct c aat t t t t aaa t caat t gaca t ct t t aat ga act t gat aaa t agt act gaa	1980
ccacat t t ca t acgt t gt at t aaaccaaat gaaaaat aaaa aaccat t aga at ggt gt gaa	2040
ccaaaaat at t aat t cagct t cat gcct t a t caat t t t ag aagcat t agt at t aagacaa	2100
t t aggat at t ct t at agaag aacct t t gaa gaat t ct t at at caat at aa at t t gt ggac	2160
at t gct gct g ct gaagat t c at cagt t gaa aaccaaata aat gt gt t aa t at at t aaag	2220
t t gt ct ggac t at ct gaat c cat gt at aag at aggaaaaa gcat ggt ct t t t t gaaacaa	2280
gaaggt gcaa aaat at t gac aaaaat acaa agagagaaac t t gt t gaat g ggaaaaat t gt	2340
gt gagt gt aa t t gaagct gc t at act t aaa caaaaat aca aacaaaaggt t aacaaaaat	2400
at acct t ct c t t t t gagagt acaagct cat at aagaaaaa aaat ggt agc t caat aa	2457

<210> 106  
 <211> 818  
 <212> PRT  
 <213> Pl asmodi um fal ci par um

<220>  
 <221> M SC\_FEATURE  
 <222> (1) . . (818)  
 <223> MyoA

<400> 106

N3027PCT\_sequ.list.txt

Met Ala Val Thr Asn Gu Gu Ile Lys Thr Ala Ser Lys Ile Val Arg  
1 5 10 15

Arg Val Ser Asn Val Gu Ala Phe Asp Lys Ser Gly Ser Val Phe Lys  
20 25 30

Gly Tyr Gn Ile Trp Thr Asp Ile Ser Pro Thr Ile Gu Asn Asp Pro  
35 40 45

Asn Ile Met Phe Val Lys Cys Val Val Gn Gn Gly Ser Lys Lys Gu  
50 55 60

Lys Leu Thr Val Val Gn Ile Asp Pro Pro Gly Thr Gly Thr Pro Tyr  
65 70 75 80

Asp Ile Asp Pro Thr His Ala Trp Asn Cys Asn Ser Gn Val Asp Pro  
85 90 95

Met Ser Phe Gly Asp Ile Gly Leu Leu Asn His Thr Asn Ile Pro Cys  
100 105 110

Val Leu Asp Phe Leu Lys His Arg Tyr Leu Lys Asn Gn Ile Tyr Thr  
115 120 125

Thr Ala Val Pro Leu Ile Val Ala Ile Asn Pro Tyr Lys Asp Leu Gly  
130 135 140

Asn Thr Thr Asn Gu Trp Ile Arg Arg Tyr Arg Asp Thr Ala Asp His  
145 150 155 160

Thr Lys Leu Pro Pro His Val Phe Thr Cys Ala Arg Gu Ala Leu Ser  
165 170 175

Asn Leu His Gly Val Asn Lys Ser Gn Thr Ile Ile Val Ser Gly Gu  
180 185 190

Ser Gly Ala Gly Lys Thr Gu Ala Thr Lys Gn Ile Met Arg Tyr Phe  
195 200 205

Ala Ser Ser Lys Ser Gly Asn Met Asp Leu Arg Ile Gn Thr Ala Ile  
210 215 220

Met Ala Ala Asn Pro Val Leu Gu Ala Phe Gly Asn Ala Lys Thr Ile  
225 230 235 240

Arg Asn Asn Asn Ser Ser Arg Phe Gly Arg Phe Met Gn Leu Val Ile  
245 250 255

Ser His Gu Gly Gly Ile Arg Tyr Gly Ser Val Val Ala Phe Leu Leu  
260 265 270

Gu Lys Ser Arg Ile Ile Thr Gn Asp Asp Asn Gu Arg Ser Tyr His  
Page 509

```

I l e P h e T y r G n P h e L e u L y s G y A l a A s n S e r T h r M e t L y s S e r L y s
 290                               295                               300

P h e G y L e u L y s G y V a l T h r G u T y r L y s L e u L e u A s n P r o A s n S e r
305                               310                               315                               320

T h r G u V a l S e r G y V a l A s p A s p V a l L y s A s p P h e G u G u V a l I l e
                               325                               330                               335

G u S e r L e u L y s A s n M e t G u L e u S e r G u S e r A s p I l e G u V a l I l e
                               340                               345                               350

P h e S e r I l e V a l A l a G y I l e L e u T h r L e u G y A s n V a l A r g L e u I l e
                               355                               360                               365

G u L y s G n G u A l a G y L e u S e r A s p A l a A l a A l a I l e M e t A s p G u
 370                               375                               380

A s p M e t G y V a l P h e A s n L y s A l a O y s G u L e u M e t T y r L e u A s p P r o
385                               390                               395                               400

G u L e u I l e L y s A r g G u I l e L e u I l e L y s V a l T h r V a l A l a G y G y
                               405                               410                               415

T h r L y s I l e G u G y A r g T r p A s n L y s A s n A s p A l a G u V a l L e u L y s
                               420                               425                               430

S e r S e r L e u O y s L y s A l a M e t T y r G u L y s L e u P h e L e u T r p I l e I l e
                               435                               440                               445

A r g H i s L e u A s n S e r A r g I l e G u P r o G u G y G y P h e L y s T h r P h e
                               450                               455                               460

M e t G y M e t L e u A s p I l e P h e G y P h e G u V a l P h e L y s A s n A s n S e r
465                               470                               475                               480

L e u G u G n L e u P h e I l e A s n I l e T h r A s n G u M e t L e u G n L y s A s n
                               485                               490                               495

P h e V a l A s p I l e V a l P h e G u A r g G u S e r L y s L e u T y r L y s A s p G u
                               500                               505                               510

G y I l e S e r T h r A l a G u L e u L y s T y r T h r S e r A s n L y s G u V a l I l e
                               515                               520                               525

A s n V a l L e u O y s G u L y s G y L y s S e r V a l L e u S e r T y r L e u G u A s p
                               530                               535                               540

G n O y s L e u A l a P r o G y G y T h r A s p G u L y s P h e V a l S e r S e r O y s
545                               550                               555                               560

```

N3027PCT\_sequ.list.txt

Ala Thr Asn Leu Lys 565 Glu Asn Asn Lys Phe 570 Thr Pro Ala Lys Val 575 Ala

Ser Asn Lys Asn 580 Phe Ile Ile Gn His 585 Thr Ile Gly Pro Ile 590 Gn Tyr

Cys Ala Glu 595 Ser Phe Leu Leu Lys 600 Asn Lys Asp Val Leu 605 Arg Gly Asp

Leu Val 610 Glu Val Ile Lys Asp 615 Ser Pro Asn Pro Ile 620 Val Gn Gn Leu

Phe 625 Glu Gly Gn Val Ile 630 Glu Lys Gly Lys Ile 635 Ala Lys Gly Ser Leu 640

Ile Gly Ser Gn Phe 645 Leu Asn Gn Leu Thr 650 Ser Leu Met Asn 655 Leu Ile

Asn Ser Thr Glu 660 Pro His Phe Ile Arg 665 Cys Ile Lys Pro Asn 670 Glu Asn

Lys Lys Pro 675 Leu Glu Trp Cys Glu 680 Pro Lys Ile Leu Ile 685 Gn Leu His

Ala Leu 690 Ser Ile Leu Glu Ala 695 Leu Val Leu Arg Gn 700 Leu Gly Tyr Ser

Tyr 705 Arg Arg Thr Phe Glu 710 Glu Phe Leu Tyr Gn 715 Tyr Lys Phe Val Asp 720

Ile Ala Ala Ala Glu 725 Asp Ser Ser Val Glu 730 Asn Gn Asn Lys Cys 735 Val

Asn Ile Leu Lys 740 Leu Ser Gly Leu Ser 745 Glu Ser Met Tyr Lys 750 Ile Gly

Lys Ser Met 755 Val Phe Leu Lys Gn 760 Glu Gly Ala Lys Ile 765 Leu Thr Lys

Ile Gn 770 Arg Glu Lys Leu Val 775 Glu Trp Glu Asn Cys 780 Val Ser Val Ile

Glu 785 Ala Ala Ile Leu Lys 790 His Lys Tyr Lys Gn 795 Lys Val Asn Lys Asn 800

Ile Pro Ser Leu Leu 805 Arg Val Gn Ala His 810 Ile Arg Lys Lys Met 815 Val

Ala Gn

# N3027PCT\_sequ. list .txt

<210> 107  
 <211> 5940  
 <212> DNA  
 <213> Pl asmodi um fal ci par um

<220>  
 <221> mi sc\_f eat ur e  
 <222> (1) . (5940)  
 <223> MyoF

<400> 107  
 at gacggcat ct t ct gcaga t ggggcgt ct gccccgggag gcggcgaccc gggagaggag 60  
 gaggt ccgct gcgccgt t gg aaccaagat c t acgt ccct g acgccgt ga t gt t t ggaga 120  
 acagcggaag t ggt gaagat ccaagaggat ggcagt ct ca ccgccagagt cgat gcagac 180  
 aat gaact gg t gcagct caa aaaaaacgat at at ggt at c t gt gcaat ac cgat gt gt gg 240  
 aacaccaccg gact gagt gc gccgacagat t t gacgat gc t gacgcat t t gcat gaggcg 300  
 gccgt cct cg act ct ct caa cct ccgct t c gat at cgacg agat ct acac t t t cacgggt 360  
 cccat t ct ga t t gcgggt caa t cct t t t aaa cagat cacag gt ct ct acga cat gaagcaa 420  
 t t ggt t cggt acat cgcgag t t cggagct g ccgat gcccg gagt gcct t c t t cct cgt cc 480  
 ggct ct t ct t ccaacgcacc cgt cgcgct g ccgat at ct c gacagcct ca cgt ct t cgcc 540  
 t cgagcagcg ccgcgt acca gggcat gt gc aacgagaagc agagt cagac gat t ct gat t 600  
 t ct ggggaga gcggagcagg caagacagaa agcacgaaat t cgt gat gaa gt t cct cgcc 660  
 t gt gccggca gcgaagact t ggagcgccgg t cgcaagt cg aggcgcaagt cct cgagagc 720  
 aat cct ct cc t ggaagcat t cggaaacgcc cggacgct gc gaaacgacaa cagcagt cgc 780  
 t t cggaagt t cat t gaact ccagt t ccaa acaagcaaag ccaagcggat gt ct ggaaac 840  
 cgcggcaggc t ct gt ggagc t cgaat t caa acgt at t t gc t ggagaagggt ccgcgt ct gc 900  
 gaccagcaag agggagagag gaact at cac at ct t ct acc aact t t gt gc agct gcagaa 960  
 gct gcagct c agacgggagg cat ct at t ac t t ccct t ccc cgaaat t ccg aaaagccgca 1020  
 gat gcaaagg cacaagagat ggat at gt ct ct ct t cgagc cgcgcgacaa at t caagt at 1080  
 t t gaccaaga gcagct gcc a ccagct gcag ggcgt ggacg act gcgagga gt t cgagagc 1140  
 acgct ct t cg cgat gcagac ggt t ggcat c t ccccgagg agcaaat gag cat t ct ct cg 1200  
 gt cgt gggcg ccgt t ct t t g t ct gggaaat gt t t ct t t cg agact ccgaa ggccaat agc 1260  
 gaaggat cgc aggt cgcagc gagct gcact gagt acgt ct gcaaggcct g ccgcct t ct g 1320  
 ggcgt ccaga gggaggct ct gcaagaggcg at gt gct acc gaacaat caa gaccgcacac 1380  
 gagagct acc ggaagccgt t gaagacagac gaagcat ggg agat gaagga cgcgct gt gt 1440  
 cgggcgct gt acggt t gt ct gt t t ct gcaa gt t gt cgca agacgaacgc gt ct at aggt 1500  
 t acct gaagg aggt gcagag t gcagacgat t t gct t ct gt t t t gcggagt gct ggacat t 1560  
 t t cggt t t cg aat gt t t cca gt t caact cg t t cgagcagc t gt gcat caa ct t caccaac 1620  
 gagcgt ct gc agaat t t ct t caat acgt t c gt ct t caagt gcgaggaaga gct ct accgc 1680

N3027PCT\_sequ. list . txt

gccgaaggca t ccagt ggaa ccct ct ggac tt cccggaca acgcagact g cgt cgcgct g	1740
ct gcaggaaa agccgct cgg t ct gt t ct cc at gct cgacg aagagt gcat gt t ccccgca	1800
ggcaaagacc gaggat t caa caacaaagt c t gccagaaac acggcggt ca caaacgt t t c	1860
ggcgt gat ca aaacgaaacc t aat t gct t c gt ggt gcacc act t t gccgg cagcgt agag	1920
t act gct ccg acggat t t ct ggagaagaac aaggaccagc t gt ccgt gga t ct gcaggag	1980
gcagt gaagg ct t cgacgat cccgt t cgt c t ccaact t gt t t t ct gcgt t cct gaaccgc	2040
ggcacagcgg aagacggat c ggggaagaag cgaaagt t cg t gacggt gt c gagcgagt t t	2100
cgcgagcaac t cggcgcgct gat ggagacc gt cgacaaga cggcaccgca ct t cat t cgc	2160
t gcat caaac ccaat ccgca gaacct ccca gacct ct t cg accgcgcgac agt gaacgag	2220
cagct ccgat at ggaggcgt cct gcaagcg gt gcaggt ca gccgt gcagg gt accct gt g	2280
cgcct ct cgc accgcgact g ct t ct t cgac t at agggcgc t cgcagacgg agcgt t gct	2340
gcgcagct gt cgcagggcac agagacgcc gaggcct ggc gcggccgcgc t gaggct ct g	2400
ct ccgccacc t ggacgagaa gct gaagct c gaccgccgga aaaaagagac agact ccccg	2460
gaccgaacct gggccgt cgg gaagacct c t gct t ct t ca aaaacgaagc gt acgagat t	2520
ct t t cggcga act t gat gag cgt gagggg g gct gcggcga cggcgat t ga ggcgaggt ac	2580
aagt gct t t g t gcagaggcg at t ct t cct g at gt at cggc agact gt cgt t t t t ct gcag	2640
t ct cacat t c gcat gt t t ct t t gcaagt t g gaggccaga gact gcgaga gt cacgcgt	2700
gcgcggcgcg t ggagaact t cat gcgaggc gccgt t gcgc gt ct gcggt a cct gcggact	2760
ct ggagaaca t cgggcgaat t caggcggcc t ggcgaggca agcagacaag gt cgcagct t	2820
cgcgat cgaa agct cgagga agccgccagt aaaat ccagg cgt t ct ggaa gat gcacaag	2880
caacgcat gt t ct acacgaa t t t gaagaaa gcct cgact a t t gct caact caagt ggaag	2940
agaat t ct gg ct cggcgcat gct gcggcga ct gcgagagg aggct cgca ggt ct caggc	3000
ct t ct gaaga aggcgcaaga t ct gcagcgc gact t gt gcg aagagaagaa caagagaagc	3060
gacgcggaaa gccat gt t ct t cagt t gcag gcgaaaaacg aagat ct cct caaagaaat c	3120
cagaaact cc agagggaaact cgaacgcgcg aaagaagat g t cgct t ct ct acaagcat ct	3180
aacgacgact t t gct t caca agt aaagcag ct gaaggaga gt t t gacggt gggct ct t cg	3240
acgccaacga cgcct cagat gacat t cggg acccacaaga gaagggt gt c gaacaacgca	3300
gat gt ccccc at t ct caaga gaaggacaag t t t ccgacag acgaggagt t gaaggct t t g	3360
cggacagagt t ggagagacg cgacgcggag gct caacagc agcaggcaga gcacgaggct	3420
ct cat cgcgg agct ccgagc ggcgt t gaag gacgt gaga gt gcat gt ga at acgagcga	3480
acgcaacgca aagaagct ga ggcgcggt ac cgact ggt cc t cgaagact c gagcgcaagc	3540
agt act cacg t ccgcgcgt c gt ct gcct ca aaggct gcgg t cgcgact c t gcgcccaca	3600
gct ct gt t ga gagagaagt g t at ggagagc gacat ggcga cagggcgacc t ggagact cg	3660
ct cgcgt ct t cggc cgcgt c cgct gct cct ct ct cgcct c cggc cgcgct ggagcct gaa	3720
ct t t gggagt cggc gct gca cgaccagcgg t ggat cgact t gct t ct gct gggc cct gcc	3780

N3027PCT\_sequ. list . . txt

ggcgt gggca agacaggt t t gct ggagcaa t t t ct t gt ga agt t gggaga cgaagt t cat	3840
ct ggagcagc t ccgagt gag ccgaaagat g gaggaccaag cgccct t cag caagct gccg	3900
caacact acg aact cgt ct a ct ct cccgac agccaggaag gccgt gaacg agaagaagct	3960
cgagt gaacg t act cgact t t ccaggcct c t cgct acca agcagaat cc cgctgt gagg	4020
gt caagcagg cct t cgt cgt cgcgggt cgt c t t cgat ccca ccagacct ga aact t gt gca	4080
gaggcgct gc aaat ct t gac caacgt cgt g ct gcct gct c ggcccaaagt ct ct gcacaa	4140
gacccgt t gg ggcct gcat cagcggcaga gt t t acct cg t t gaaaacgg gt ggcgcgca	4200
gccgcaaag aagct gct gt gcaagt cgac act gcagct g t cagagacaa agct gcgggt	4260
ct ccgct gt c act accgcga at t ggt gcat ct ggagt ct c t ggt cgacga aat t gt gcct	4320
ct gat gt cga gct ggagaga t ct gct t cag cagcagagac t t gccat gct gcagcaccac	4380
gcgcggct gc agccgggt gg gcct t ct ccg cat gcgt ct c cgt t ct ccct gcct cgct cg	4440
cagacaggt c gcggagct t c gct ct t cgcc act gcgt cgc agt ct ggagc t ct aggcgcc	4500
t ccgct gt cg gaggacagga gaacggagt t gagaagt cgt cgt cgggct ct ct gct cac	4560
agacagggag gct t gt ct gc gaact t ct t c gacagcat t c gct ct t t cct ct cacagt cg	4620
t cgat gcgac ct gcggggaa cgt t ct ggct t ct ggaaagc aggccgcgga cct gaagct g	4680
ct cagaccga gcat gaagcc t gggggcacc gcgat gat ga agaaact gaa gacgcgaagt	4740
ct cgaccaac act cgggt cgt ccct gt gcag gaact gcagg act cggact c t gcgat cacc	4800
t gcgt ggt gt t t ggcaagga gaaagaaaac cgggact aca t t ct t ct cgc ggct gcgagc	4860
aaagacggca gcgt agt gat ct accggt gt t accgt ct ag aagct gaaag acaaat gt t c	4920
gaccaggagc aagt t t ct ct agt cact cct gcggct t cgc ggaccact ga cagcaaggag	4980
cacat cgggc ct t ct gt ct c cgt gcact cg cgact cgt gg ggcacagccg cgccgt cacc	5040
t gt ct ct t ct t ct cgct ct t ggaagaccag ct gat t acaa ct t caat cga caagt ct gt g	5100
cgat t t t ggc at gt cgat ac gggggacat g ct gaaagt ct t cacagact c t t ct cct gcg	5160
ct ggct gccg cct t cct ccc gt t caacccc acagcct t t g t cgct cgaa ct caaact cc	5220
at t ct t cggc t ggt ct gcgc caccagt gga cgcgt gat t c agaagct gaa agt ggagagc	5280
gaagt gaggg cgct caagt t cgacgacaca gggct ct t ct gt t t t gct gg aacgaaggca	5340
ggagcagt cc acgt t ct gga ggccagcgac acagt caaca t t cgat t t aa at t caagact	5400
t ct t t gggga agggcgct gt gacgt gcat c acct t t gt gc cgagcacagg acct ggacag	5460
t at ccgcgcc t cct cat caa ct gct gcgac t ccagcgt cg ccgt cgt cga gt gt at ct ac	5520
ggccgcct c cgggcgt cct caccaact t g ct cgt t cgcc accgt gt gag aat cgccac	5580
agt ct gct t c ct ct aagat g ct ggt t ct ca aact t t ggag gaggggt ggct t at caccggt	5640
agt gaggaca aggacgt gt a ct gt t t ct ct ct t caacaag gcgcgaact t caaggcaat c	5700
t cgct caaac at caccaggt aacgcct gaa ct gacagaga t cat ggggt cc ct cat cgaat	5760
t t cagagaca gct gt t t t t ct t ct t caca ccct t cat ct t cagt ct t t g t cat t t ct ct	5820

N3027PCT\_sequ.list.txt

cagt cgg t t t t g t a t c t c t g t c t c a t c t g t a t c g g a t t t t c t c c c c g t a g c t t t c c c 5880  
t g t c t g t a c t c t g t t t t c a g c c t c t g t c c g c t g c g c t a t g t g t g t g t g t c t c t t g t g a 5940

<210> 108  
<211> 1979  
<212> PRT  
<213> P l a s m o d i u m f a l c i p a r u m

<220>  
<221> M S C \_ F E A T U R E  
<222> ( 1 ) . . ( 1 9 7 9 )  
<223> M y o F

<400> 108

M e t T h r A l a S e r S e r A l a A s p G l y A l a S e r A l a P r o G l y G l y G l y A s p  
1 5 10 15

P r o G l y G u G u G u V a l A r g C y s A l a V a l G l y T h r L y s I l e T y r V a l  
20 25 30

P r o A s p A l a A l a A s p V a l T r p A r g T h r A l a G u V a l V a l L y s I l e G l n  
35 40 45

G l u A s p G l y S e r L e u T h r A l a A r g V a l A s p A l a A s p A s n G l u L e u V a l  
50 55 60

G l n L e u L y s L y s A s n A s p I l e T r p T y r L e u C y s A s n T h r A s p V a l T r p  
65 70 75 80

A s n T h r T h r G l y L e u S e r A l a P r o T h r A s p L e u T h r M e t L e u T h r H i s  
85 90 95

L e u H i s G u A l a A l a V a l L e u A s p S e r L e u A s n L e u A r g P h e A s p I l e  
100 105 110

A s p G u I l e T y r T h r P h e T h r G l y P r o I l e L e u I l e A l a V a l A s n P r o  
115 120 125

P h e L y s G l n I l e T h r G l y L e u T y r A s p M e t L y s G l n L e u V a l A r g T y r  
130 135 140

I l e A l a S e r S e r G u L e u P r o M e t P r o G l y V a l P r o S e r S e r S e r S e r  
145 150 155 160

G l y S e r S e r S e r A s n A l a P r o V a l A l a L e u P r o I l e S e r A r g G l n P r o  
165 170 175

H i s V a l P h e A l a S e r S e r S e r A l a A l a T y r G l n G l y M e t C y s A s n G l u  
180 185 190

L y s G l n S e r G l n T h r I l e L e u I l e S e r G l y G u S e r G l y A l a G l y L y s  
195 200 205

N3027PCT\_sequ.list.txt

Thr	Glu	Ser	Thr	Lys	Phe	Val	Met	Lys	Phe	Leu	Ala	Cys	Ala	Gly	Ser
	210					215					220				
Glu	Asp	Leu	Glu	Arg	Arg	Ser	Gln	Val	Glu	Ala	Gln	Val	Leu	Glu	Ser
225					230					235					240
Asn	Pro	Leu	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Arg	Thr	Leu	Arg	Asn	Asp
				245					250					255	
Asn	Ser	Ser	Arg	Phe	Gly	Lys	Phe	Ile	Glu	Leu	Gln	Phe	Gln	Thr	Ser
			260					265					270		
Lys	Ala	Lys	Arg	Met	Ser	Gly	Asn	Arg	Gly	Arg	Leu	Cys	Gly	Ala	Arg
		275					280					285			
Ile	Gln	Thr	Tyr	Leu	Leu	Glu	Lys	Val	Arg	Val	Cys	Asp	Gln	Gln	Glu
	290					295					300				
Gly	Glu	Arg	Asn	Tyr	His	Ile	Phe	Tyr	Gln	Leu	Cys	Ala	Ala	Ala	Glu
305					310					315					320
Ala	Ala	Ala	Gln	Thr	Gly	Gly	Ile	Tyr	Tyr	Phe	Pro	Ser	Pro	Lys	Phe
				325					330					335	
Arg	Lys	Ala	Ala	Asp	Ala	Lys	Ala	Gln	Glu	Met	Asp	Met	Ser	Leu	Phe
			340					345					350		
Glu	Pro	Arg	Asp	Lys	Phe	Lys	Tyr	Leu	Thr	Lys	Ser	Ser	Cys	His	Gln
		355					360					365			
Leu	Gln	Gly	Val	Asp	Asp	Cys	Glu	Glu	Phe	Glu	Ser	Thr	Leu	Phe	Ala
	370					375					380				
Met	Gln	Thr	Val	Gly	Ile	Ser	Pro	Glu	Glu	Gln	Met	Ser	Ile	Leu	Ser
385					390					395					400
Val	Val	Gly	Ala	Val	Leu	Cys	Leu	Gly	Asn	Val	Ser	Phe	Glu	Thr	Pro
				405					410					415	
Lys	Ala	Asn	Ser	Glu	Gly	Ser	Gln	Val	Ala	Ala	Ser	Cys	Thr	Glu	Tyr
			420					425					430		
Val	Cys	Lys	Ala	Cys	Arg	Leu	Leu	Gly	Val	Gln	Arg	Glu	Ala	Leu	Gln
		435					440					445			
Glu	Ala	Met	Cys	Tyr	Arg	Thr	Ile	Lys	Thr	Ala	His	Glu	Ser	Tyr	Arg
	450					455					460				
Lys	Pro	Leu	Lys	Thr	Asp	Glu	Ala	Trp	Glu	Met	Lys	Asp	Ala	Leu	Cys
465					470					475					480

N3027PCT\_sequ.list.txt

Arg Ala Leu Tyr Gly 485 Cys Leu Phe Leu Gln 490 Val Val Ala Lys Thr 495 Asn

Ala Ser Ile Gly 500 Tyr Leu Lys Glu 505 Val Gln Ser Ala Asp 510 Asp Leu Leu

Leu Phe Cys 515 Gly Val Leu Asp 520 Ile Phe Gly Phe Glu 525 Cys Phe Gln Phe

Asn Ser 530 Phe Glu Gln Leu Cys 535 Ile Asn Phe Thr 540 Asn Glu Arg Leu Gln

Asn 545 Phe Phe Asn Thr Phe 550 Val Phe Lys Cys Glu 555 Glu Glu Leu Tyr Arg 560

Ala Glu Gly Ile Gln 565 Trp Asn Pro Leu Asp 570 Phe Pro Asp Asn 575 Ala Asp

Cys Val Ala 580 Leu Leu Gln Glu Lys Pro 585 Leu Gly Leu Phe Ser 590 Met Leu

Asp Glu 595 Glu Cys Met Phe Pro Ala 600 Gly Lys Asp Arg 605 Gly Phe Asn Asn

Lys Val 610 Cys Gln Lys His Gly 615 Gly His Lys Arg Phe 620 Gly Val Ile Lys

Thr 625 Lys Pro Asn Cys Phe 630 Val Val His His Phe 635 Ala Gly Ser Val Glu 640

Tyr Cys Ser Asp 645 Gly Phe Leu Glu Lys Asn 650 Lys Asp Gln Leu Ser 655 Val

Asp Leu Gln 660 Glu Ala Val Lys Ala Ser 665 Thr Ile Pro Phe 670 Val Ser Asn

Leu Phe Ser 675 Ala Phe Leu Asn Arg 680 Gly Thr Ala Glu Asp 685 Gly Ser Gly

Lys Lys 690 Arg Lys Phe Val Thr 695 Val Ser Ser Glu Phe 700 Arg Glu Gln Leu

Gly 705 Ala Leu Met Glu Thr 710 Val Asp Lys Thr Ala 715 Pro His Phe Ile Arg 720

Cys Ile Lys Pro 725 Asn Pro Gln Asn Leu Pro 730 Asp Leu Phe Asp Arg 735 Ala

Thr Val Asn 740 Glu Gln Leu Arg Tyr Gly 745 Gly Val Leu Gln Ala 750 Val Gln

Val Ser Arg Ala Gly Tyr Pro Val Arg Leu Ser His Arg Asp Cys Phe

755

Phe Asp Tyr Arg Ala Leu Ala Asp Gly Ala Leu Ala Ala Gln Leu Ser  
770 775 780

Gln Gly Thr Glu Thr Pro Glu Ala Trp Arg Gly Arg Ala Glu Ala Leu  
785 790 795 800

Leu Arg His Leu Asp Glu Lys Leu Lys Leu Asp Arg Arg Lys Lys Glu  
805 810 815

Thr Asp Ser Pro Asp Arg Thr Trp Ala Val Gly Lys Thr Leu Cys Phe  
820 825 830

Phe Lys Asn Glu Ala Tyr Glu Ile Leu Ser Ala Asn Leu Met Ser Val  
835 840 845

Arg Val Ala Ala Ala Thr Ala Ile Glu Ala Arg Tyr Lys Cys Phe Val  
850 855 860

Gln Arg Arg Phe Phe Leu Met Tyr Arg Gln Thr Val Val Phe Leu Gln  
865 870 875 880

Ser His Ile Arg Met Phe Leu Cys Lys Leu Glu Ala Gln Arg Leu Arg  
885 890 895

Glu Ser Arg Ala Ala Arg Arg Val Glu Asn Phe Met Arg Gly Ala Val  
900 905 910

Ala Arg Leu Arg Tyr Leu Arg Thr Leu Glu Asn Ile Arg Arg Ile Gln  
915 920 925

Ala Ala Trp Arg Gly Lys Gln Thr Arg Ser Gln Leu Arg Asp Arg Lys  
930 935 940

Leu Glu Glu Ala Ala Ser Lys Ile Gln Ala Phe Trp Lys Met His Lys  
945 950 955 960

Gln Arg Met Phe Tyr Thr Asn Leu Lys Lys Ala Ser Thr Ile Ala Gln  
965 970 975

Leu Lys Trp Lys Arg Ile Leu Ala Arg Arg Met Leu Arg Arg Leu Arg  
980 985 990

Glu Glu Ala Arg Glu Val Ser Gly Leu Leu Lys Lys Ala Gln Asp Leu  
995 1000 1005

Gln Arg Asp Leu Cys Glu Glu Lys Asn Lys Arg Ser Asp Ala Glu  
1010 1015 1020

Ser His Val Leu Gln Leu Gln Ala Lys Asn Glu Asp Leu Leu Lys  
1025 1030 1035

N3027PCT\_sequ.list.txt

G u	I l e	G n	L y s	L e u	G n	A r g	G u	L e u	G u	A r g	A l a	L y s	G u	A s p
	1040					1045					1050			
V a l	A l a	S e r	L e u	G n	A l a	S e r	A s n	A s p	A s p	P h e	A l a	S e r	G n	V a l
	1055					1060					1065			
L y s	G n	L e u	L y s	G u	S e r	L e u	T h r	V a l	G y	S e r	S e r	T h r	P r o	T h r
	1070					1075					1080			
T h r	P r o	G n	M e t	T h r	P h e	G y	T h r	H i s	L y s	A r g	A r g	V a l	S e r	A s n
	1085					1090					1095			
A s n	A l a	A s p	V a l	P r o	H i s	S e r	G n	G u	L y s	A s p	L y s	P h e	P r o	T h r
	1100					1105					1110			
A s p	G u	G u	L e u	L y s	A l a	L e u	A r g	T h r	G u	L e u	G u	A r g	A r g	A s p
	1115					1120					1125			
A l a	G u	A l a	G n	G n	G n	G n	A l a	G u	H i s	G u	A l a	L e u	I l e	A l a
	1130					1135					1140			
G u	L e u	A r g	A l a	A l a	L e u	L y s	A s p	A l a	G u	S e r	A l a	C y s	G u	T y r
	1145					1150					1155			
G u	A r g	T h r	G n	A r g	L y s	G u	A l a	G u	A l a	A r g	T y r	A r g	L e u	V a l
	1160					1165					1170			
L e u	G u	A s p	S e r	S e r	A l a	S e r	S e r	T h r	H i s	V a l	A r g	A l a	S e r	S e r
	1175					1180					1185			
A l a	S e r	L y s	A l a	A l a	V a l	A l a	A s p	S e r	A l a	P r o	T h r	A l a	L e u	L e u
	1190					1195					1200			
A r g	G u	L y s	C y s	M e t	G u	S e r	A s p	M e t	A l a	T h r	G y	A r g	P r o	G y
	1205					1210					1215			
A s p	S e r	L e u	A l a	S e r	S e r	V a l	A l a	S e r	A l a	A l a	P r o	L e u	S e r	P r o
	1220					1225					1230			
P r o	V a l	A l a	L e u	G u	P r o	G u	L e u	T r p	G u	S e r	V a l	L e u	H i s	A s p
	1235					1240					1245			
G n	A r g	T r p	I l e	A s p	L e u	L e u	L e u	L e u	G y	P r o	A l a	G y	V a l	G y
	1250					1255					1260			
L y s	T h r	G y	L e u	L e u	G u	G n	P h e	L e u	V a l	L y s	L e u	G y	A s p	G u
	1265					1270					1275			
V a l	H i s	L e u	G u	G n	L e u	A r g	V a l	S e r	A r g	L y s	M e t	G u	A s p	G n
	1280					1285					1290			

N3027PCT\_sequ.list.txt

Ala	Pro	Phe	Ser	Lys	Leu	Pro	Gln	His	Tyr	Glu	Leu	Val	Tyr	Ser
	1295					1300					1305			
Pro	Asp	Ser	Gln	Glu	Gly	Arg	Glu	Arg	Glu	Glu	Ala	Arg	Val	Asn
	1310					1315					1320			
Val	Leu	Asp	Phe	Pro	Gly	Leu	Ser	Arg	Thr	Lys	Gln	Asn	Pro	Ala
	1325					1330					1335			
Leu	Arg	Val	Lys	Gln	Ala	Phe	Val	Val	Ala	Val	Val	Phe	Asp	Pro
	1340					1345					1350			
Thr	Arg	Pro	Glu	Thr	Cys	Ala	Glu	Ala	Leu	Gln	Ile	Leu	Thr	Asn
	1355					1360					1365			
Val	Val	Leu	Pro	Ala	Arg	Pro	Lys	Val	Ser	Ala	Gln	Asp	Pro	Leu
	1370					1375					1380			
Gly	Ala	Cys	Ile	Ser	Gly	Arg	Val	Tyr	Leu	Val	Glu	Asn	Gly	Trp
	1385					1390					1395			
Arg	Ala	Ala	Ala	Lys	Glu	Ala	Ala	Val	Gln	Val	Asp	Thr	Ala	Ala
	1400					1405					1410			
Val	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Arg	Cys	His	Tyr	Arg	Glu	Leu
	1415					1420					1425			
Val	His	Leu	Glu	Ser	Leu	Val	Asp	Glu	Ile	Val	Pro	Leu	Met	Ser
	1430					1435					1440			
Ser	Trp	Arg	Asp	Leu	Leu	Gln	Gln	Gln	Arg	Leu	Ala	Met	Leu	Gln
	1445					1450					1455			
His	His	Ala	Arg	Leu	Gln	Pro	Gly	Gly	Pro	Ser	Pro	His	Ala	Ser
	1460					1465					1470			
Pro	Phe	Ser	Leu	Pro	Arg	Ser	Gln	Thr	Gly	Arg	Gly	Ala	Ser	Leu
	1475					1480					1485			
Phe	Ala	Thr	Ala	Ser	Gln	Ser	Gly	Ala	Leu	Gly	Ala	Ser	Ala	Val
	1490					1495					1500			
Gly	Gly	Gln	Glu	Asn	Gly	Val	Glu	Lys	Ser	Ser	Ser	Gly	Val	Ser
	1505					1510					1515			
Ala	His	Arg	Gln	Gly	Gly	Leu	Ser	Ala	Asn	Phe	Phe	Asp	Ser	Ile
	1520					1525					1530			
Arg	Ser	Phe	Leu	Ser	Gln	Ser	Ser	Met	Arg	Pro	Ala	Gly	Asn	Val
	1535					1540					1545			

Leu Ala Ser Gly Lys Gln Ala Ala Asp Leu Lys Leu Leu Arg Pro  
 1550 1555 1560  
 Ser Met Lys Pro Gly Gly Thr Ala Met Met Lys Lys Leu Lys Thr  
 1565 1570 1575  
 Arg Ser Leu Asp Gln His Ser Val Val Pro Val Gln Glu Leu Gln  
 1580 1585 1590  
 Asp Ser Asp Ser Ala Ile Thr Cys Val Val Phe Gly Lys Glu Lys  
 1595 1600 1605  
 Glu Asn Arg Asp Tyr Ile Leu Leu Ala Ala Ala Ser Lys Asp Gly  
 1610 1615 1620  
 Ser Val Val Ile Tyr Arg Cys Tyr Arg Leu Glu Ala Glu Arg Gln  
 1625 1630 1635  
 Met Phe Asp Gln Glu Gln Val Ser Leu Val Thr Pro Ala Ala Ser  
 1640 1645 1650  
 Arg Thr Thr Asp Ser Lys Glu His Ile Gly Pro Ser Val Ser Val  
 1655 1660 1665  
 His Ser Arg Leu Val Gly His Ser Arg Ala Val Thr Cys Leu Phe  
 1670 1675 1680  
 Phe Ser Leu Leu Glu Asp Gln Leu Ile Thr Thr Ser Ile Asp Lys  
 1685 1690 1695  
 Ser Val Arg Phe Trp His Val Asp Thr Gly Asp Met Leu Lys Val  
 1700 1705 1710  
 Phe Thr Asp Ser Ser Pro Ala Leu Ala Ala Ala Phe Leu Pro Phe  
 1715 1720 1725  
 Asn Pro Thr Ala Phe Val Ala Ser Asn Ser Asn Ser Ile Leu Arg  
 1730 1735 1740  
 Leu Val Cys Ala Thr Ser Gly Arg Val Ile Gln Lys Leu Lys Val  
 1745 1750 1755  
 Glu Ser Glu Val Arg Ala Leu Lys Phe Asp Asp Thr Gly Leu Phe  
 1760 1765 1770  
 Cys Phe Ala Gly Thr Lys Ala Gly Ala Val His Val Leu Glu Ala  
 1775 1780 1785  
 Ser Asp Thr Val Asn Ile Arg Phe Lys Phe Lys Thr Ser Leu Gly  
 1790 1795 1800  
 Lys Gly Ala Val Thr Cys Ile Thr Phe Val Pro Ser Thr Gly Pro

1805

1810

1815

Gly Gln Tyr Pro Arg Leu Leu Ile Asn Cys Cys Asp Ser Ser Val  
1820 1825 1830

Ala Val Val Glu Cys Ile Tyr Gly Pro Pro Pro Gly Val Leu Thr  
1835 1840 1845

Asn Leu Leu Val Arg His Arg Val Arg Ile Ala His Ser Leu Leu  
1850 1855 1860

Pro Leu Arg Cys Trp Phe Ser Asn Phe Gly Gly Gly Trp Leu Ile  
1865 1870 1875

Thr Gly Ser Glu Asp Lys Asp Val Tyr Cys Phe Ser Leu Gln Gln  
1880 1885 1890

Gly Ala Asn Phe Lys Ala Ile Ser Leu Lys His His Gln Val Thr  
1895 1900 1905

Pro Glu Leu Thr Glu Ile Met Gly Pro Ser Ser Asn Phe Arg Asp  
1910 1915 1920

Ser Cys Phe Phe Phe Phe Thr Pro Phe Ile Phe Ser Leu Cys His  
1925 1930 1935

Phe Ser Gln Ser Val Phe Val Ser Leu Ser Leu Ile Cys Ile Gly  
1940 1945 1950

Phe Ser Pro Arg Ser Phe Pro Cys Leu Tyr Ser Val Phe Ser Leu  
1955 1960 1965

Cys Pro Leu Arg Tyr Val Cys Val Cys Leu Leu  
1970 1975

<210> 109  
<211> 12227  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(12227)  
<223> myosin VA heavy chain 12 myosin MYO5A

<400> 109  
accccgggca ggtggagcgc tgcgggctgc tgcgggcgag cccgggagtg atggcgaggc 60  
ccctgcgggc ggccagcgcc tgaggcgccc cgccccgcc cgccccgcgc ggccctcccc 120  
gcccggccct gccctgccct gctccctgcc ggcggctgcg ggcgcttcct agtccgctcg 180  
ggcggccgcc caggcgaggt gcggcctccg cacaggcggg gggcgtaggc gcgcggggcc 240  
cgccatggct gcgtcggagc tctacacaaa gt ttgccagg gt ttggat ac ctgatccaga 300

N3027PCT\_sequ. list . txt

ggaagt ct gg aagt cagcag agct gct caa agat t at aag ccaggagat a aagt cct cct	360
gct t cacct c gaggaaggaa aggat t t gga at accat ct a gat ccaaaga ccaaggagct	420
gcct cact t a cgaaat cct g acat act t gt t ggt gaaaat gacct cacag ccct cagct a	480
t ct t cat gag cct gct gt gc t ccat aat ct cagagt ccgc t t t at t gat t ccaaact t at	540
t t at acgt at t gt ggt at ag t cct agt agc t at aaat ccc t at gaacagc t gcct at t t a	600
t ggagaagat at t at t aat g cat acagt gg t cagaacat g ggt gat at gg at ccacat at	660
ct t t gcagt a gct gaagaag ct t acaagca aat ggccaga gat gaacgaa at cagt ccat	720
cat cgt aagt ggagagt ct g gggcaggaaa aacagt ct ca gct aagt at g ccat gcgat a	780
ct t t gcaact gt gagt ggt t ct gccagt ga ggccaat gt g gagggaaaagg t ct t ggcct c	840
caaccccat c at ggagt cca t t ggaaat gc t aaaacaacc aggaat gat a at agcagccg	900
t t t t gggaag t at at t gaga t t ggt t t t ga t aagagat at cgaat cat t g gt gccaat at	960
gagaact t at ct t t t agaga aat ccagagt ggt at t ccag gcagaagagg agagaaact a	1020
t cat at ct t c t at cagct t t gt gcct cagc aaagt t acct gaat t t aaaa t gct acgat t	1080
aggaaat gca gat aact t t a at t acacaaa acaaggaggc agt cct gt ga t t gaaggagt	1140
ggat gat gca aaggagat gg cacat act ag gcaggcct gc act t t gct ag gaat t agt ga	1200
at ct cat caa at gggaat t t t ccgaat act t gct ggcct c ct t cact t ag gcaat gt t gg	1260
at t t acat cc cgagat gcag acagct gcac aat acct ccc aagcat gaac ct ct ct gcct	1320
ct t ct gt gaa ct cat ggggt g t ggact at ga ggagat gt gt cact ggct ct gccat cggaa	1380
act ggct act gccacagaga cat acat caa gcccat ct cc aagct gcagg ccacaaat gc	1440
ccgcgat gct t t ggccaagc acat ct at gc caagct ct t t aact ggat t g t agat aat gt	1500
caat caggct ct ccat t ct g ct gt caaaca gcact ct t t t at t ggt gt gc t agacat t t a	1560
cggat t t gaa acat t t gaga t aaat agt t t t gaacagt t t t gcat aaat t at gcaaat ga	1620
aaaact acag caacaat t ca at at gcat gt ct t caaat t g gagcaagaag aat at at gaa	1680
ggaacaaat t ccat ggacac t cat agat t t t t at gat aat cagcct t gt a t t aat ct t at	1740
agaat caaaa ct aggcatt c t agat t t act ggat gaggaa t gcaagat gc ct aaaggcac	1800
agat gacacc t gggcccaaa aat t gt acaa cacacat t t g aacaaat gt g cact ct t t ga	1860
aaagcct cgt ct at caaaca aagct t t cat cat ccaacat t t t gct gaca aagt ggaat a	1920
ccagt gt gaa ggat t t ct cg aaaagaat aa agacaccgt t t t t gaagaac aaat t aaagt	1980
t ct t aaat ca agcaagt t t a agat gct acc agaact at t t caagat gat g agaaggccat	2040
cagt ccaact t cagccacct cct cagggcg cacaccct c acacgaact c ct gcaaagcc	2100
caccaaaggc agaccaggcc aaat ggccaa agagcacaag aaaacagt gg ggcat cagt t	2160
cagaaact cc ct gcacct gc t t at ggagac act caat gcc act accct c act at gt gcg	2220
ct gt at caag cct aat gact t caagt t ccc at t cacgt t t gat gagaaga gggcagt gca	2280
gcagct gaga gcat gt ggt g t cct ggaaac cat ccgaat c agt gcggccg gt t t cccct c	2340
acggt ggact t accaagaat t t t t cagccg ct accgt gt c ct aat gaagc agaaagat gt	2400

N3027PCT\_sequ. list . . txt

gct gagt gac	agaaagcaaa	cat gcaagaa	tgt gt t agag	aaact gat ac	t ggacaagga	2460
caaat accag	t t t ggt aaga	caaagat ct t	t t t ccgt gcc	ggg caagt gg	cct at ct aga	2520
aaaat t gaga	gct gacaaac	t gagagct gc	ct gcat ccgg	at ccagaaga	ccat ccgagg	2580
gt ggct gct g	agaaagaagt	acct acgcat	gcggaaggca	gccat cacca	t gcagagat a	2640
cgt gcggggc	t accaggccc	gat gct at gc	t aagt t t ct g	cgcagaacca	aggcagcaac	2700
cat cat t caa	aagt act ggc	gcat gt at gt	ggg ccgcagg	aggt acaaga	t t agacgagc	2760
t gccact at c	gt t ct t cagt	ct t act t gcg	aggct t ct t g	gccagaaat a	ggg at cgcaa	2820
gat act ccgt	gagcaciaag	cagt cat cat	t cagaagcga	gt ccggggct	ggct ggcccg	2880
cacacact ac	aagaggagca	t gcat gccat	cat ct acct t	cagt gct gct	t caggcggat	2940
gat ggccaag	cgt gagct aa	agaagct caa	aat cgaggct	cgct cagt gg	agcgct at aa	3000
gaagct gcac	at cggcat gg	agaacaagat	cat gcagct g	cagcgcaaag	t t gat gagca	3060
gaacaaagac	t acaaat gcc	t t gt ggagaa	act aaccaat	ct ggaaggaa	t at acaact c	3120
t gagact gag	aaact acgaa	gt gact t aga	acgt ct t caa	ct aagt gaag	aggaagcgaa	3180
agt t gccact	gggcgggt cc	t t agt ct gca	ggaagaaat t	gccaagct cc	ggaaagacct	3240
ggagcaaact	cgt t cagaga	aaaaat gcat	t gaggaacat	gcagat cgat	acaaacaaga	3300
aacagagcag	ct ggt at caa	at ct gaagga	agaaaat act	t t gct gaagc	aagaaaaaga	3360
agccct caat	caccgcat cg	t gcagcaggc	t aaggagat g	acagaaact a	t ggagaagaa	3420
gt t agt agaa	gaaacgaaac	aact ggaact	cgacct t aat	gat gaaaggc	t gagat at ca	3480
gaacct t ct g	aat gagt t ca	gt cgcct gga	agaaagat at	gat gacct ca	aggaagagat	3540
gaccct t at g	gt gcat gt gc	ct aagcct gg	acacaagaga	acagact cca	cccacagcag	3600
caacgagt ct	gaat at at ct	t t agct ct ga	aat t gcagaa	at ggaagaca	t t ccat caag	3660
gacagaggaa	ccaagt gaga	agaaggt acc	t ct ggacat g	t cat t gt t cc	t t aagct cca	3720
gaagcgggt c	acagagct gg	agcaggagaa	gcaggt gat g	caggat gagc	t ggaccgcaa	3780
ggaggagcag	gt gct ccgca	gcaaggccaa	ggaagaagaa	agaccacaaa	t t agaggt gc	3840
agaact ggaa	t at gagt cac	t caagcgt ca	agaact agaa	t cagaaaaca	aaaaact gaa	3900
gaat gagct a	aat gagt t gc	gcaaggccct	cagt gagaaa	agt gccccag	aggt gaccgc	3960
cccaggt gca	cct gcct acc	gt gt cct cat	ggagcagct g	acct ct gt ga	gcgaggagct	4020
t gat gt ccgc	aaggaggaag	t cct cat ct t	aagggt ct caa	ct ggt gagcc	agaaagaggc	4080
cat ccaaccc	aaggat gaca	agaat acaat	gacagat t cc	acaat act t t	t ggaagat gt	4140
acaaaaaat g	aaagat aaag	gt gaaat agc	acaagcat ac	at t ggt t t ga	aagaaacaaa	4200
t agat cat ct	gct ct ggat t	accat gagt t	gaat gaggat	ggagagct gt	ggct ggt t t a	4260
t gaaggggt t a	aaacaagcca	acaggct cct	ggaat cccag	ct gcagt cac	agaagaggag	4320
ccat gagaat	gaggccgagg	ccct ccgt gg	ggagat ccag	agcct gaagg	aggagaacaa	4380
ccgacagcag	cagct gct gg	cccagaacct	gcagct gccc	ccagaggccc	gcat t gaggc	4440

N3027PCT\_sequ. list.txt

cagcctgcag caccgagatca cccggctgac caacgaaaac ttggatttga t ggaacaact	4500
t gaaaaacag gat aagacgg tccgt aaact gaaaaaaciaa ct gaaagt at ttgccaaaaa	4560
aat tggcgaa ct agaagt gg gccagat gga gaacat at cc ccaggacaga t cat t gat ga	4620
acccat ccga ccagt caaca ttcccaggaa agaaaaggat ttccaaggga t gct ggaat a	4680
caagaaggag gat gagcaaa aact t gtt aa gaacct gat t ct ggaact ga agccacgt gg	4740
tgt agcagtc aat tt gat t c caggat t acc ggcat at at c ctgt t cat gt gtgt t cgaca	4800
t gct gact ac ct gaat gat g at cagaaagt aagggt cgt t g ct aacat caa caat t aacag	4860
cat caaaaaa gt at t gaaga aaagagggt ga t gat t t t gaa accgt ct cct t ct ggct ct c	4920
t aacacat gc cgat t t t t gc act gct t gaa acagt acagt ggagaagagg gct t t at gaa	4980
gcacaacaca t ct cgccaga at gaacact g cct caccaat t t t gacct gg ct gagt at cg	5040
gcagggt gct g agt gact t gg ccat t cagat ct accagcag ct cgt gcggg t gt t agagaa	5100
cat cct t cag ccaat gat t g t ct caggcat gct ggaacat gaaacgat t c agggcgt gt c	5160
t ggggt gaag cccacagggt t gagaaagcg aacct ccagt at cgccgat g agggcacct a	5220
cacact ggac t ccat cct cc ggagct caa ct cct t ccac t cggt cat gt gt cagcat gg	5280
cat ggaccct gaact gat ca agcagggt ggt caagcagat g t t ct acat ca t aggggccat	5340
caccct gaac aacct t ct cc t gcggaagga cat gt gct cc t ggagt aaag gcat gcagat	5400
cagggt acaat gt cagt caac t ggaagaat g gct gcgt gac aagaat ct ga t gaat agt gg	5460
ggct aaagaa accct ggaac ct ct cat t ca ggct gct caa ct t t t gcaag t gaaaaagaa	5520
aacagat gat gat gcagaag ccat t t gtt c t at gt gcaat gct t t aact a ct gccagat	5580
tgt gaaagt g tt gaat t t gt at act ccagt t aat gagt t t gaagaaagag t ct ct gt gt c	5640
gt t cat t cgt act at acaga t gcgt t t acg agacaggaaa gact ct cccc agct gct cat	5700
ggat gct aaa cacat ct t t c ctgt cacct t t cct t t caac ccat ct t ccc t cgcact aga	5760
aacat ccag at t ccagcca gcct cggcct gggct t cat t t cacgggt ct gaaagt gat g	5820
t ccaggcaaa aat t gacaat acat t t ct t g cccgaaat aa gaacccat t a t t t ccagt ga	5880
gt t act gaaa at acat t t t t aaagagaaag t act gat t at ct cccaaat g agaagt cat t	5940
aact ggaaat ct cct agaa t act t t cat c act t t ggaaa caaagat agg ct ct t t cgt g	6000
ct gt gt t at c t t t at agcaa cact cat cct t aaccaact a ggt accgt ga gt t t acat ac	6060
aggagaat ga t ggaaggaag ggaggaagga aaggaggaga aaaat gt gt c t t cagct ggc	6120
agcat t t at t t t aaat cct t agcact gagt t t gaat ggt a t aaaaagt at aact t ccat a	6180
gat gagct gt t gt t aggaag gcaccaaaga acct cct ct g cact aaacag gagaat ggaa	6240
agaaaagt ct ccat t gagt a cat at cat gt cagt t t agt a at caat t at g t t gat at t gt	6300
t aaact ggt t caaagaaat a aact ggcaat at gt aaagt a at t cct cat t t gt gt cact a	6360
t gat at agag at at t aaagg aat gt t ggt t t gct aaat ag t at agat gt c cat t t gt act	6420
at agt t t act gagcat t t t a aat t gct gct acat act gt c t t ct t aaaat gt aagt gat a	6480
t t aggcact a caat aagt t t ct ct t gt caa t t ct gt t t ac aat t caat ca gat cacagt t	6540

N3027PCT\_sequ.list.txt

t t aact ggat	t at at gcaaa	t acct acaga	t t cacct gca	caagt agcag	acact ggaaa	6600
gt cat gt agt	aat at gacaa	aat gct t gac	at t t aggggt	aggat t agac	aaagt ggct a	6660
t t gt t gat gt	cat t at t t at	t caggat gt a	t t acat t gat	gt gct cat t a	at t t t ccct g	6720
ggg ggat at t	gcgt cagggt	acagt gt t ct	gt gaagt gac	t t at t t t t aa	ct accagat c	6780
t gat t cct t c	agt gcat at t	t t caacct t g	acagggt t t t c	t ct ct t ct t a	at t t at t aag	6840
aat t aat ct c	ggct gggcgc	ggg ggct cac	gcct gt aat c	ccagcact t t	gggaagccaa	6900
ggg gggcggg	t cact t cagg	t t aggagt t g	gagaccagcc	t ggccaacat	ggcgaaaccc	6960
t gt ct ct act	aaaaat acaa	aaat t agccg	ggcgt ggt gg	cact t gcct g	t aat cccagc	7020
t act cgggag	gct gaggcac	gagaat cgat	t aaacct ggg	aggcggagat	t gcaat gaga	7080
t cgaaccact	gcact ccagc	ct ggggt gaca	gagagagaca	ct gcct t gga	aaaaaaaaaga	7140
at ct cact ca	ct at ct agag	aggat t gt ca	gaat at t cac	gat t caggt c	t t gaaact t t	7200
gat t at gcaa	aagaaggt at	at aat aaat a	t t t cat t at g	at t cagt t t t	t aaggct t t g	7260
cagct t ct at	aagt gt t ct c	agat gccact	agat aat t t t	aaaagcat ca	t at t agaaat	7320
act t t aagaa	gact t at at a	agaaat agaa	gat t gt t gaa	t t t t acagag	gat t t ggt t c	7380
at t aagaccc	agat t ct gt a	agt t t t cat t	ct gaaat t ct	agt t aaacat	at t caccat t	7440
t t t ct t agga	at ct t at aca	at aaat cct t	cagggt t gcac	aaaagcaa	t at t agt t t t	7500
cat t agaaac	t ct ggt t ct g	aat t acaat c	at aggt t at a	t aaat t t aac	t gt t agat gg	7560
t ct at aaat c	t t at t aaaa	at gt gcaat a	t t t at ggaag	t caaacagct	t cat at cagt	7620
gat aaagat t	gt t at t aaaa	gat aaat act	gt ct gt t aat	t t acat gggc	ct caagt t cc	7680
t cgt t t at aa	aat aagagag	t t ggacact g	at t ct t aaca	t ct cct ccac	at t t aaaaat t	7740
ct ct ct t ct c	agccct t aga	t t ct agagag	aaaaagct gc	agt t act cag	t aagt ccat t	7800
ct ct gat gga	aagaccagt g	t gt agt gcct	gt caat t cct	t aggat t aat	caaat gt aaa	7860
at cacaagt t	t gt gt agct g	t aacct t t ct	t aaat gt aca	t gat t t at gt	acat gct t t t	7920
agaaggt cct	act at at t t g	t at t at aat t	agt t t aagt a	at t t t t at t a	cat cat gt at	7980
t gct t t at t c	agt t t gaat a	cat t t at t t a	t t t at t t gca	gt at caacca	gaaacact ac	8040
caat t gcat c	aaat t ct ccc	agt t t t t cct	ggg t gt caat	gcggt t t t ca	at gcacaat t	8100
aagt cat agc	cat t t ggt t c	gt accaaat g	t gt cagaat c	t aacagcat c	cgat aggct g	8160
t aagt t gggg	agt t gct aag	aaaat gcaac	gt ggt acagg	ct gt ccgcct	cagccct gga	8220
aat ct cccag	acct ccccca	gct t cat cct	gt gt agcacg	act caacgt g	caccct gaat	8280
ct t ct caggt	ct t ccaggt c	at gct gt agc	t gt cact gcc	at gcagccct	t t t t t t t act	8340
ccggacagct	cat gt act ga	agcgt cat ga	aagaaaggct	gt ggt ct gag	ccct t ct ct c	8400
ccat ct cct g	t ct t t gt cct	gt caagt gct	ggagccagag	ct cct acagc	t gccct t ggt	8460
ggg t t ct cct	gt t cagcgat	ggg ggcacaa	aggt t ct gct	at t ccagggc	t ccagct t cc	8520
t cccaggt ct	accagagct	ccagat gggg	gt ct gaat t a	acct ct ct t g	gt ggcct gga	8580

N3027PCT\_sequ. list.txt

gat t t t t agt	cat t gacaag	aat acct t gt	aaccagggaa	ccccaaggcc	cagt aaat ga	8640
t t ct gt at ac	cat t t t ct t g	aaggt acaag	aagat t ct gc	cgact at ggg	gat ct t t ggg	8700
ccag t t t gag	gat t gct t t c	cct ct gaggt	t ct t t ct ct c	t gt cagccac	act t t ct cac	8760
ccaact t cag	acacaccct g	ccagcct t t c	ccct act cat	t cact ct t cc	cct t ccct ca	8820
act t aat cgt	ct at cccgt t	gcct gct gt t	t gact gt gca	ct gaaggcag	gt ggat ggag	8880
t cagt cct ca	gt t gccct g	ct ggcct t cc	t ggt gct t ac	cat cagccca	at ct t t gcac	8940
agt cct t gt t	gt t ct t act t	ct ct gcat gc	at t cct t cag	aagat cagt c	at caact t t t	9000
t ct t aat t cc	t ct gt gacac	acaat gggaa	t t caaaggaa	gagat ct t aa	aagt cacaac	9060
agt t ct t t at	ct t aat aat c	ccct ccccat	t cacct t act	acat gcagac	t cacct caca	9120
ccct t acaac	t t gaagct ga	aaat t t aaaa	gt aat t t ccc	t t t t t gcagc	t t t t cct cag	9180
gt t aaggct t	t gat ct gcct	gagagt aact	ct aaaaggag	ggaagat aaa	t at gggat aa	9240
aat ccacaaa	gt gt agct t c	t aat t cct t t	ggaagt t t aa	aaaat t t cca	cat at ct gat	9300
gct t ct t t t g	t caggt gcag	aagcacaaaa	acat at t ccg	aagccaact g	at agggaat t	9360
t ggggat t at	t gt cagt t t g	gagaat t t gc	t gt gt t at t t	ct t cat t t cc	at ggat agct	9420
cat agt t ggc	t ct t t ct ggg	t gagt aat t a	t gt gt aat at	agat caaat c	t t t t act aag	9480
gt t acagct a	cat gt t aggg	gaggct at ga	aaat act at a	t t at t at aat	t t cagt gcag	9540
t gat t gt t gt	gagaaat aac	t t t cat ggt a	accct aggaa	aat gggcacc	t gccacat c	9600
ct gagaagt c	ct cacacaat	gccct t t ct c	t ct t acacac	acacacacac	acat acacac	9660
acacacacccc	ccgt cact aa	t t cat agagt	t cct t agcag	gcat agt caa	ggat cct ct g	9720
ggg aat gt ca	gct gct t agt	gat aaaacag	agccaaaact	agt gcat cct	gt t gaaagt a	9780
at gcagaaac	agt acct ggg	t ccagat at g	ct t t cct gcg	gcgct t t cct	ct gt t acct c	9840
gt t t cat cct	cacagcagca	t ggacggg ag	gt ggggt cgc	t t ct acaat c	at t t ct gat g	9900
at agct t ggg	aat agagat a	ggggcagt ga	ct t gcct gat	gt cgcacagc	cct ct ggct g	9960
t cct gct t t c	ccat at ggag	cagt ggt ggt	gt gggcacct	gt gat gcagg	agact t t aaa	10020
aat gt cgt ga	ggg cagct gc	t gcccct cct	ggg acgt gt g	gaat gccct	ggccagcaag	10080
gggt gct t t t	t t at cagagt	t ggcagct gg	cat gt gggaa	ccgagcaagt	gct gcgt acc	10140
aagt t act t g	t t t t aaggag	accaagt gct	cagcgccagg	t ggt t t t ct t	t t t t gt cat a	10200
gt t act t gct	at aact cagc	t t gact t ct g	t cat gaat ca	gt gct ct ct g	ggaggat gca	10260
at act ct gt t	t gggcat t aa	t t ggt agcag	gt t gt ct caa	ccaaaaagac	aggaaacagc	10320
aaaagcct ct	ct gaaat t aa	gaggaaagt t	act ct cccca	cacccat cag	agt ct t t at t	10380
ggagccacca	ggg gagct gt	gcagcct gga	caggcct gca	gct at aggcc	acct t cccag	10440
t t t aggt cct	cagcacaggg	gagcccaagt	cact ggggt gc	ct t ccgaggg	ct gt cact gg	10500
gcaggccat a	t acaagt cag	t gt gt gcgt g	ggcact gcag	t gt gt gcat g	ccgt aggt gt	10560
t gat ggggt gc	t aggaggggt	gt cgt gt gca	t gcgcgt t ga	agaggat ct g	t at t gccgt g	10620
acct ct gt t c	at ggat gagt	gcat t gt aat	t t gt t ct cag	gct gt gct gt	gagggccgcc	10680

N3027PCT\_sequ.list.txt

t t a a c c c t t g	c t c c c t t c c c	t t c t a g a g c t	g c c t t a a g t t	c t c c a g a a c t	t t t c t t c t g t	10740
a a a g g a t a t c	t t g c c t g g a a	g g g a t a t c t t	g c c c t g t t t c	t c a a g g t t t t	g t g a g a g t t t	10800
t g a c t g g a t g	t g g c c c t g c a	t g a c c c t c c t	t c t c c t g t a c	t t c c t c t t t c	c t t t c c a a a t	10860
g g g a a t t a g a	a c t g t g g g g c	a g c a a c a g t c	t c a g a g c c a g	t g a g a g g c c a	g c t t a g a g a a	10920
t g c t t c t g a g	t t a g t g g g a c	t c t g t g t c a c	a a g t a a g c a a	a t g a a t a t a t	g a a a g a a a t t	10980
a t g g a g a t a a	g t t a g a t t c t	t g g t a a t a c t	t a a a t g t c t t	g c t t t c t a c t	a a c c t t t t g t	11040
t a c t a a a g g t	a a a g g g t a t a	a c t c a a a c t t	t t t g t g g a c a	t t c t t t t c a a	a a t t t t t t a a	11100
g a a c c c t g t a	c t a t a a a a g g	t t g a g t a a a a	a c a g g a a a g c	g t g c t a t a a g	t t c a a a t c t g	11160
t t g t a t t a c c	c t a a a t t a g a	t a a a c c a a c c	t g a a t t a t a g	t a g a t t t c t c	a a t a g a t g a g	11220
g a a c t g a a a a	a t a c t a t g t a	a a a t a t c t t c	c a a a a t g c t t	t t t a t a c t t t	t t t t a t t t g t	11280
a a t t t g g t c t	a t c t a a a a t g	t t c g t t a g c t	t a a c t t a a t g	g g c g t t a t t g	g a t t c a t a t g	11340
a c t a a c g t t t	c c t c a g t a t t	g t a a t g c t t g	a a a t a t t t g a	a a g a a a a a a t	g t t g t t t t t t	11400
a g t t g a a a c t	g g t a t a t a t a	a t t c a g t g c t	t g g c a g g t t a	g t a t a t t t t t	a t g c a t t t t t	11460
c a g a g t c a g c	a g t t t c a a a t	c t t a t t g t t a	t c a t g t t a t a	a a a t t t t a g c	c c a c a t t t c a	11520
g g c t c c g t a a	a t c a t t t g a g	c c a t t a t t t t	t t c c c a a c a a	a t g g t g a a t t	t t t t c t t t a a	11580
a t g t g g a t a t	a t a t g t t g t a	a t t t a t g a t t	c c t g g t t a t g	t a t t t t t g t g	g g a t c c t g c a	11640
g t a a a a t t g a	c t t t t t t g t g	t c t t t g g g a g	a t t t a a a t t g	c g c t a a c a g t	g t t g c g c a a a	11700
a a t g a g t t c a	t g c c a t t t a a	c a t a t t g t a t	t t t a a t t a t t	a a c t g t a t t a	a t t t a c t a t g	11760
a a a t g g a c a t	c c t t t t a a c t	a a a a t g g a a t	t g a a c a t t g c	a g t t t t c a a a	t a t t t t t c c t	11820
t g t t g g g t c t	g g a a a a g g a a	t t c t a c t t t g	a t c t g c a t a g	a a a a t t t t g a	t a c a a t t t t t	11880
t g a a a g t t c t	t a g g t g a a a c	a t t t a c c c a t	t a a a a a g g a a	g c a g a a a t a c	t g a g a c a t g a	11940
a a g g c a t t a t	c a a c t a a c t c	t a g a c t c t a g	a a c c c a t t c t	a g c a t a t c t c	a c g t g c a a t t	12000
t t t a a a a a t a	a g t t a a t a a t	t c a t c t c a t a	t c a a c a a a a g	c c t t t g a a a c	a t g g g t t t t c	12060
a c t a g a t a t c	a c c t a g t g c t	a a g a t a a a a a	c c a a a a c a a t	a t c a g a a t t a	c a t t t a t g c t	12120
c t a a a t t t g t	a g t t g t c c a t	t g t t g t g c t t	a g t a a a t g t g	t g t c a t t a a t	g c t g t a t t c t	12180
c c t a g c t a t t	a t g g a a a c t t	g t t t a a a t a a	a g a t a t g g a t	a t a a a g a		12227