

35259127- seq1 - 000001  
SEQUENCE LISTING

<110> Prince Henry's Institute of Medical Research trading as the Hudson Institute of Medical Research

<120> Inhibin analogs

<130> 35259127/EJH

<150> AU 2015904898

<151> 2015-11-26

<160> 44

<170> Patent In version 3.5

<210> 1

<211> 1281

<212> DNA

<213> artificial

<220>

<223> Nucleotide sequence encoding wild type human inhibin betaA-subunit

<400> 1

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gccgccct cc caaaggat gt acccaact ct cagccagaga t ggt ggaggc cgt caagaag	180
cacat t t t aa acat gct gca ct t gaagaag agacccgat g t caccagcc ggt acccaag	240
gcggcgct t c t gaacgcgat cagaaagct t cat gt gggca aagt cgggga gaacgggt at	300
gt ggagat ag aggat gacat t ggaaggagg gcagaaat ga at gaact t at ggagcagacc	360
t cggagat ca t cacgt t t gc cgagt cagga acagccagga agacgt gca ct t cgagat t	420
t ccaaggaag gcagt gacct gt cagt ggt g gagcgt gcag aagt ct ggct ct t cct aaaa	480
gt cccaagg ccaacaggac caggaccaa gt caccat cc gcct ct t cca gcagcagaag	540
caccgcgagg gcagct t gga cacaggggaa gaggccgagg aagt gggct t aaagggggag	600
aggagt gaac t gt t gct ct c t gaaaaagt a gt agacgct c ggaagagcac ct ggcat gt c	660
t t ccct gt ct ccagcagcat ccagcgg t g ct ggaccagg gcaagagct c cct ggacgt t	720
cggat t gcct gt gagcagt g ccaggagagt ggcgccagct t ggt t ct cct gggcaagaag	780
aagaagaaaag aagaggaggg ggaagggaaa aagaagggcg gaggt gaagg t ggggcagga	840
gcagat gagg aaaaggagca gt cgcacaga cct t t cct ca t gct gcaggc ccggcagt ct	900
gaagaccacc ct cat cgccg gcgt cggcgg ggct t ggagt gt gat ggcaa ggt caacat c	960
t gct gt aaga aacagt t ct t t gt cagt t t c aaggacat cg gct ggaat ga ct ggat cat t	1020
gct ccct ct g gct at cat gc caact act gc gagggt gagt gcccagacca t at agcaggc	1080
acgt ccgggt cct cact gt c ct t ccact ca acagt cat ca accact accg cat gcggggc	1140
cat agcccct t t gccaacct caaat cgt gc t gt gt gccca ccaagct gag acccat gt cc	1200
at gt t gt act at gat gat gg t caaaacat c at caaaaagg acat t cagaa cat gat cgt g	1260

gaggagt gt g ggt gct cat a g

<210> 2  
 <211> 426  
 <212> PRT  
 <213> artificial

&lt;220&gt;

&lt;223&gt; Amino acid sequence of wild type human inhibin betaA-subunit

&lt;400&gt; 2

Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
 1 5 10 15

Ile Val Arg Ser Ser Pro Thr Pro Gly Ser Glu Gly His Ser Ala Ala  
 20 25 30

Pro Asp Cys Pro Ser Cys Ala Leu Ala Ala Leu Pro Lys Asp Val Pro  
 35 40 45

Asn Ser Gln Pro Glu Met Val Glu Ala Val Lys Lys His Ile Leu Asn  
 50 55 60

Met Leu His Leu Lys Lys Arg Pro Asp Val Thr Gln Pro Val Pro Lys  
 65 70 75 80

Ala Ala Leu Leu Asn Ala Ile Arg Lys Leu His Val Gly Lys Val Gly  
 85 90 95

Glu Asn Gly Tyr Val Glu Ile Glu Asp Asp Ile Gly Arg Arg Ala Glu  
 100 105 110

Met Asn Glu Leu Met Glu Gln Thr Ser Glu Ile Ile Thr Phe Ala Glu  
 115 120 125

Ser Gly Thr Ala Arg Lys Thr Leu His Phe Glu Ile Ser Lys Glu Gly  
 130 135 140

Ser Asp Leu Ser Val Val Glu Arg Ala Glu Val Trp Leu Phe Leu Lys  
 145 150 155 160

Val Pro Lys Ala Asn Arg Thr Arg Thr Lys Val Thr Ile Arg Leu Phe  
 165 170 175

Gln Gln Gln Lys His Pro Gln Gly Ser Leu Asp Thr Gly Glu Glu Ala  
 180 185 190

Glu Glu Val Gly Leu Lys Gly Glu Arg Ser Glu Leu Leu Leu Ser Glu  
 195 200 205

Lys Val Val Asp Ala Arg Lys Ser Thr Trp His Val Phe Pro Val Ser  
 210 215 220

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Ser Ser Ile Gln Arg Leu Leu Asp Gln Gly Lys Ser Ser Leu Asp Val  
225 230 235 240

Arg Ile Ala Cys Glu Gln Cys Gln Glu Ser Gly Ala Ser Leu Val Leu  
245 250 255

Leu Gly Lys Lys Lys Lys Lys Glu Glu Glu Gly Glu Gly Lys Lys Lys  
260 265 270

Gly Gly Gly Glu Gly Gly Ala Gly Ala Asp Glu Glu Lys Glu Gln Ser  
275 280 285

His Arg Pro Phe Leu Met Leu Gln Ala Arg Gln Ser Glu Asp His Pro  
290 295 300

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile  
305 310 315 320

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn  
325 330 335

Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly  
340 345 350

Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe  
355 360 365

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe  
370 375 380

Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser  
385 390 395 400

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln  
405 410 415

Asn Met Ile Val Glu Glu Cys Gly Cys Ser  
420 425

<210> 3

<211> 1323

<212> DNA

<213> artificial

<220>

<223> Nucleotide sequence encoding super-cut variant of human inhibin  
betaA-subunit with FLAG tag

<400> 3

atgcccttgc tttggctgag aggatttctg ttggcaagtt gctggattat agtgaggagt 60

gactacaaag acgacgacga caaatcccc accccaggat ccgaggggca cagcgcggcc 120

cccgactgtc cgtcctgtgc gctggccgcc ctcccaaagg atgtacccaa ctctcagcca 180

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gagat ggt gg aggccgt caa gaagcacat t t t aaacat gc t gcact t gaa gaagagaccc 240  
gat gt ccccc agccggg acc caaggcggcg ct t ct gaacg cgat cagaaa gct t cat gt g 300  
ggcaaagt cg gggagaacgg gt at gt ggag at agaggat g acat t ggaag gagggcagaa 360  
at gaat gaac t t at ggagca gacct cggag at cat cacgt t t gccgagt c aggaacagcc 420  
aggaagacgc t gcact t cga gat t t ccaag gaaggcagt g acct gt cagt ggt ggagcgt 480  
gcagaagt ct ggct ct t cct aaaagt cccc aaggccaaca ggaccaggac caaagt cacc 540  
at ccgcct ct t ccagcagca gaagcaccgg cagggcagct t ggacacagg ggaagaggcc 600  
gaggaagt gg gct t aaaggg ggagaggagt gaact gt t gc t ct ct gaaaa agt agt agac 660  
gct cggaaga gcacct ggca t gt ct t ccct gt ct ccagca gcat ccagcg gt t gct ggac 720  
cagggcaaga gct ccct gga cgt t cggat t gcct gt gagc agt gccagga gagt ggcgcc 780  
agct t ggt t c t cct gggcaa gaagaagaag aaagaagagg agggggaagg gaaaaagaag 840  
ggcggaggt g aaggt ggggc aggagcagat gaggaaaagg agcagt cgca cagacct t t c 900  
ct cat gct gc agggccggca gt ct gaagac caccct cat a t ct cat cgag aaagaaacgc 960  
t cagt ct cat cgggct t gga gt gt gat ggc aaggt caaca t ct gct gt aa gaaacagt t c 1020  
t t t gt cagt t t caaggacat cggct ggaat gact ggat ca t t gct ccct c t ggct at cat 1080  
gccaact act gcgagggt ga gt gcccagac cat at agcag gcacgt ccgg gt cct cact g 1140  
t cct t ccact caacagt cat caaccact ac cgcat gcggg gccat agccc ct t t gccaac 1200  
ct caaat cgt gct gt gt gcc caccaagct g agacccat gt ccat gt t gt a ct at gat gat 1260  
ggc caaaaca t cat caaaaa ggacat t cag aacgcgat cg t ggaggagt g t gggg gct ca 1320  
t ag 1323

<210> 4  
<211> 440  
<212> PRT  
<213> a r t i f i c i a l

<220>  
<223> Amino acid sequence of super-cut variant of inhibin betaA-subunit with FLAG tag

<400> 4

Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
1 5 10 15

Ile Val Arg Ser Asp Tyr Lys Asp Asp Asp Lys Ser Pro Thr Pro  
20 25 30

Gly Ser Glu Gly His Ser Ala Ala Pro Asp Cys Pro Ser Cys Ala Leu  
35 40 45

Ala Ala Leu Pro Lys Asp Val Pro Asn Ser Glu Pro Glu Met Val Glu  
50 55 60

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Ala Val Lys Lys His Ile Leu Asn Met Leu His Leu Lys Lys Arg Pro  
 65 70 75 80  
 Asp Val Thr Gln Pro Val Pro Lys Ala Ala Leu Leu Asn Ala Ile Arg  
 85 90 95  
 Lys Leu His Val Gly Lys Val Gly Glu Asn Gly Tyr Val Glu Ile Glu  
 100 105 110  
 Asp Asp Ile Gly Arg Arg Ala Glu Met Asn Glu Leu Met Glu Gln Thr  
 115 120 125  
 Ser Glu Ile Ile Thr Phe Ala Glu Ser Gly Thr Ala Arg Lys Thr Leu  
 130 135 140  
 His Phe Glu Ile Ser Lys Glu Gly Ser Asp Leu Ser Val Val Glu Arg  
 145 150 155 160  
 Ala Glu Val Trp Leu Phe Leu Lys Val Pro Lys Ala Asn Arg Thr Arg  
 165 170 175  
 Thr Lys Val Thr Ile Arg Leu Phe Gln Gln Gln Lys His Pro Gln Gly  
 180 185 190  
 Ser Leu Asp Thr Gly Glu Glu Ala Glu Glu Val Gly Leu Lys Gly Glu  
 195 200 205  
 Arg Ser Glu Leu Leu Leu Ser Glu Lys Val Val Asp Ala Arg Lys Ser  
 210 215 220  
 Thr Trp His Val Phe Pro Val Ser Ser Ser Ile Gln Arg Leu Leu Asp  
 225 230 235 240  
 Gln Gly Lys Ser Ser Leu Asp Val Arg Ile Ala Cys Glu Gln Cys Gln  
 245 250 255  
 Glu Ser Gly Ala Ser Leu Val Leu Leu Gly Lys Lys Lys Lys Lys Glu  
 260 265 270  
 Glu Glu Gly Glu Gly Lys Lys Lys Gly Gly Gly Glu Gly Gly Ala Gly  
 275 280 285  
 Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu Gln  
 290 295 300  
 Ala Arg Gln Ser Glu Asp His Pro His Ile Ser Ser Arg Lys Lys Arg  
 305 310 315 320  
 Ser Val Ser Ser Gly Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys  
 325 330 335

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Lys Lys Gl n Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp  
340 345 350

Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Gl u Gl y Gl u Cys  
355 360 365

Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser  
370 375 380

Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn  
385 390 395 400

Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met Leu  
405 410 415

Tyr Tyr Asp Asp Gly Gl n Asn Ile Ile Lys Lys Asp Ile Gl n Asn Ala  
420 425 430

Ile Val Gl u Gl u Cys Gly Cys Ser  
435 440

<210> 5  
<211> 1101  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding wild type human inhibin  
alpha-subunit

<400> 5  
at ggt gct gc acct act gct ct t ct t gct g ct gacccac agggg gggca cagct gccag 60  
gggct ggagc tggcccggga act t gt t ct g gccaaagg ga gggccct gt t ct t ggat gcc 120  
t t ggggcccc ccgcggg gac caggggaagg ggggaccct g gagt caggcg gct gccccga 180  
agacat gccc tgggggggct t cacacacagg ggct ct gaggc cggaggaaga ggaggat gt c 240  
t cccaagcca t cct t t t ccc agccacagat gccagct gt g aggacaagt c agct gccaga 300  
gggct ggccc aggaggct ga ggagggcct c t t cagat aca t gt t ccggcc at cccagcat 360  
acacgcagcc gccagg gac t t cagcccag ct gt ggt t cc acaccgggct ggacaggcag 420  
ggcacagcag cct ccaat ag ct ct gagccc ct gct aggcc t gct ggcact gt caccggga 480  
ggacccgt gg ct gt gccat gt ct t t gggc cat gct cccc ct cact gggc cgt gct gcac 540  
ct ggccacct ct gct ct ct c t ct gct gacc caccctgt cc t ggt gct gct gct ggcgt gt 600  
cccct ct gt a cct gct cagc ccggcct gag gccacgccct t cct ggt ggc ccacact cgg 660  
accagaccac ccagt ggagg ggagagagcc cgacgct caa ct cccct gat gt cct ggcct 720  
t ggt ct ccct ct gct ct gcg cct gct gcag aggcct ccgg aggaaccggc t gccat gcc 780  
aact gccaca gagt agcact gaacat ct cc t t ccaggagc t gggct ggga acggt ggat c 840  
gt gt accct c ccagt t t cat ct t ccact ac t gt cat ggt g gt t gt gggct gcacat ccca 900

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ccaaacctgt cccttccagt ccctggggct cccctaccc cagcccagcc ctactccttg 960  
ctgccagggg ccagccctg ctgtgctgct ctcccaggga ccatgaggcc cctacatgtc 1020  
cgcaccacct cggatggagg ttactctttc aagtatgaga cagtgcccaa ccttctcacg 1080  
cagcactgtg cttgtatcta a 1101

<210> 6  
<211> 366  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of wild type human inhibin alpha-subunit  
<400> 6

Met Val Leu His Leu Leu Leu Phe Leu Leu Leu Thr Pro Gln Gly Gly  
1 5 10 15

His Ser Cys Gln Gly Leu Glu Leu Ala Arg Glu Leu Val Leu Ala Lys  
20 25 30

Val Arg Ala Leu Phe Leu Asp Ala Leu Gly Pro Pro Ala Val Thr Arg  
35 40 45

Glu Gly Gly Asp Pro Gly Val Arg Arg Leu Pro Arg Arg His Ala Leu  
50 55 60

Gly Gly Phe Thr His Arg Gly Ser Glu Pro Glu Glu Glu Glu Asp Val  
65 70 75 80

Ser Gln Ala Ile Leu Phe Pro Ala Thr Asp Ala Ser Cys Glu Asp Lys  
85 90 95

Ser Ala Ala Arg Gly Leu Ala Gln Glu Ala Glu Glu Gly Leu Phe Arg  
100 105 110

Tyr Met Phe Arg Pro Ser Gln His Thr Arg Ser Arg Gln Val Thr Ser  
115 120 125

Ala Gln Leu Trp Phe His Thr Gly Leu Asp Arg Gln Gly Thr Ala Ala  
130 135 140

Ser Asn Ser Ser Glu Pro Leu Leu Gly Leu Leu Ala Leu Ser Pro Gly  
145 150 155 160

Gly Pro Val Ala Val Pro Met Ser Leu Gly His Ala Pro Pro His Trp  
165 170 175

Ala Val Leu His Leu Ala Thr Ser Ala Leu Ser Leu Leu Thr His Pro  
180 185 190

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Val Leu Val Leu Leu Leu Arg Cys Pro Leu Cys Thr Cys Ser Ala Arg  
195 200 205

Pro Glu Ala Thr Pro Phe Leu Val Ala His Thr Arg Thr Arg Pro Pro  
210 215 220

Ser Gly Gly Glu Arg Ala Arg Arg Ser Thr Pro Leu Met Ser Trp Pro  
225 230 235 240

Trp Ser Pro Ser Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro  
245 250 255

Ala Ala His Ala Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln  
260 265 270

Glu Leu Gly Trp Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe  
275 280 285

His Tyr Cys His Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser  
290 295 300

Leu Pro Val Pro Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu  
305 310 315 320

Leu Pro Gly Ala Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg  
325 330 335

Pro Leu His Val Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr  
340 345 350

Glu Thr Val Pro Asn Leu Leu Thr Gln His Cys Ala Cys Ile  
355 360 365

<210> 7  
<211> 1146  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding super-cut variant 1 of human inhibin  
alpha-subunit with HIS tag

<400> 7  
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gggct ggagc tggcccgga act t gt t ct g gccaaagt ga gggccct gt t ct t ggat gcc 120  
t t ggggcccc ccgcggt gac caggaaggt ggggaccct g gagt caggcg gct gccccga 180  
agacat gcc tggggggct t cacacacagg ggct ct gagc ccgaggaaga ggaggat gt c 240  
t cccaagcca t cct t t t ccc agccacagat gccagct gt g aggacaagt c agct gccaga 300  
gggct ggccc aggaggct ga ggagggcct c t t cagat aca t gt t ccggcc at ccagcat 360  
acacgcagcc gccaggt gac t t cagcccag ct gt ggt t cc acaccgggct ggacaggcag 420



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ggacccgt gg ct gt gcccat gt ct t t gggc cat gct cccc ct cact gggc cgt gct gcac 540  
ct ggccacct ct gct ct ct c t ct gct gacc caccctgt cc t ggt gct gct gct gcgct gt 600  
cccct ct gt a cct gct cagc ccggcct gag gccacgccct t cct ggt ggc ccacact cgg 660  
accagaccac ccagt ggagg ggagcat cat caccat cacc accat cat ca cat ct cat cg 720  
agaaagaaac gct cagt ct c at caact ccc ct gat gt cct ggcct t ggt c t ccct ct gct 780  
ct gcgct gc t gcagaggcc t ccggaggaa ccggct gccc at gccaaact g ccacagagt a 840  
gcact gaaca t ct cct t cca ggagct gggc t gggaacggt ggat cgt gt a ccct ccagt 900  
t t cat ct t cc act act gt ca t ggt ggt t gt gggct gcaca t cccacaaa cct gt ccct t 960  
ccagt ccct g gggct cct cc t accccagcc cagccct act cct t gct gcc aggggcccag 1020  
ccct gct gt g ct gct ct ccc agggacat g agggccct ac at gt ccgcac cacct cggat 1080  
ggaggt t act ct t t caagt a t gagacagt g cccaacct t c t cagcagca ct gt gct t gt 1140  
at ct aa 1146

<210> 8

<211> 381

<212> PRT

<213> a r t i f i c i a l

<220>

<223> Amino acid sequence of super-cut variant 1 of human inhibin  
alpha-subunit with HIS tag

<400> 8

Met Val Leu His Leu Leu Leu Phe Leu Leu Leu Thr Pro Gln Gly Gly  
1 5 10 15

His Ser Cys Gln Gly Leu Glu Leu Ala Arg Glu Leu Val Leu Ala Lys  
20 25 30

Val Arg Ala Leu Phe Leu Asp Ala Leu Gly Pro Pro Ala Val Thr Arg  
35 40 45

Glu Gly Gly Asp Pro Gly Val Arg Arg Leu Pro Arg Arg His Ala Leu  
50 55 60

Gly Gly Phe Thr His Arg Gly Ser Glu Pro Glu Glu Glu Glu Asp Val  
65 70 75 80

Ser Gln Ala Ile Leu Phe Pro Ala Thr Asp Ala Ser Cys Glu Asp Lys  
85 90 95

Ser Ala Ala Arg Gly Leu Ala Gln Glu Ala Glu Glu Gly Leu Phe Arg  
100 105 110

Tyr Met Phe Arg Pro Ser Gln His Thr Arg Ser Arg Gln Val Thr Ser  
115 120 125

## 35259127- seq1 - 000001

Ala Gln Leu Trp Phe His Thr Gly Leu Asp Arg Gln Gly Thr Ala Ala  
130 135 140

Ser Asn Ser Ser Glu Pro Leu Leu Gly Leu Leu Ala Leu Ser Pro Gly  
145 150 155 160

Gly Pro Val Ala Val Pro Met Ser Leu Gly His Ala Pro Pro His Trp  
165 170 175

Ala Val Leu His Leu Ala Thr Ser Ala Leu Ser Leu Leu Thr His Pro  
180 185 190

Val Leu Val Leu Leu Leu Arg Cys Pro Leu Cys Thr Cys Ser Ala Arg  
195 200 205

Pro Glu Ala Thr Pro Phe Leu Val Ala His Thr Arg Thr Arg Pro Pro  
210 215 220

Ser Gly Gly Glu His His His His His His His His His Ile Ser Ser  
225 230 235 240

Arg Lys Lys Arg Ser Val Ser Ser Thr Pro Leu Met Ser Trp Pro Trp  
245 250 255

Ser Pro Ser Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala  
260 265 270

Ala His Ala Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu  
275 280 285

Leu Gly Trp Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His  
290 295 300

Tyr Cys His Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu  
305 310 315 320

Pro Val Pro Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu  
325 330 335

Pro Gly Ala Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro  
340 345 350

Leu His Val Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu  
355 360 365

Thr Val Pro Asn Leu Leu Thr Gln His Cys Ala Cys Ile  
370 375 380

&lt;210&gt; 9

&lt;211&gt; 1146

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<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding super-cut variant 2 of human inhibin alpha-subunit with HIS tag

<400> 9  
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t t ggggcccc ccgcggg gac caggggaaggt ggggaccct g gagt caggcg gcgacgt cga 180  
agacat gccc tgggggggct t cacacacagg ggct ct gaggc ccgaggaaga ggaggat gt c 240  
t cccaagcca t cct t t t ccc agccacagat gccagct gt g aggacaagt c agct gccaga 300  
gggct ggccc aggaggct ga ggagggcct c t t cagat aca t gt t ccggcc at cccagcat 360  
acacgcagcc gccaggt gac t t cagcccag ct gt ggt t cc acaccgggct ggacaggcag 420  
ggcacagcag cct ccaat ag ct ct gagccc ct gct aggcc t gct ggcact gt caccggga 480  
ggaccct gt ct gt gccat gt ct t t gggc cat gct cccc ct cact gggc cgt gct gcac 540  
ct ggccacct ct gct ct ct c t ct gct gacc caccctgt cc t ggt gct gct gct gcgct gt 600  
cccct ct gt a cct gct cagg ccggcct gag gccacgccct t cct ggt ggc ccacact cgg 660  
accagaccac ccagt ggagg ggagcat cat caccat cacc accat cat ca cat ct cat cg 720  
agaaagaaac gct cagt ct c at caact ccc ct gat gt cct ggct t ggt c t cct ct gct 780  
ct gcgcct gc t gcagaggcc t ccggaggaa ccggct gccc at gccaaact g ccacagagt a 840  
gcact gaaca t ct cct t cca ggagct gggc t gggaacggg ggat cgt gt a ccct cccagt 900  
t t cat ct t cc act act gt ca t ggt ggt t gt gggct gcaca t cccacaaa cct gt ccct t 960  
ccagt ccct g gggct cct cc t accccagcc cagccct act cct t gct gcc agggggccag 1020  
ccct gct gt g ct gct ct ccc aggaccat g agggccct ac at gt ccgcac cacct cggat 1080  
ggaggt t act ct t t caagt a t gagacagt g cccaacct t c t cagcagca ct gt gct t gt 1140  
at ct aa 1146

<210> 10  
<211> 381  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of super-cut variant 2 of human inhibin alpha-subunit with HIS tag

<400> 10  
Met Val Leu His Leu Leu Leu Phe Leu Leu Leu Thr Pro Gl n Gly Gly  
1 5 10 15  
His Ser Cys Gl n Gly Leu Gl u Leu Ala Arg Gl u Leu Val Leu Ala Lys  
20 25 30

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Val Arg Ala Leu Phe Leu Asp Ala Leu Gly Pro Pro Ala Val Thr Arg  
35 40 45

Gly Gly Gly Asp Pro Gly Val Arg Arg Arg Arg Arg Arg His Ala Leu  
50 55 60

Gly Gly Phe Thr His Arg Gly Ser Glu Pro Glu Glu Glu Glu Asp Val  
65 70 75 80

Ser Gln Ala Ile Leu Phe Pro Ala Thr Asp Ala Ser Cys Glu Asp Lys  
85 90 95

Ser Ala Ala Arg Gly Leu Ala Gln Glu Ala Glu Glu Gly Leu Phe Arg  
100 105 110

Tyr Met Phe Arg Pro Ser Gln His Thr Arg Ser Arg Gln Val Thr Ser  
115 120 125

Ala Gln Leu Trp Phe His Thr Gly Leu Asp Arg Gln Gly Thr Ala Ala  
130 135 140

Ser Asn Ser Ser Glu Pro Leu Leu Gly Leu Leu Ala Leu Ser Pro Gly  
145 150 155 160

Gly Pro Val Ala Val Pro Met Ser Leu Gly His Ala Pro Pro His Trp  
165 170 175

Ala Val Leu His Leu Ala Thr Ser Ala Leu Ser Leu Leu Thr His Pro  
180 185 190

Val Leu Val Leu Leu Leu Arg Cys Pro Leu Cys Thr Cys Ser Ala Arg  
195 200 205

Pro Glu Ala Thr Pro Phe Leu Val Ala His Thr Arg Thr Arg Pro Pro  
210 215 220

Ser Gly Gly Glu His His His His His His His His His Ile Ser Ser  
225 230 235 240

Arg Lys Lys Arg Ser Val Ser Ser Thr Pro Leu Met Ser Trp Pro Trp  
245 250 255

Ser Pro Ser Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala  
260 265 270

Ala His Ala Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu  
275 280 285

Leu Gly Trp Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His  
290 295 300

35259127-seql - 000001

Tyr Cys His Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu  
305 310 315 320

Pro Val Pro Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu  
325 330 335

Pro Gly Ala Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro  
340 345 350

Leu His Val Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu  
355 360 365

Thr Val Pro Asn Leu Leu Thr Gln His Cys Ala Cys Ile  
370 375 380

<210> 11  
<211> 1884  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding wild type human inhibin  
betaB-subunit

<400> 11  
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ccacccccgc caccggatc cccgggtggc tcgaggaca cctgtacgtc gtgcggcggc 180  
ttccggcggc cagaggagct cggccgagt gacggcgact tcctggaggc ggtgaagcgg 240  
cacatcttga gccgcctgca gatgcggggc cggcccaaca tcacgcacgc cgtgcct aag 300  
gccgccatgg tcacggccct gcgcaagct gacgcgggca aggtgcgcga ggacggccgc 360  
gtggagatcc cgcacctcga cggccacgcc agcccgggcg ccgacggcca ggagcgcgtt 420  
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atggacgggc tggccggtcg ggcgctgggg gccgcctgcc ttctgctgct ggcggccggc 720  
tggctggggc ctgaggcctg gggctcacc acgccccgc cgacgcctgc cgcgccggcg 780  
ccacccccgc caccggatc cccgggtggc tcgaggaca cctgtacgtc gtgcggcggc 840  
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cacatcttga gccgcctgca gatgcggggc cggcccaaca tcacgcacgc cgtgcct aag 960  
gccgccatgg tcacggccct gcgcaagct gacgcgggca aggtgcgcga ggacggccgc 1020  
gtggagatcc cgcacctcga cggccacgcc agcccgggcg ccgacggcca ggagcgcgtt 1080  
tccgaaatca tcagcttcgc cgagacagat ggcctcgcct cctcccggt ccgcctat ac 1140

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t t c t t c a t c t c c a a c g a a g g c a a c c a g a a c c t g t t t g t g g t c c a g g c c a g c c t g t g g c t t 1200  
t a c c t g a a a c t c c t g c c c t a c g t c c t g g a g a a g g g c a g c c g g c g g a a g g t g c g g g t c a a a 1260  
g t g t a c t t c c a g g a g c a g g c c a c g g t g a c a g g t g g a a c a t g g t g g a g a a g a g g g t g g a c 1320  
c t c a a g c g c a g c g g c t g g c a t a c c t t c c c a c t c a c g g a g g c c a t c c a g g c c t t g t t t g a g 1380  
c g g g g c g a g c g g c g a c t c a a c c t a g a c g t g c a g t g t g a c a g c t g c c a g g a g c t g g c c g t g 1440  
g t g c c g g t g t t c g t g g a c c c a g g c g a a g a g t c g c a c c g g c c c t t t g t g g t g g t g c a g g c t 1500  
c g g c t g g g c g a c a g c a g g c a c c g c a t t c g c a a g c g a g g c c t g g a g t g c g a t g g c c g g a c c 1560  
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a t c a t a g c a c c c a c c g g c t a c t a c g g g a a c t a c t g t g a g g g c a g c t g c c c a g c c t a c c t g 1680  
g c a g g g g t c c c c g g c t c t g c c t c c t t c c a c a c g g c t g t g g t g a a c c a g t a c c g c a t g 1740  
c g g g g t c t g a a c c c c g g c a c g g t g a a c t c c t g c t g c a t t c c c a c c a a g c t g a g c a c c a t g 1800  
t c c a t g c t g t a c t t c g a t g a t g a g t a c a a c a t c g t c a a g c g g g a c g t g c c c a a c a t g a t t 1860  
g t g g a g g a g t g c g g c t g c g c c t g a 1884

<210> 12  
<211> 407  
<212> PRT  
<213> a r t i f i c i a l

<220>  
<223> A m i n o a c i d s e q u e n c e o f w i l d t y p e h u m a n i n h i b i n b e t a B - s u b u n i t  
<400> 12

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1 5 10 15

Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro  
20 25 30

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

Gly Gly Ser Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro  
50 55 60

Glu Glu Leu Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg  
65 70 75 80

His Ile Leu Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His  
85 90 95

Ala Val Pro Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala  
100 105 110

Gly Lys Val Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly  
115 120 125

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His Ala Ser Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile  
 130 135 140  
 Ser Phe Ala Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr  
 145 150 155 160  
 Phe Phe Ile Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala  
 165 170 175  
 Ser Leu Trp Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly  
 180 185 190  
 Ser Arg Arg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His  
 195 200 205  
 Gly Asp Arg Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser  
 210 215 220  
 Gly Trp His Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu  
 225 230 235 240  
 Arg Gly Glu Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln  
 245 250 255  
 Glu Leu Ala Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His  
 260 265 270  
 Arg Pro Phe Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg  
 275 280 285  
 Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys  
 290 295 300  
 Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp  
 305 310 315 320  
 Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys  
 325 330 335  
 Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr  
 340 345 350  
 Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val  
 355 360 365  
 Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr  
 370 375 380  
 Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile  
 385 390 395 400

Val Glu Glu Cys Gly Cys Ala  
405

<210> 13  
<211> 1257  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding super-cut variant of human inhibin  
betaB-subunit with FLAG tag

<400> 13  
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tggctggggc ctgaggcctg gggcgactac aaagacgacg acgacaaatc acccagcccc 120  
ccgccgacgc ctgccgcgcc gccgccaccc ccgccacccg gatccccggg tggctcgacg 180  
gacacctgta cgtcgtgcgg cggcttccgg cggccagagg agctcggccg agtggacggc 240  
gacttcctgg aggcgggtgaa gcggcacatc ttgagccgcc tgcagatgcg gggccggccc 300  
aacatcacgc acgccgtgcc taaggccgcc atggc cacgg ccctgcgcaa gctgcacgcg 360  
ggcaaggtgc gcgaggacgg ccgcgtggag atccgcacc tgcacggcca cgccagcccc 420  
ggcgccgacg gccaggagcg cgtttccgaa atcatcagct tgcgcgagac agatggcctc 480  
gcctcctccc gggtccgcct atacttcttc atctccaacg aaggcaacca gaacctgttt 540  
gtggtccagg ccagcctgtg gctttacctg aaactcctgc cctacgtcct ggagaagggc 600  
agccggcgga aggtgcgggt caaagtgtac ttccaggagc agggccacgg tgacaggtgg 660  
aacatggtgg agaagagggt ggacctcaag cgcagcggct ggcatacct cccactcacg 720  
gaggccatcc aggccttgtt tgagcggggc gagcggcgac tcaacctaga cgtgcagtgt 780  
gacagctgcc aggagctggc cgtggtgccg gtgttcgtgg acccaggcga agagtgcac 840  
cggccctttg tgggtggtgca ggctcggctg ggcgacatct catcgagaaa gaaacgctca 900  
gtctcatcgg gcctggagtgc cgatggccgg accaacctct gtgcaggca acagtctctc 960  
attgacttcc gcctcatcgg ctggaacgac tggatcatag caccacccgg ctactacggg 1020  
aactactgtg agggcagctg cccagcctac ctggcagggg tccccggctc tgcctcctcc 1080  
ttccacacgg ctgtggtgaa ccagtaccgc atgcggggctc tgaaccccgg cacggtgaac 1140  
tcctgctgca ttcccaccaa gctgagcacc atgtccatgc tgtacttga tgatgagtac 1200  
aacatcgtca agcgggacgt gcccaacgcg attgtggagg agtgcggctg cgcctga 1257

<210> 14  
<211> 418  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of super-cut variant of human inhibin  
betaB-subunit with FLAG tag

<400> 14



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Met Asp Gly Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu  
1 5 10 15

Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Asp Tyr Lys Asp  
20 25 30

Asp Asp Asp Lys Ser Pro Thr Pro Pro Pro Thr Pro Ala Ala Pro Pro  
35 40 45

Pro Pro Pro Pro Pro Gly Ser Pro Gly Gly Ser Gl n Asp Thr Cys Thr  
50 55 60

Ser Cys Gly Gly Phe Arg Arg Pro Gl u Gl u Leu Gly Arg Val Asp Gly  
65 70 75 80

Asp Phe Leu Gl u Ala Val Lys Arg Hi s Ile Leu Ser Arg Leu Gl n Met  
85 90 95

Arg Gly Arg Pro Asn Ile Thr Hi s Ala Val Pro Lys Ala Ala Met Val  
100 105 110

Thr Ala Leu Arg Lys Leu Hi s Ala Gly Lys Val Arg Gl u Asp Gly Arg  
115 120 125

Val Gl u Ile Pro Hi s Leu Asp Gly Hi s Ala Ser Pro Gly Ala Asp Gly  
130 135 140

Gl n Gl u Arg Val Ser Gl u Ile Ile Ser Phe Ala Gl u Thr Asp Gly Leu  
145 150 155 160

Ala Ser Ser Arg Val Arg Leu Tyr Phe Phe Ile Ser Asn Gl u Gly Asn  
165 170 175

Gl n Asn Leu Phe Val Val Gl n Ala Ser Leu Trp Leu Tyr Leu Lys Leu  
180 185 190

Leu Pro Tyr Val Leu Gl u Lys Gly Ser Arg Arg Lys Val Arg Val Lys  
195 200 205

Val Tyr Phe Gl n Gl u Gl n Gly Hi s Gly Asp Arg Trp Asn Met Val Gl u  
210 215 220

Lys Arg Val Asp Leu Lys Arg Ser Gly Trp Hi s Thr Phe Pro Leu Thr  
225 230 235 240

Gl u Ala Ile Gl n Ala Leu Phe Gl u Arg Gly Gl u Arg Arg Leu Asn Leu  
245 250 255

Asp Val Gl n Cys Asp Ser Cys Gl n Gl u Leu Ala Val Val Pro Val Phe  
260 265 270

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Val Asp Pro Gly Gl u Gl u Ser Hi s Arg Pro Phe Val Val Val Gl n Al a  
275 280 285

Arg Leu Gly Asp Ile Ser Ser Arg Lys Lys Arg Ser Val Ser Ser Gly  
290 295 300

Leu Gl u Cys Asp Gly Arg Thr Asn Leu Cys Cys Arg Gl n Gl n Phe Phe  
305 310 315 320

Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp Ile Ile Al a Pro Thr  
325 330 335

Gly Tyr Tyr Gly Asn Tyr Cys Gl u Gly Ser Cys Pro Al a Tyr Leu Al a  
340 345 350

Gly Val Pro Gly Ser Al a Ser Ser Phe Hi s Thr Al a Val Val Asn Gl n  
355 360 365

Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val Asn Ser Cys Cys Ile  
370 375 380

Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr Phe Asp Asp Gl u Tyr  
385 390 395 400

Asn Ile Val Lys Arg Asp Val Pro Asn Al a Ile Val Gl u Gl u Cys Gly  
405 410 415

Cys Al a

<210> 15  
<211> 24  
<212> DNA  
<213> arti f i ci al

<220>  
<223> Nucl eoti de sequence encodi ng FLAG tag

<400> 15  
gact acaaag acgacgacga caaa

24

<210> 16  
<211> 8  
<212> PRT  
<213> arti f i ci al

<220>  
<223> Ami no aci d sequence of FLAG tag

<400> 16

Asp Tyr Lys Asp Asp Asp Lys  
1 5

<210> 17

<211> 33  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence encoding super-cut site

<400> 17  
 atctcatcga gaaagaaacg ct cagt ct ca t cg

33

<210> 18  
 <211> 11  
 <212> PRT  
 <213> artificial

<220>  
 <223> Amino acid sequence of super-cut site

<400> 18  
 Ile Ser Ser Arg Lys Lys Arg Ser Val Ser Ser  
 1 5 10

<210> 19  
 <211> 26  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence encoding poly-histidine TAG (x9)

<400> 19  
 atcatcacca t caccacat cat cac

26

<210> 20  
 <211> 9  
 <212> PRT  
 <213> artificial

<220>  
 <223> Amino acid sequence of poly-histidine TAG (x9)

<400> 20  
 His His His His His His His His His  
 1 5

<210> 21  
 <211> 15  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence encoding super-cut site 2

<400> 21  
 aggcgcgac gt cga

15

<210> 22  
 <211> 5  
 <212> PRT  
 <213> artificial

&lt;220&gt;

&lt;223&gt; Amino acid sequence of super-cut site 2

&lt;400&gt; 22

Arg Arg Arg Arg Arg  
1 5

&lt;210&gt; 23

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of alpha-NHE1 sense primer

&lt;400&gt; 23

ctaggctagc atggcgctgc acctactgct cttc

34

&lt;210&gt; 24

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of alpha-ECOR1 antisense primer

&lt;400&gt; 24

ctaggaattc ttagatacaa gcacagtgc gcg

33

&lt;210&gt; 25

&lt;211&gt; 66

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of alpha-SCUT (site1) sense primer

&lt;400&gt; 25

cgatgagact gagcggtttct ttctcgatga gatctcccct ccactgggtg gtctgggtccg

60

agtgtg

66

&lt;210&gt; 26

&lt;211&gt; 66

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of alpha-SCUT (site1) antisense primer

&lt;400&gt; 26

atctcatcga gaaagaaacg ct cagtctca tgcactcccc t gatgtcctg gccttgggtct

60

ccctct

66

&lt;210&gt; 27

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of alpha-SCUT (site2) sense primer

<400> 27  
ccctggagt c aggcggcgac gt cgaagaca t gccc 35

<210> 28  
<211> 35  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence of alpha-SCUT (site2) antisense primer

<400> 28  
gggcatgtct t cgacgt cgc cgcctgact c caggg 35

<210> 29  
<211> 62  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence of alpha-pol yH1 Stage sense primer

<400> 29  
atctcatcga gaaagaaacg ct cagt ct ca t caact cccc t gat gt cct g gcct t ggt ct 60  
cc 62

<210> 30  
<211> 62  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence of alpha-pol yH1 Stage antisense primer

<400> 30  
tgagactgag cgtttctttc t cgatgagat gt gat gat gg t ggt gat ggt gat gat gct c 60  
cc 62

<210> 31  
<211> 33  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence of betaAXBA1 sense primer

<400> 31  
ctagtctaga atgcccttgc tttggctgag agg 33

<210> 32  
<211> 40  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence of betaA-NOT1 antisense primer

<400> 32  
gctagcggcc gcctatgagc acccacact c ctccacgat c 40

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<210> 33  
 <211> 66  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence of betaA-SCUT (site1) sense primer

<400> 33  
 atctcatcga gaaagaaacg ct cagtctca t cgggcttgg agtgtgatgg caaggtcaac 60  
 atctgc 66

<210> 34  
 <211> 66  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence of betaA-SCUT (site1) antisense primer

<400> 34  
 cgatgagact gagcgtttct ttctcgatga gatatgaggg tggcttcag actgccgggc 60  
 ctgcag 66

<210> 35  
 <211> 27  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence of betaA-M418A sense primer

<400> 35  
 gacattcaga acgcgatcgt ggaggag 27

<210> 36  
 <211> 27  
 <212> DNA  
 <213> artificial

<220>  
 <223> Nucleotide sequence of betaA-M418A antisense primer

<400> 36  
 ctctccacg atcgcggttct gaatgtc 27

<210> 37  
 <211> 426  
 <212> PRT  
 <213> artificial

<220>  
 <223> Amino acid sequence of human betaA-subunit with A347H mutation

<400> 37  
 Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
 1 5 10 15

Ile Val Arg Ser Ser Pro Thr Pro Gly Ser Glu Gly His Ser Ala Ala  
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Pro Asp Cys<sub>35</sub> Pro Ser Cys Ala<sub>40</sub> Leu Ala Ala Leu Pro Lys<sub>45</sub> Asp Val Pro  
 Asn Ser<sub>50</sub> Gl n Pro Gl u Met Val<sub>55</sub> Gl u Ala Val Lys<sub>60</sub> Lys His Ile Leu Asn  
 Met<sub>65</sub> Leu His Leu Lys<sub>70</sub> Lys Arg Pro Asp Val Thr<sub>75</sub> Gl n Pro Val Pro Lys<sub>80</sub>  
 Ala Ala Leu Leu Asn<sub>85</sub> Ala Ile Arg Lys<sub>90</sub> Leu His Val Gly Lys Val<sub>95</sub> Gly  
 Gl u Asn Gly Tyr<sub>100</sub> Val Gl u Ile Gl u Asp<sub>105</sub> Asp Ile Gly Arg Arg Ala Gl u  
 Met Asn Gl u<sub>115</sub> Leu Met Gl u Gl n Thr<sub>120</sub> Ser Gl u Ile Ile Thr<sub>125</sub> Phe Ala Gl u  
 Ser Gly<sub>130</sub> Thr Ala Arg Lys Thr<sub>135</sub> Leu His Phe Gl u Ile Ser Lys Gl u Gly  
 Ser<sub>145</sub> Asp Leu Ser Val Val<sub>150</sub> Gl u Arg Ala Gl u Val<sub>155</sub> Trp Leu Phe Leu Lys<sub>160</sub>  
 Val Pro Lys Ala Asn<sub>165</sub> Arg Thr Arg Thr Lys<sub>170</sub> Val Thr Ile Arg Leu Phe  
 Gl n Gl n Gl n Lys<sub>180</sub> His Pro Gl n Gly Ser<sub>185</sub> Leu Asp Thr Gly Gl u Gl u Ala  
 Gl u Gl u Val<sub>195</sub> Gly Leu Lys Gly Gl u Arg Ser Gl u Leu Leu<sub>205</sub> Leu Ser Gl u  
 Lys Val<sub>210</sub> Val Asp Ala Arg Lys<sub>215</sub> Ser Thr Trp His Val<sub>220</sub> Phe Pro Val Ser  
 Ser<sub>225</sub> Ser Ile Gl n Arg Leu<sub>230</sub> Leu Asp Gl n Gly Lys<sub>235</sub> Ser Ser Leu Asp Val<sub>240</sub>  
 Arg Ile Ala Cys Gl u<sub>245</sub> Gl n Cys Gl n Gl u Ser<sub>250</sub> Gly Ala Ser Leu Val<sub>255</sub> Leu  
 Leu Gly Lys Lys<sub>260</sub> Lys Lys Lys Gl u Gl u Gl u Gly Gl u Gly Lys<sub>270</sub> Lys Lys  
 Gly Gly Gly Gl u Gly Gly Ala Gl y<sub>280</sub> Ala Asp Gl u Gl u Lys<sub>285</sub> Gl u Gl n Ser  
 His Arg Pro Phe Leu Met Leu Gl n Ala Arg Gl n Ser Gl u Asp His Pro

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290

295

300

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile  
305 310 315 320

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn  
325 330 335

Asp Trp Ile Ile Ala Pro Ser Gly Tyr His His Asn Tyr Cys Glu Gly  
340 345 350

Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe  
355 360 365

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe  
370 375 380

Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser  
385 390 395 400

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln  
405 410 415

Asn Met Ile Val Glu Glu Cys Gly Cys Ser  
420 425

<210> 38

<211> 426

<212> PRT

<213> artificial

<220>

<223> Amino acid sequence of human betaA-subunit with Y345G mutation

<400> 38

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Ile Val Arg Ser Ser Pro Thr Pro Gly Ser Glu Gly His Ser Ala Ala  
20 25 30

Pro Asp Cys Pro Ser Cys Ala Leu Ala Ala Leu Pro Lys Asp Val Pro  
35 40 45

Asn Ser Gln Pro Glu Met Val Glu Ala Val Lys Lys His Ile Leu Asn  
50 55 60

Met Leu His Leu Lys Lys Arg Pro Asp Val Thr Gln Pro Val Pro Lys  
65 70 75 80

Ala Ala Leu Leu Asn Ala Ile Arg Lys Leu His Val Gly Lys Val Gly  
85 90 95



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

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His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe  
370 375 380

Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser  
385 390 395 400

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln  
405 410 415

Asn Met Ile Val Glu Glu Cys Gly Cys Ser  
420 425

<210> 39

<211> 426

<212> PRT

<213> artificial

<220>

<223> Amino acid sequence of human betaA-subunit with A347H/Y345G mutation

<400> 39

Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
1 5 10 15

Ile Val Arg Ser Ser Pro Thr Pro Gly Ser Glu Gly His Ser Ala Ala  
20 25 30

Pro Asp Cys Pro Ser Cys Ala Leu Ala Ala Leu Pro Lys Asp Val Pro  
35 40 45

Asn Ser Gln Pro Glu Met Val Glu Ala Val Lys Lys His Ile Leu Asn  
50 55 60

Met Leu His Leu Lys Lys Arg Pro Asp Val Thr Gln Pro Val Pro Lys  
65 70 75 80

Ala Ala Leu Leu Asn Ala Ile Arg Lys Leu His Val Gly Lys Val Gly  
85 90 95

Glu Asn Gly Tyr Val Glu Ile Glu Asp Asp Ile Gly Arg Arg Ala Glu  
100 105 110

Met Asn Glu Leu Met Glu Gln Thr Ser Glu Ile Ile Thr Phe Ala Glu  
115 120 125

Ser Gly Thr Ala Arg Lys Thr Leu His Phe Glu Ile Ser Lys Glu Gly  
130 135 140

Ser Asp Leu Ser Val Val Glu Arg Ala Glu Val Trp Leu Phe Leu Lys  
145 150 155 160

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Val Pro Lys Ala Asn Arg Thr Arg Thr Lys Val Thr Ile Arg Leu Phe  
165 170 175

Gln Gln Gln Lys His Pro Gln Gly Ser Leu Asp Thr Gly Glu Glu Ala  
180 185 190

Glu Glu Val Gly Leu Lys Gly Glu Arg Ser Glu Leu Leu Leu Ser Glu  
195 200 205

Lys Val Val Asp Ala Arg Lys Ser Thr Trp His Val Phe Pro Val Ser  
210 215 220

Ser Ser Ile Gln Arg Leu Leu Asp Gln Gly Lys Ser Ser Leu Asp Val  
225 230 235 240

Arg Ile Ala Cys Glu Gln Cys Gln Glu Ser Gly Ala Ser Leu Val Leu  
245 250 255

Leu Gly Lys Lys Lys Lys Lys Glu Glu Glu Gly Glu Gly Lys Lys Lys  
260 265 270

Gly Gly Gly Glu Gly Gly Ala Gly Ala Asp Glu Glu Lys Glu Gln Ser  
275 280 285

His Arg Pro Phe Leu Met Leu Gln Ala Arg Gln Ser Glu Asp His Pro  
290 295 300

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile  
305 310 315 320

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn  
325 330 335

Asp Trp Ile Ile Ala Pro Ser Gly Gly His His Asn Tyr Cys Glu Gly  
340 345 350

Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe  
355 360 365

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe  
370 375 380

Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser  
385 390 395 400

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln  
405 410 415

Asn Met Ile Val Glu Glu Cys Gly Cys Ser  
420 425

## 35259127- seq1 - 000001

&lt;210&gt; 40

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Amino acid sequence of human betaA-subunit supercut with A361H mutation

&lt;400&gt; 40

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

Thr Trp His Val Phe Pro Val Ser Ser Ser Ile Gln Arg Leu Leu Asp

225 230 235 240

Gln Gly Lys Ser Ser Leu Asp Val Arg Ile Ala Cys Glu Gln Cys Gln  
 245 250 255

Gl u Ser Gl y Ala Ser Leu Val Leu Leu Gl y Lys Lys Lys Lys Lys Gl u  
260 265 270

Glu Glu Gly Glu Gly Lys Lys Lys Gly Gly Gly Glu Gly Gly Ala Gly  
275 280 285

Ala Asp Glu Glu Lys Glu Glu Ser His Arg Pro Phe Leu Met Leu Glu  
290 295 300

Ala Arg Gln Ser Glu Asp His Pro His Ile Ser Ser Arg Lys Lys Arg  
305 310 315 320

Ser Val Ser Ser Gl y Leu Gl u Cys Asp Gl y Lys Val Asn Ile Cys Cys  
325 330 335

Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp  
340 345 350

I l e I l e A l a P r o S e r G l y T y r H i s H i s A s n T y r C y s G l u G l y G l u C y s  
355 360 365

Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser  
370 375 380

Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn  
385 390 395 400

Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met Leu  
405 410 415

Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln Asn Ala  
420 425 430

I l e Val Gl u Gl u Cys Gl y Cys Ser  
435 440

<210> 41

$\langle 211 \rangle$  440

<212> PRT

<213> artificial

<220>

<223> Amino acid sequence of human betaA-subunit supercut with Y359G mutation

<400> 41

Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
1 5 10 15

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I l e Val Arg Ser 20 Asp Tyr Lys Asp 25 Asp Asp Lys Ser Pro 30 Thr Pro  
 Gl y Ser Gl u 35 Gl y Hi s Ser Al a 40 Al a Pro Asp Cys Pro 45 Cys Al a Leu  
 Al a Al a 50 Leu Pro Lys Asp Val 55 Pro Asn Ser Gl n Pro 60 Gl u Met Val Gl u  
 Al a Val 65 Lys Lys Hi s 70 I l e Leu Asn Met Leu 75 Hi s Leu Lys Lys Arg Pro 80  
 Asp Val Thr Gl n 85 Pro Val Pro Lys Al a 90 Al a Leu Leu Asn Al a 95 I l e Arg  
 Lys Leu Hi s 100 Val Gl y Lys Val Gl y Gl u 105 Asn Gl y Tyr Val Gl u 110 I l e Gl u  
 Asp Asp 115 I l e Gl y Arg Arg Al a Gl u 120 Met Asn Gl u Leu Met 125 Gl u Gl n Thr  
 Ser Gl u 130 I l e I l e Thr Phe Al a 135 Gl u Ser Gl y Thr Al a 140 Arg Lys Thr Leu  
 Hi s 145 Phe Gl u I l e Ser Lys 150 Gl u Gl y Ser Asp Leu 155 Ser Val Val Gl u Arg 160  
 Al a Gl u Val Trp 165 Leu Phe Leu Lys Val Pro 170 Lys Al a Asn Arg Thr 175 Arg  
 Thr Lys Val Thr 180 I l e Arg Leu Phe Gl n 185 Gl n Gl n Lys Hi s Pro 190 Gl n Gl y  
 Ser Leu Asp 195 Thr Gl y Gl u Gl u Al a 200 Gl u Gl u Val Gl y Leu 205 Lys Gl y Gl u  
 Arg Ser 210 Gl u Leu Leu Leu Ser 215 Gl u Lys Val Val Asp 220 Al a Arg Lys Ser  
 Thr 225 Trp Hi s Val Phe Pro 230 Val Ser Ser Ser I l e 235 Gl n Arg Leu Leu Asp 240  
 Gl n Gl y Lys Ser Ser 245 Leu Asp Val Arg I l e 250 Al a Cys Gl u Gl n Cys 255 Gl n  
 Gl u Ser Gl y Al a 260 Ser Leu Val Leu 265 Leu Gl y Lys Lys Lys Lys Lys Gl u  
 Gl u Gl u Gl y 275 Gl u Gl y Lys Lys Lys 280 Gl y Gl y Gl y Gl u Gl y 285 Gl y Al a Gl y

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Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu Gln  
290 295 300

Ala Arg Gln Ser Glu Asp His Pro His Ile Ser Ser Arg Lys Lys Arg  
305 310 315 320

Ser Val Ser Ser Gly Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys  
325 330 335

Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp  
340 345 350

Ile Ile Ala Pro Ser Gly Gly His Ala Asn Tyr Cys Glu Gly Glu Cys  
355 360 365

Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser  
370 375 380

Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn  
385 390 395 400

Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met Leu  
405 410 415

Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln Asn Ala  
420 425 430

Ile Val Glu Glu Cys Gly Cys Ser  
435 440

<210> 42  
<211> 440  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of human betaA-subunit supercut with  
A361H/Y359G mutation

<400> 42

Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile  
1 5 10 15

Ile Val Arg Ser Asp Tyr Lys Asp Asp Asp Asp Lys Ser Pro Thr Pro  
20 25 30

Gly Ser Glu Gly His Ser Ala Ala Pro Asp Cys Pro Ser Cys Ala Leu  
35 40 45

Ala Ala Leu Pro Lys Asp Val Pro Asn Ser Gln Pro Glu Met Val Glu  
50 55 60

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Ala Val Lys Lys His Ile Leu Asn Met Leu His Leu Lys Lys Arg Pro  
65 70 75 80

Asp Val Thr Gln Pro Val Pro Lys Ala Ala Leu Leu Asn Ala Ile Arg  
85 90 95

Lys Leu His Val Gly Lys Val Gly Glu Asn Gly Tyr Val Glu Ile Glu  
100 105 110

Asp Asp Ile Gly Arg Arg Ala Glu Met Asn Glu Leu Met Glu Gln Thr  
115 120 125

Ser Glu Ile Ile Thr Phe Ala Glu Ser Gly Thr Ala Arg Lys Thr Leu  
130 135 140

His Phe Glu Ile Ser Lys Glu Gly Ser Asp Leu Ser Val Val Glu Arg  
145 150 155 160

Ala Glu Val Trp Leu Phe Leu Lys Val Pro Lys Ala Asn Arg Thr Arg  
165 170 175

Thr Lys Val Thr Ile Arg Leu Phe Gln Gln Gln Lys His Pro Gln Gly  
180 185 190

Ser Leu Asp Thr Gly Glu Glu Ala Glu Glu Val Gly Leu Lys Gly Glu  
195 200 205

Arg Ser Glu Leu Leu Leu Ser Glu Lys Val Val Asp Ala Arg Lys Ser  
210 215 220

Thr Trp His Val Phe Pro Val Ser Ser Ser Ile Gln Arg Leu Leu Asp  
225 230 235 240

Gln Gly Lys Ser Ser Leu Asp Val Arg Ile Ala Cys Glu Gln Cys Gln  
245 250 255

Glu Ser Gly Ala Ser Leu Val Leu Leu Gly Lys Lys Lys Lys Lys Glu  
260 265 270

Glu Glu Gly Glu Gly Lys Lys Lys Gly Gly Gly Glu Gly Gly Ala Gly  
275 280 285

Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu Gln  
290 295 300

Ala Arg Gln Ser Glu Asp His Pro His Ile Ser Ser Arg Lys Lys Arg  
305 310 315 320

Ser Val Ser Ser Gly Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys  
325 330 335



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Lys Lys Gl n Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp  
340 345 350

Ile Ile Ala Pro Ser Gly Gly His His Asn Tyr Cys Gl u Gl y Gl u Cys  
355 360 365

Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser  
370 375 380

Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn  
385 390 395 400

Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met Leu  
405 410 415

Tyr Tyr Asp Asp Gly Gl n Asn Ile Ile Lys Lys Asp Ile Gl n Asn Ala  
420 425 430

Ile Val Gl u Gl u Cys Gly Cys Ser  
435 440

<210> 43  
<211> 1224  
<212> DNA  
<213> artificial

<220>  
<223> Nucleotide sequence encoding super-cut variant of human inhibin  
betaB-subunit with FLAG tag: with a modified signal sequence

<400> 43  
at ggacgggc t gcccggc g ggcgct gggg gccgcct gcc t t ct gct gct ggcggccggc 60  
t ggct ggggc ct gaggcct g gggct ccccc acgccccgc cgacgcct gc cgcgccgcgc 120  
ccacccccgc caccggat c cccgggt ggc t cgcaggaca cct gt acgt c gt gcggcggc 180  
t t ccggcggc cagaggagct cggccgagt g gacggcgact t cct ggaggc ggt gaagcgg 240  
cacat ct t ga gccgcct gca gat gcggggc cggcccaaca t cacgcacgc cgt gcct aag 300  
gccgccat gg t cacggccct gcgcaagct g cacgcgggca aggt gcgcga ggacggccgc 360  
gt ggagat cc cgacact cga cggccacgcc agcccgggcg ccgacggcca ggagcgcgt t 420  
t ccgaaat ca t cagct t cgc cgagacagat ggcct cgcct cct cccgggt ccgcct at ac 480  
t t ct t cat ct ccaacgaagg caaccagaac ct gt t t gt gg t ccaggccag cct gt ggct t 540  
t acct gaaac t cct gccct a cgt cct ggag aagggcagcc ggcggaaggt gcgggt caaa 600  
gt gt act t cc aggagcagg ccacggg gac aggt ggaaca t ggt ggagaa gagggt ggac 660  
ct caagcgca gcggct ggca t acct t ccca ct cacggagg ccat ccaggc ct t gt t t gag 720  
cggggcgagc ggcgact caa cct agacgt g cagt gt gaca gct gccagga gct ggccgt g 780  
gt gccggt gt t cgt ggaccc aggcgaagag t cgcaccggc cct t t gt ggt ggt gcaggct 840  
cggt gggcg acagcaggca ccgcat t cgc aagcgaggcc t ggagt gcga t ggccggacc 900

35259127- seq1 - 000001

aacctctgtt gcaggcaaca gttcttcat t gacttccgcc tcatcggctg gaacgactgg 960  
atcatagcac ccaccggcta ctacgggaac tactgtgagg gcagctgccc agcctacctg 1020  
gcagggtcc ccggctctgc ctctctctc cacacggctg tggagaacca gtaccgcatg 1080  
cggggtctga accccggcac ggtgaactcc tctgcatctc ccaccaagct gagcaccatg 1140  
tccatgctgt acttcgatga tgagtacaac atcgtcaagc gggacgtgcc caacatgat t 1200  
gtggaggagt gcggctgcgc ctga 1224

<210> 44  
<211> 418  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of super-cut variant of human inhibin  
betaB-subunit: with a modified signal sequence

<400> 44

Met Asp Gly Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu  
1 5 10 15

Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Asp Tyr Lys Asp  
20 25 30

Asp Asp Asp Lys Ser Pro Thr Pro Pro Pro Thr Pro Ala Ala Pro Pro  
35 40 45

Pro Pro Pro Pro Pro Gly Ser Pro Gly Gly Ser Gln Asp Thr Cys Thr  
50 55 60

Ser Cys Gly Gly Phe Arg Arg Pro Glu Glu Leu Gly Arg Val Asp Gly  
65 70 75 80

Asp Phe Leu Glu Ala Val Lys Arg His Ile Leu Ser Arg Leu Gln Met  
85 90 95

Arg Gly Arg Pro Asn Ile Thr His Ala Val Pro Lys Ala Ala Met Val  
100 105 110

Thr Ala Leu Arg Lys Leu His Ala Gly Lys Val Arg Glu Asp Gly Arg  
115 120 125

Val Glu Ile Pro His Leu Asp Gly His Ala Ser Pro Gly Ala Asp Gly  
130 135 140

Gln Glu Arg Val Ser Glu Ile Ile Ser Phe Ala Glu Thr Asp Gly Leu  
145 150 155 160

Ala Ser Ser Arg Val Arg Leu Tyr Phe Phe Ile Ser Asn Glu Gly Asn  
165 170 175

## 35259127- seq1 - 000001

Gln Asn Leu Phe Val Val Gln Ala Ser Leu Trp Leu Tyr Leu Lys Leu  
 180 185 190  
 Leu Pro Tyr Val Leu Glu Lys Gly Ser Arg Arg Lys Val Arg Val Lys  
 195 200 205  
 Val Tyr Phe Gln Glu Gln Gly His Gly Asp Arg Trp Asn Met Val Glu  
 210 215 220  
 Lys Arg Val Asp Leu Lys Arg Ser Gly Trp His Thr Phe Pro Leu Thr  
 225 230 235 240  
 Glu Ala Ile Gln Ala Leu Phe Glu Arg Gly Glu Arg Arg Leu Asn Leu  
 245 250 255  
 Asp Val Gln Cys Asp Ser Cys Gln Glu Leu Ala Val Val Pro Val Phe  
 260 265 270  
 Val Asp Pro Gly Glu Glu Ser His Arg Pro Phe Val Val Val Gln Ala  
 275 280 285  
 Arg Leu Gly Asp Ile Ser Ser Arg Lys Lys Arg Ser Val Ser Ser Gly  
 290 295 300  
 Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys Arg Gln Gln Phe Phe  
 305 310 315 320  
 Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp Ile Ile Ala Pro Thr  
 325 330 335  
 Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys Pro Ala Tyr Leu Ala  
 340 345 350  
 Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr Ala Val Val Asn Gln  
 355 360 365  
 Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val Asn Ser Cys Cys Ile  
 370 375 380  
 Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr Phe Asp Asp Glu Tyr  
 385 390 395 400  
 Asn Ile Val Lys Arg Asp Val Pro Asn Ala Ile Val Glu Glu Cys Gly  
 405 410 415  
 Cys Ala