

DE2010-156 ST25.txt
SEQUENCE LISTING

<110> SANOFI
<120> Peptide or peptide complex binding to alpha 2 integrin and methods and uses involving the same
<130> DE2010/156
<140> EP10305929.1
<141> 2010-08-31
<160> 54
<170> PatentIn version 3.5
<210> 1
<211> 111
<212> PRT
<213> Artificial Sequence
<220>
<223> Light chain variable domain of anti-alpha2-integrin mAb
<400> 1

Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
20 25 30

Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 2
<211> 117
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<220>
<223> Heavy chain variable domain of anti-alpha2-integrin mAb
<400> 2

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Seite 1

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 3
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<223> CDR1 of the heavy chain variable domain
<400> 3

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn
1 5 10

<210> 4
<211> 16
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<223> CDR2 of the heavy chain variable domain
<400> 4

Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

<210> 5
<211> 8
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<213> Artificial Sequence

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<223> CDR3 of the heavy chain variable domain
<400> 5

Val Gly Arg Gly Tyr Phe Asp Tyr
1 5

<210> 6
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1 of the light chain variable domain

<400> 6

Arg Ala Ser Glu Ser Val Glu Ser Tyr Gly Asn Ser Phe Ile Tyr
 1 5 10 15

<210> 7
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2 of the light chain variable domain

<400> 7

Leu Ala Ser Asn Leu Ala Ser
 1 5

<210> 8
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 of the light chain variable domain

<400> 8

Gln Gln Asn Asn Glu Asp Pro Tyr Thr
 1 5

<210> 9
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric (anti-alpha2-VL-IGKC-CL) light chain

<400> 9

Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
 20 25 30

Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 Seite 3

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

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Ile Gln Leu Ser Ser₈₅ Leu Thr Ser Glu Asp₉₀ Ser Ala Val Tyr Tyr₉₅ Cys

Ala Lys Val Gly₁₀₀ Arg Gly Tyr Phe Asp₁₀₅ Tyr Trp Gly Gln Gly₁₁₀ Thr Thr

Leu Thr Val₁₁₅ Ser Ser Ala Ser Thr₁₂₀ Lys Gly Pro Ser Val₁₂₅ Phe Pro Leu

Ala Pro₁₃₀ Cys Ser Arg Ser Thr₁₃₅ Ser Glu Ser Thr Ala₁₄₀ Ala Leu Gly Cys

Leu Val₁₄₅ Lys Asp Tyr Phe₁₅₀ Pro Glu Pro Val₁₅₅ Thr Val Ser Trp Asn Ser₁₆₀

Gly Ala Leu Thr Ser₁₆₅ Gly Val His Thr Phe₁₇₀ Pro Ala Val Leu Gln Ser₁₇₅

Ser Gly Leu Tyr₁₈₀ Ser Leu Ser Ser Val₁₈₅ Val Thr Val Pro Ser₁₉₀ Ser Ser

Leu Gly Thr₁₉₅ Lys Thr Tyr Thr Cys₂₀₀ Asn Val Asp His Lys₂₀₅ Pro Ser Asn

Thr Lys₂₁₀ Val Asp Lys Arg Val₂₁₅ Glu Ser Lys Tyr Gly₂₂₀ Pro Pro Cys Pro

Pro Cys Pro Ala Pro Glu₂₃₀ Phe Glu Gly Gly Pro₂₃₅ Ser Val Phe Leu Phe₂₄₀

Pro Pro Lys Pro Lys₂₄₅ Asp Thr Leu Met Ile₂₅₀ Ser Arg Thr Pro Glu₂₅₅ Val

Thr Cys Val Val₂₆₀ Val Asp Val Ser Gln₂₆₅ Glu Asp Pro Glu Val₂₇₀ Gln Phe

Asn Trp Tyr₂₇₅ Val Asp Gly Val Glu₂₈₀ Val His Asn Ala Lys₂₈₅ Thr Lys Pro

Arg Glu₂₉₀ Glu Gln Phe Asn Ser₂₉₅ Thr Tyr Arg Val Val₃₀₀ Ser Val Leu Thr

Val₃₀₅ Leu His Gln Asp Trp₃₁₀ Leu Asn Gly Lys Glu₃₁₅ Tyr Lys Cys Lys Val₃₂₀

Ser Asn Lys Gly₃₂₅ Leu Pro Ser Ser Ile Glu₃₃₀ Lys Thr Ile Ser Lys₃₃₅ Ala

Lys Gly Gln Pro₃₄₀ Arg Glu Pro Gln Val₃₄₅ Tyr Thr Leu Pro Pro₃₅₀ Ser Gln

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 11
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VH-IGHG1-CH1) heavy chain Fab fragment

<400> 11

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

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Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr His His His His His His
225 230

<210> 12
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain variable domain of anti-alpha2-integrin mAb"

<400> 12
aacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atatcctgca gagccagtga aagtgttgag agttatggca acagttttat ttactggtac 120
cagcagaaac caggacaggc acccaaactc ctcatctatc ttgcatccaa cctagcatct 180
ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240
cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtac 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 13
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain variable domain of anti-alpha2-integrin mAb

<400> 13
caggtccaac tgcacagcc tggggctgaa cttgtgaagc ctggggctcc agtgaagctg 60
tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120
cctggacgag gcctcgagt gattggcagg attgatcctt ccgatagtga aactcactac 180
aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac 240
atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga 300
cgggggtact ttgactactg gggccaaggc accactctca cagtctcctc a 351

<210> 14

<211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric (anti-alpha2-VL-IGKC-CL) light chain

<400> 14
 aacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atatcctgca gagccagtga aagtgttgag agttatggca acagttttat ttactggtac 120
 cagcagaaac caggacaggc acccaaactc ctcatctatc ttgcatccaa cctagcatct 180
 ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240
 cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtac 300
 acgttcggag gggggaccaa gctggaaata aaacgtacgg tggccgctcc ttccgtgttc 360
 atcttcctc cctccgacga gcagctgaag tccggcaccg cctccgtggt gtgtctgctg 420
 aacaacttct accctcggga ggccaagggt cagtgggaagg tggacaacgc cctgcagtcc 480
 ggcaactccc aggagtccgt caccgagcag gactccaagg acagcaccta ctccctgtcc 540
 tccaccctga ccctgtccaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
 acccaccagg gcctgtccag ccctgtgacc aagtccttca accggggcga gtgc 654

<210> 15
 <211> 1329
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric (anti-alpha2-VH-IGHG4-CH1) mAb

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 tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120
 cctggacgag gcctcgagtg gattggcagg attgatcctt ccgatagtga aactcactac 180
 aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac 240
 atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga 300
 cgggggtact ttgactactg gggccaaggc accactctca cagtctcctc agccagcacc 360
 aagggccctt ccgtgttccc tctggcccct tgctcccgtt ccacctccga gtccaccgcc 420
 gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480
 ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540
 tccctgtcct ccgtgggtgac cgtgccttcc tcctccctgg gcaccaagac ctacacctgt 600
 aacgtggacc acaagccttc caacaccaag gtggacaagc ggggtggagtc caagtacggc 660
 cctccttgcc ctccctgccc tgcccctgag ttcgagggcg gacctagcgt gttcctgttc 720
 cctcctaagc ctaaggacac cctgatgatc tcccggaacc ctgaggtgac ctgtgtggtg 780
 gtggacgtgt cccaggagga ccctgaggtc cagttcaact ggtacgtgga cggcgtggag 840
 gtgcacaacg ccaagaccaa gcctcgggag gagcagttca attccaccta ccgggtggtg 900

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tctgtgctga ccgtgctgca ccaggactgg ctgaacggca aagaatacaa gtgtaaggtc	960
tccaacaagg gcctgccctc ctccatcgag aaaaccatct ccaaggccaa gggccagcct	1020
agggagcctc aggtgtacac cctgcctcct agccaggaag agatgaccaa gaaccaggtg	1080
tccctgacct gtctggtgaa gggcttctac ctttccgaca tcgccgtgga gtgggagtcc	1140
aacggccagc ctgagaacaa ctacaagacc acccctcctg tgctggactc cgacggctcc	1200
ttcttcctgt actccaggct gaccgtggac aagtcccggg ggcaggaggg caacgtcttt	1260
tcctgtcccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg	1320
tctctgggc	1329

<210> 16
 <211> 693
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric (anti-alpha2-VH-IGHG1-CH1) heavy chain Fab fragment

<400> 16	
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tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg	120
cctggacgag gcctcgagt gattggcagg attgatcctt ccgatagtga aactcactac	180
aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac	240
atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga	300
cgggggtact ttgactactg gggccaaggc accactctca cagtctctc agccagcacc	360
aagggcccat ccgtgttccc tctggcccct tcctccaagt ccacctccgg cggcaccgcc	420
gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct	480
ggcgccctga ccagcggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac	540
tccctgtcct ccgtggtgac cgtgccttcc tcctccctgg gcacccagac ctacatctgt	600
aacgtgaacc acaagccctc caacaccaag gtggacaaga aggtggagcc taagtctctg	660
gacaagaccc acacccatca ccataccat cac	693

<210> 17
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IGKC protein (Swiss-Prot: Q502W4)

<400> 17

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
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Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
			20					25					30		

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 18
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHG4 protein (Swiss-Prot: P01861.1 (S108P, L115E))
<400> 18

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 19
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHG1 protein (Swiss-Prot: Q569F4)

<400> 19

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

50

55

60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 20
 <211> 1181
 <212> PRT
 <213> Homo sapiens

<400> 20

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Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
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Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
      20      25      30

Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
      35      40      45

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

Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val
65      70      75      80

Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn
      85      90      95

Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn
      100     105     110

Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe
      115     120     125

Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr
      130     135     140

Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala
145      150     155     160

Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val
      165     170     175

Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys
      180     185     190

Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
      195     200     205

Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe
      210     215     220

Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser
225      230     235     240

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Gln Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile
 245 250 255
 Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg
 260 265 270
 Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp
 275 280 285
 Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile
 290 295 300
 Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu
 305 310 315 320
 Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro
 325 330 335
 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu
 340 345 350
 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
 355 360 365
 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
 370 375 380
 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
 385 390 395 400
 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
 405 410 415
 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
 420 425 430
 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
 435 440 445
 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
 450 455 460
 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
 465 470 475 480
 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
 485 490 495
 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
 500 505 510
 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
 Seite 14

515

Leu Phe Thr Ile Lys Glu Gly Ile Leu Gly Gln His Gln Phe Leu Glu
530 535 540

Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
545 550 555 560

Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
565 570 575

Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
580 585 590

Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
595 600 605

Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
610 615 620

Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
625 630 635 640

Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
645 650 655

Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
660 665 670

Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
675 680 685

Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
690 695 700

Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
705 710 715 720

Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
725 730 735

Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
740 745 750

Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
755 760 765

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

Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
785 790 795 800

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 Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
 835 840 845
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 850 855 860
 Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
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 Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys
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<213> Homo sapiens
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Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
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Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
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Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
65          70          75          80

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Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
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Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile Thr
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Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
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Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
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Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
145          150          155          160

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

Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
195 200 205

Ser Glu Gln Asn Cys Thr Ser Pro Phe Ser Tyr Lys Asn Val Leu Ser
210 215 220

Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
225 230 235 240

Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
245 250 255

Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
260 265 270

Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
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Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
290 295 300

Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
305 310 315 320

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

Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
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Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
355 360 365

Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
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Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
385 390 395 400

Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
405 410 415

Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
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Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu
Seite 20

435

Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
450 455 460

Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
465 470 475 480

Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val
485 490 495

Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met
500 505 510

Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn
515 520 525

Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr
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Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys
565 570 575

Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
580 585 590

Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn
595 600 605

Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys
610 615 620

Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
625 630 635 640

Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
645 650 655

Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
660 665 670

Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
675 680 685

Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
690 695 700

Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
705 710 715 720

Pro Glu Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
725 730 735Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
740 745 750

Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
755 760 765

Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys
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<212> DNA
<213> Homo sapiens
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<220>
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<400> 25	
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<210> 26
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 <223> CKFOR: 3'-primer internal to murine Ck region for amplifying variable domains of anti-alpha2-integrin mAb

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<210> 28
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<210> 29
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<220>
 <223> alpha2mAB mAB-VH FOR: primer for amplifying the heavy chain of anti-alpha2-integrin mAb

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 <211> 54
 <212> DNA
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<220>
 <223> Leader FOR1-54: primer for introducing leader sequence into the variable chains of anti-alpha2-integrin mAb

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<210> 32
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Leader FOR1-23: primer for introducing leader sequence into the variable chains of anti-alpha2-integrin mAb

<400> 32
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<210> 33
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC1: Light chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 33

Asn Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
 20 25 30

Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 65 70 75 80

Pro Val Gln Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
 85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 34
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC2: Light chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 34

Asn Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
 20 25 30

Gly Gln Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 65 70 75 80

Pro Val Gln Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 35
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC3: Light chain variable domain of anti-alpha2-integrin mAb with
humanizing and stabilizing mutations

<400> 35

Asn Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
20 25 30

Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80

Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 36
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC4: Light chain variable domain of anti-alpha2-integrin mAb with
humanizing and stabilizing mutations

<400> 36

Asn Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
20 25 30

Gly Gln Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80

Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 37

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> LC5: Light chain variable domain of anti-alpha2-integrin mAb with grafted mutations

<400> 37

Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1 5 10 15

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
20 25 30

Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asp Asp Thr Ala Asn Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 38

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> HC1: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 38

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
Seite 28

1 5 10 15
 Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110
 Leu Thr Val Val Ser
 115

<210> 39
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC2: Heavy chain variable domain of anti-alpha2-integrin mAb with
 humanizing mutations

<400> 39

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ser Glu Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Leu Thr Val Val Ser
115

<210> 40
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC3: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 40

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 41
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC4: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 41

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Leu Thr Val Val Ser
 115

<210> 42
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC5: Heavy chain variable domain of anti-alpha2-integrin mAb with
 humanizing and stabilizing mutations

<400> 42

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Ile Asp Pro Ser Glu Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Leu Thr Val Val Ser
 115

<210> 43
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>

<223> HC6: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 43

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Glu Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 44

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> HC7: Heavy chain variable domain of anti-alpha2-integrin mAb with grafted mutations

<400> 44

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 45
<211> 717
<212> DNA
<213> Mus musculus

<400> 45
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<210> 46
<211> 1401
<212> DNA
<213> Mus musculus

<400> 46
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aagccctgtc ctccatgcaa atgccagca cctaacctct tgggtggacc atccgtcttc      780
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gtggtggtg atgtgagcga ggatgacca gatgtccaga tcagctggtt tgtgaacaac      900
gtggaagtac acacagctca gacacaaacc catagagagg attacaacag tactctccg      960
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aaggtcaaca acaaagacct ccagcgccc atcgagagaa ccatctcaa acccaaagg      1080
tcagtaagag ctccacaggt atatgtctt cctccaccag aagaagagat gactaagaaa     1140
caggtcactc tgacctgcat ggtcacagac ttcatgcctg aagacattta cgtggagtgg     1200
accaacaacg ggaaaacaga gctaaactac aagaacactg aaccagtcct ggactctgat     1260
ggttcttact tcatgtacag caagctgaga gtggaaaaga agaactgggt ggaaagaaat     1320
agctactcct gttcagtggg ccacgagggt ctgcacaatc accacacgac taagagcttc     1380
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<210> 47
 <211> 218
 <212> PRT
 <213> Mus musculus

<400> 47

Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
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Gly Asn Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 65 70 75 80

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
 85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 48
 <211> 447
 <212> PRT
 <213> Mus musculus

<400> 48

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu
 115 120 125

Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys
 130 135 140

Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser
 145 150 155 160

Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp
 180 185 190
 Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr
 195 200 205
 Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
 210 215 220
 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
 245 250 255
 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
 260 265 270
 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
 275 280 285
 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
 290 295 300
 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
 305 310 315 320
 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
 325 330 335
 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
 340 345 350
 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
 355 360 365
 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
 370 375 380
 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
 405 410 415
 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
 420 425 430

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His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 49
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> IGLKV79_IGLKJ2

<400> 49

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1 5 10 15

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Ser Phe Leu
20 25 30

Gly Ile Asn Leu Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Gln Ala Ser Asn Lys Asp Thr Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Leu Gln Ser Lys
85 90 95

Asn Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 50
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV11_IGHD33_IGHJ8

<400> 50

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

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Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Thr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 51
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> vk1LC

<400> 51

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 52
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> vh1b

<400> 52

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Seite 38

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Trp Gly Tyr Asp Tyr Asp Val Phe Tyr Tyr Ala Met Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 53
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain of anti-integrin 2 mAb

<400> 53

Asp Phe Val Met Thr Gln Ser Pro Ala Phe Leu Ser Val Thr Pro Gly
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Gln Ser Ser Val Asn Tyr Ile
 20 25 30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ala Pro Lys Lys Leu Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Thr Asn Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

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Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 54
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable domain of anti-integrin 2 mAb
<400> 54

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1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Ile His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Arg Gly Phe Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ala Asn Asp Gly Val Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

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Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
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Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly
		435					440					445