# SEQUENCE LISTING:

<110> AC Immune

<120> Humanized Antibody

<130> 089667-0156

<141> 2008-10-03

<150> US 60/960,617

<151> 2007-10-05

<160> 32

<170> PatentIn version 3.3

<210> 1
<211> 10
<212> PRT
<213> Mus musculus

<220>
<223> C2 HuVH AF 4 humanised heavy chain variable region (CDR1)

<400> 1

Gly Phe Thr Phe Ser Ser Tyr Gly Met Ser
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<210> 2
<211> 17
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<220>
<223> C2 HuVH AF 4 humanised heavy chain variable region (CDR2)

<400> 2

Ser Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10
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Gly

<210> 3
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<213> Mus musculus

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<223> C2 HuVH AF 4 humanised heavy chain variable region (CDR3)

<400> 3

Gly Asp Tyr
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<210> 4
<211> 16
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<220>
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<400> 4

Arg Ser Ser Gln Ser Leu Val Tyr Ser Asn Gly Asp Thr Tyr Leu His
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<210> 5
<211> 7
<212> PRT
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<220>
<223> C2 HuVK 1 humanised light chain variable region (CDR2)

<400> 5

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 6
<211> 9
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<220>
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<400> 6

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 7
<211> 6
<212> PRT

<213> Homo sapiens

<220>
<223> Aβ epitope, region 2

<400> 7

Val Phe Phe Ala Glu Asp
1 5

<210> 8
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> Aβ epitope, region 1

<400> 8

His Gln Lys Leu Val
1 5

<210> 9
<211> 6
<212> PRT
<213> Homo sapiens

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<222> (1)..(1)
<223> Xaa can be Ala, Val, Leu, norleucine, Met, Phe, or Ile

<220>
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<222> (4)..(4)
<223> Xaa can be Ala, Val, Leu, Ser or Ile

<220>
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<222> (5)..(5)
<223> Xaa can be Glu or Asp

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<222> (6)..(6)
<223> Xaa can be Glu or Asp

<400> 9

Xaa Phe Phe Xaa Xaa Xaa
1 5

<210> 10
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> Xaa can be His, Asn, Gln Lys, or Arg

<220>
<221> misc_feature
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<223> Xaa can be Asn or Gln

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be Ala, Val, Leu, norleucine, Met, Phe, or Ile

<400> 10

Xaa Xaa Lys Leu Xaa
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<210> 11
<211> 10
<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa can be His, Asn, Gln Lys, or Arg

<220>
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<223> Xaa can be Asn or Gln

<220>
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<223> Xaa can be Ala, Val, Leu, norleucine, Met, Phe, or Ile

<220>
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<222> (8)..(8)
<223> Xaa can be Ala, Val, Leu, Ser or Ile

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<222> (9)..(9)
<223> Xaa can be Glu or Asp

<220>
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<222> (10)..(10)
<223> Xaa can be Glu or Asp

<400> 11

Xaa Xaa Lys Leu Xaa Phe Phe Xaa Xaa Xaa
1 5 10

<210> 12
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> artificial humanized C2 HuVK 1 variable light chain

<400> 12

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

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

Asn Gly Asp Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
85 90
95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 13
<211> 219
<212> PRT
<213> artificial sequence

<220>
<223> artificial humanized C2 light chain

<400> 13

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

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

Asn Gly Asp Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
85 90
95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155
160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170
175

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 14
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> artificial humanized C2 light chain constant region

<400> 14

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10
15

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> 15

<211> 112

<212> PRT

<213> artificial sequence

<220>

<223> artificial humanized C2 HuVH AF 4 variable heavy chain

<400> 15

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val

35 40 45

Ala Ser Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75
80

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

Ala Ser Gly Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

<210> 16
<211> 439
<212> PRT
<213> artificial sequence

<220>
<223> artificial humanized C2 heavy chain

<400> 16

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val
35 40 45

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

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

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

Ala Ser Gly Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

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

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

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

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

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

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235
240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250
255

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu

305 310 315
320

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330
335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
340 345 350

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395
400

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Leu Gly Lys

435

<210> 17

<211> 326

<212> PRT

<213> Homo sapiens

<220>
<223> IG GAMMA-4 CHAIN C REGION - modified

<400> 17

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

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 Leu 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
325

<210> 18
<211> 51
<212> DNA
<213> Mus musculus

<220>
<223> C2 HuVH AF 4 humanised heavy chain variable region (CDR2)

<400> 18
agcatcaata gtaatggtgg tagcacctat tatccagaca gtgtgaaggg c
51

<210> 19
<211> 9
<212> DNA
<213> Mus musculus

<220>
<223> C2 HuVH AF 4 humanised heavy chain variable region (CDR3)

<400> 19
ggtgactac
9

<210> 20
<211> 49
<212> DNA
<213> Mus musculus

<220>
<223> C2 HuVK 1 humanised light chain variable region (CDR1)

<400> 20
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49

<210> 21
<211> 635
<212> DNA
<213> artificial sequence

<220>
<223> artificial humanized C2 Hu VK 1 variable light chain

<400> 21
gatattgtga tgacccaatc tccactctcc ctgcctgtca ctcctggtga gcctgcctcc
60

atctcttgca gatctagtca gagccttgta tatagtaatg gagacaccta tttacattgg
120

tacctgcaga agccaggcca gtctccacag ctcctgatct acaaagtttc caaccgattt
180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc
240

agcagagtgg aggctgagga tgtgggagtt tattactgct ctcaaagtac acatgttcct
300

tggacgttcg gccaaggcac caaggtggaa atcaaa
336

<210> 22
<211> 657
<212> DNA
<213> artificial sequence

<220>
<223> artificial humanized C2 light chain

<400> 22
gatattgtga tgacccaatc tccactctcc ctgcctgtca ctcctggtga gcctgcctcc
60

atctcttgca gatctagtca gagccttgta tatagtaatg gagacaccta tttacattgg
120

tacctgcaga agccaggcca gtctccacag ctcctgatct acaaagtttc caaccgattt
180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc
240

agcagagtgg aggctgagga tgtgggagtt tattactgct ctcaaagtac acatgttcct
300

tggacgttcg gccaaggcac caaggtggaa atcaaaagga ctgtggctgc accatctgtc
360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg
420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa
480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc
540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa
600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt
657

<210> 23
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<223> artificial humanized C2 light chain constant region

<400> 23
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ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag
120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac
180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag
240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag
300

agcttcaaca ggggagagtg t
321

<210> 24
<211> 798
<212> DNA
<213> artificial sequence

<220>
<223> artificial humanized C2 HuVH AF variable heavy chain

<400> 24
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60

tcctgtgcag cctctggatt cactttcagt agctatggca tgtcttgggt tcgccaggct
120

ccaggcaagg gtctcgaatt ggtcgcaagc atcaatagta atggtggtag cacctattat
180

ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac
240

ctgcaaatga acagtctgag agctgaggac accgccgtgt attactgtgc aagtggtgac
300

tactggggcc aaggcaccac tgtcacagtc tcctca
336

<210> 25
<211> 1317
<212> DNA

<213> artificial sequence

<220>
<223> artificial humanized C2 heavy chain

<400> 25
gaggtgcagc tggtcgagtc tgggggaggc ttagtgcagc ctggagggtc cctgagactc
60

tcctgtgcag cctctggatt cactttcagt agctatggca tgtcttgggt tcgccaggct
120

ccaggcaagg gtctcgaatt ggtcgcaagc atcaatagta atggtggtag cacctattat
180

ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac
240

ctgcaaatga acagtctgag agctgaggac accgccgtgt attactgtgc aagtggtgac
300

tactggggcc aaggcaccac tgtcacagtc tcctcagctt ccaccaaggg cccatccgtc
360

ttccccctgg cgccctgctc cagatcgacc tccgagagca cagccgccct gggctgcctg
420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc
480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg
540

gtgaccgtgc cctccagcag cttgggcacg aagacctaca cctgcaacgt agatcacaag
600

cccagcaaca ccaaggtgga caagagagtt gagtccaaat atggtccccc gtgtcccccа
660

tgcccagcac ctgagttcct gggggggacca tcagtcttcc tgttcccccc aaaacccaag
720

gacactctca tgatctcccg gacccctgag gtcacgtgcg tggtggtgga cgtgagccag
780

gaagaccccg aggtccagtt caactggtac gtggatggcg tggaggtgca taatgccaag
840

acaaagccgc gggaggagca gttcaacagc acgtaccgtg tggtcagcgt cctcaccgtc
900

ctgcaccagg actggctgaa cggcaaggag tacaagtgca aggtctccaa caaaggcctc
960

ccgtcctcca tcgagaaaac catctccaaa gccaaagggc agccccgaga gccacaggtg
1020

tacaccctgc ccccatccca ggaggagatg accaagaacc aggtcagcct gacctgcctg
1080

gtcaaaggct tctaccccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag
1140

aacaactaca agaccacgcc tcccgtcctc gattccgacg gctccttctt cctctacagc
1200

aggctaaccg tggacaagag caggtggcag gaggggaatg tcttctcatg ctccgtgatg
1260

catgaggctc tgcacaacca ctacacacag aagagcctct ccctgtctct gggtaaa
1317

<210> 26
<211> 981
<212> DNA
<213> Homo sapiens

<220>
<223> artificial humanized C2 heavy chain constant region

<400> 26
gcttccacca agggcccatc cgtcttcccc ctggcgccct gctccagatc gacctccgag
60

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg
120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca
180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc
240

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc
300

aaatatggtc ccccgtgtcc cccatgccca gcacctgagt tcctgggggg accatcagtc
360

ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg
420

tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat
480

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac
540

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag
600

tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa
660

gggcagcccc gagagccaca ggtgtacacc ctgccccccat cccaggagga gatgaccaag
720

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag
780

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt cctcgattcc
840

gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg
900

aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc
960

ctctccctgt ctctgggtaa a
981

<210> 27
<211> 112
<212> PRT
<213> Mus musculus

<400> 27

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

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

Asn Gly Asp Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90
95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 28
<211> 112
<212> PRT
<213> Mus musculus

<400> 28

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

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

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

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

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

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

<210> 29
<211> 336
<212> DNA

<213> Mus musculus

<400> 29
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc
60

atctcttgca gatctagtca gagccttgta tatagtaatg gagacaccta tttacattgg
120

tacctgcaga agccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt
180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc
240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttcct
300

tggacgttcg gtggaggcac caagctagaa atcaaa
336

<210> 30
<211> 417
<212> DNA
<213> Mus musculus

<400> 30
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat
60

gttgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc
120

tcttgcagat ctagtcagag ccttgtatat agtaatggag acacctattt acattggtac
180

ctgcagaagc caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct
240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc
300

agagtggagg ctgaggatct gggagtttat ttctgctctc aaagtacaca tgttccttgg
360

acgttcggtg gaggcaccaa gctagaaatc aaacgggctg atgctgcacc aactgta
417

<210> 31
<211> 336
<212> DNA
<213> Mus musculus

<400> 31
gaggtgcagc tggtggagtc tgggggaggc ttagtgcagc ctggagggtc cctgaaactc
60

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