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<130> M1967 EP S3

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<170> PatentIn version 3.3

<210> 1

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<212> PRT

<213> Mus musculus

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<400> 1

Gly Phe Thr Phe Ser Ser Tyr Gly Met Ser

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<210> 2

<211> 17

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<213> Mus musculus

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<400> 2

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1 5 10 15

Gly

<210> 3

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<400> 3

Gly Asp Tyr

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<210> 4

<211> 16

<212> PRT

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

<400> 4

Arg Ser Ser Gln Ser Leu Val Tyr Ser Asn Gly Asp Thr Tyr Leu His

1 5 10 15

<210> 5

<211> 7

<212> PRT

<213> Mus musculus

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Lys Val Ser Asn Arg Phe Ser

1 5

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<211> 9

<212> PRT

<213> Mus musculus

<220>

<223> C2 HuVK 1 humanised light chain variable region (CDR3)

<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

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<213> Homo sapiens

<220>
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His Gln Lys Leu Val
1 5
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<213> Homo sapiens
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<222> (1)..(1)
<223> Xaa can be Ala, Val, Leu, norleucine, Met, Phe, or Ile
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<222> (4)..(4)
<223> Xaa can be Ala, Val, Leu, Ser or Ile
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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
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<223> Xaa can be His, Asn, Gln Lys, or Arg
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<223> Xaa can be Asn or Gln

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<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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<211> 10

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

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<223> Xaa can be Asn or Gln

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<222> (5)..(5)

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

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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

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<222> (10)..(10)

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<400> 11

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<211> 112

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

agatctagtc agagccttgt atatagtaat ggagacacct atttacatt 49

<210> 21

<211> 635

<212> DNA

<213> artificial sequence

<220>

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

<400> 21

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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

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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
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agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
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<210> 23
<211> 321
<212> DNA
<213> Homo sapiens
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<223> artificial humanized C2 light chain constant region
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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
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<210> 24
<211> 798
<212> DNA
<213> artificial sequence
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<223> artificial humanized C2 HuVH AF variable heavy chain
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ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac 240
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tactggggcc aaggcaccac tgtcacagtc tcctca 336

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<212> DNA

<213> artificial sequence

<220>

<223> artificial humanized C2 heavy chain

<400> 25

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ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac 240

ctgcaaatga acagtctgag agctgaggac accgccgtgt attactgtgc aagtgggtgac 300

tactgggggcc 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 gtgtccccca 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 tcccgtgctc 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

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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 240

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300
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ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 420
tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 480
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gggcagcccc gagagccaca ggtgtacacc ctgccccccat cccaggagga gatgaccaag 720
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt cctcgattcc 840
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aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc 960
ctctccctgt ctctgggtaa a 981

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<212> PRT
<213> Mus musculus
<400> 27
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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
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<213> Mus musculus

<400> 28

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

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tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

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<210> 30

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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

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<212> DNA

<213> Mus musculus

<400> 31

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ccagacaaga ggctggaatt ggtcgcaagc atcaatagta atggtggtag cacctattat 180

ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtgc aagtggtgac 300

tactggggcc aaggctccac tctcacagtc tcctca 336

<210> 32

<211> 408

<212> DNA

<213> Mus musculus

<400> 32

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gacaagaggc tggaattggt cgcaagcatc aatagtaatg gtggtagcac ctattatcca 240

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