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<110> Glaxo Group Limited

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Asn Tyr Ala Met Ser
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<210> 14
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Gly

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Gln His Ser Arg Glu Phe Pro Phe Thr
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Asn Tyr Ala Met Ser
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<210> 20
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Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val Lys
 1   5   10   15
Gly

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 1   5   10   15

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<400> 24
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<210> 25
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ccggaaaaga gcctggagtg ggtcgcaacc attagtgatg gtggtagttt cacctactat 180
ctagacaatg taaggggccg attcaccatc tccagagaca atgccaagaa caacctgtat 240

ttgcaaatga gccatttgaa gtctgacgac acagccatgt attactgtgc aagagatgtg 300
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tca 363

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<211> 121
<212> PRT
<213> Murine

<400> 26

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			20					25					30		
Ala	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Lys	Ser	Leu	Glu	Trp	Val
		35					40					45			
Ala	Thr	Ile	Ser	Asp	Gly	Gly	Ser	Phe	Thr	Tyr	Tyr	Leu	Asp	Asn	Val
	50					55					60				
Arg	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Asn	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Ser	His	Leu	Lys	Ser	Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Asp	Val	Gly	His	Thr	Thr	Phe	Trp	Tyr	Phe	Asp	Val	Trp	Gly
			100					105					110		
Ser	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser							
		115					120								

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<212> DNA
<213> Murine

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caacagaaac caggacagcc gcccaaagtc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgtaacatat tactgtctgc acagtaggga gtttccgttc 300
acgttcggag gggggaccaa cctggaaata aaa 333

<210> 28
<211> 111
<212> PRT
<213> Murine

<400> 28

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

<210> 29
<211> 363
<212> DNA
<213> Murine

<400> 29
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tcctgtgtac cctctggatt cactttcagt agttatgcca tgtcttgggt tcgccagact 120
ccggaaaaga ggctggagtg ggtcgcaacc attagtgatg gtggtagttt cacctactat 180
tttgccaata tacagggccg attcaccatc tccagagaca ataccaagaa caacctatac 240
ctgcaaatga accatctgaa gtctgaggac gcaggcatgt attactgtgc aagagatgtg 300
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tca 363

<210> 30
<211> 121
<212> PRT
<213> Murine

<400> 30
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            20   25   30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Phe Ala Asn Ile
    50   55   60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Asn Leu Tyr
65   70   75   80
Leu Gln Met Asn His Leu Lys Ser Glu Asp Ala Gly Met Tyr Tyr Cys
                85   90   95
Ala Arg Asp Val Gly Leu Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100   105   110
Thr Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 31
<211> 333
<212> DNA
<213> Murine

<400> 31
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atctcctgca gggccagcaa aagtgtcagt ccatctggct atgatttcat gcactggtat 120
caacagaagc caggacagcc gcccaaactc ctcatcaagt atgcatccga actagaatct 180
ggggtccctg gcaggttcag tggcagtggg tctgggacag atttcaccct caacatccat 240
cctgtggagg aagaagatgc tgcaacatat ttctgtcagc acagtaggga gtttccgttc 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 32
<211> 111
<212> PRT
<213> Murine

<400> 32
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Thr Ile Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Pro Ser
            20   25   30
Gly Tyr Asp Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Lys Tyr Ala Ser Glu Leu Glu Ser Gly Val Pro Gly
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Phe Cys Gln His Ser Arg
                85   90   95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 33
<211> 364
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<213> Murine

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ccggaaaaga ggctggagtg ggtcgcgacc attagtgatg gtggtggtta cacctactat 180
ttagacaatg gacagggccg attcaccatc tccagagaca atgccaagaa caacctgtac 240
ctgcagatga gccatctgaa gtctgaggac acagccatgt attactgtgc aagagatgtg 300
ggacttacta cgttttggta ccttcgatgt ctggggcaca gggaccacgg tcaccgtctc 360
ctca 364

<210> 34
<211> 121
<212> PRT
<213> Murine

<400> 34
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1   5   10   15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser Asp Gly Gly Gly Tyr Thr Tyr Tyr Leu Asp Asn Gly
    50   55   60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65   70   75   80
Leu Gln Met Ser His Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Asp Val Gly Leu Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100   105   110
Thr Gly Thr Thr Val Thr Val Ser Ser
        115   120

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<212> DNA
<213> Murine

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caacagagac caggacagcc gcccaaactc ctcatcacgt atgcttccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aagaggatgc tgcaacatat tactgtcagc acagtaggga gtttccgttc 300
acgttcggag gggggaccag gctggaaata aaa 333

<210> 36
<211> 111
<212> PRT
<213> Murine

<400> 36
Asp Ile Val Leu Thr Gln Ser Pro Val Ser Leu Val Ile Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Pro Ser
            20   25   30
Ser Tyr Asn Phe Met His Trp Tyr Gln Gln Arg Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Thr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg

eolf-seql

85 90 95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 37
<211> 363
<212> DNA
<213> Murine

<400> 37
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ccggaaaaga ggctggagtg ggtcgcaacc attagtgatg gtggtagttt cacctactat 180
ctagacaatg taaagggccg attcaccatc tccagagaca atgccaagaa caacctgtat 240
ttgcaaatga gccatttgaa gtctgacgac acagccatgt attactgtgc aagagatgtg 300
ggacatacta cgttttggta cttcgatgtc tggggcacag ggaccacggt caccgtctcc 360
tca 363

<210> 38
<211> 121
<212> PRT
<213> Murine

<400> 38
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80
Leu Gln Met Ser His Leu Lys Ser Asp Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
100 105 110
Thr Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 39
<211> 333
<212> DNA
<213> Murine

<400> 39
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caacagaaac caggacagcc gcccaaagtc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgtaacatat tactgtcagc acagtaggga gtttccgttc 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 40
<211> 111
<212> PRT
<213> Murine

<400> 40
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1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Ala Ser
20 25 30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

eolf-seql

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Lys Val Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Glu Glu Asp Ala Val Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 41
<211> 1353
<212> DNA
<213> Chimera

<400> 41

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ccggaaaaga gcctggagtg ggtcgcaacc attagtgatg gtggtagttt cacctactat 180
ctagacaatg taaggggccg attcaccatc tccagagaca atgccaagaa caacctgtat 240
ttgcaaatga gccatttgaa gtctgacgac acagccatgt attactgtgc aagagatgtg 300
ggacatacta ccttttggta cttcgatgtc tggggctcag ggacactagt gaccgtgtcc 360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
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<210> 42
<211> 451
<212> PRT
<213> Chimera

<400> 42

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Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Ser Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65                  70                  75                  80
Leu Gln Met Ser His Leu Lys Ser Asp Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Ser Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
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```
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
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<210> 43
<211> 654
<212> DNA
<213> Chimera

<400> 43

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caacagaaac caggacagcc gcccaaagtc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
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acgttcggag gggggaccaa cctggaaata aaacgtacgg tggccgcccc cagcgtgttc 360
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ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
acccaccagg gcctgtccag ccccgtgacc aagagcttca accggggcga gtgc       654
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<210> 44
<211> 218
<212> PRT
<213> Chimera

<400> 44

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

<210> 45
<211> 1353
<212> DNA
<213> Chimera

<400> 45
gaagtacaac tggtggagtc tgggggaggc ttagtggagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt cactttcagt aactatgcca tgtcttgggt tcgccagact 120
ccggaaaaga ggctggagtg ggtcgcaacc attagtgatg gtggtagttt cacctactat 180
ctagacaatg taaagggccg attcaccatc tccagagaca atgccaagaa caacctgtat 240
ttgcaaatga gccatttgaa gtctgacgac acagccatgt attactgtgc aagagatgtg 300
ggacatacta cgttttggta cttcgatgtc tggggcacag ggacactagt gaccgtgtcc 360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgccctggg ctgcctggtg aaggactact tccccgaacc ggtgaccgtg 480
tcctggaaca gcggagccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc 540
agcggcctgt acagcctgag cagcgtggtg accgtgccca gcagcagcct gggcacccag 600
acctacatct gtaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gtgacaagac ccacacctgc ccccccctgcc ctgcccccga gctgctggga 720
ggccccagcg tgttcctgtt ccccccaag cctaaggaca ccctgatgat cagcagaacc 780
cccgaggtga cctgtgtggt ggtggatgtg agccacgagg accctgaggt gaagttcaac 840
tggtacgtgg acggcgtgga ggtgcacaat gccaagacca agcccaggga ggagcagtac 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggattg gctgaacggc 960
aaggagtaca agtgtaaggt gtccaacaag gccctgcctg cccctatcga gaaaaccatc 1020
agcaaggcca agggccagcc cagagagccc caggtgtaca ccctgccccc tagcagagat 1080
gagctgacca agaaccaggt gtccctgacc tgcctggtga agggcttcta ccccagcgac 1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cacccccct 1200
gtgctggaca gcgatggcag cttcttcctg tacagcaagc tgaccgtgga caagagcaga 1260
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caatcactac 1320
acccagaaga gcctgagcct gtcccctggc aag 1353

<210> 46
<211> 451
<212> PRT
<213> Chimera

<400> 46
```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
 1               5                  10                  15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65                  70                  75                  80
Leu Gln Met Ser His Leu Lys Ser Asp Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Thr Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

<210> 47
<211> 654
<212> DNA
<213> Chimera

<400> 47

```
gacattgtgc tgacacagtc tcctgttttc ttagttatat ctctggggca gagggccacc 60
atctcctgca gggccagcaa aagtgtcagt gcatctggct ataatttcat gcactggtac 120
caacagaaac caggacagcc gcccaaagtc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgtaacatat tactgtcagc acagtaggga gtttccgttc 300
acgttcggag gggggaccaa gctggaaata aaacgtacgg tggccgcccc cagcgtgttc 360
atcttccccc ccagcgatga gcagctgaag agcggcaccg ccagcgtggt gtgtctgctg 420
aacaacttct acccccggga ggccaaggtg cagtggaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
```

acccaccagg gcctgtccag ccccgtgacc aagagcttca accggggcga gtgc 654

<210> 48
<211> 218
<212> PRT
<213> Chimera

<400> 48
Asp Ile Val Leu Thr Gln Ser Pro Val Phe Leu Val Ile Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Ala Ser
20 25 30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Val Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Glu Glu Asp Ala Val Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 49
<211> 294
<212> DNA
<213> Homo Sapiens

<400> 49
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaga 294

<210> 50
<211> 98
<212> PRT
<213> Human

<400> 50
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
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val 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 Arg

<210> 51
<211> 300
<212> DNA
<213> Homo Sapiens

<400> 51
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

<210> 52
<211> 100
<212> PRT
<213> Homo Sapiens

<400> 52
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20   25   30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Thr
            100

<210> 53
<211> 363
<212> DNA
<213> Artifical Sequence

<220>
<223> Homo Sapiens and Mus musculus

<400> 53
gaggtgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc aactacgcca tgagctgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtggccacc atcagcgacg gcggcagctt cacctactat 180
ctggacaacg tgaggggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag ggccgaggat accgccgtgt actactgcgc cagggacgtc 300
ggccacacca ccttctggta cttcgacgtc tggggcaggg gcacactagt gaccgtgtcc 360
agc   363

<210> 54
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo Sapiens and Mus musculus

<400> 54
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 Asn Tyr

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```
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 55
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 55

```
gagatgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc aactacgcca tgagctgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtggccacc atcagcgacg gcggcagctt cacctactat 180
ctggacaacg tgaggggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag ggccgaggat accgccgtgt actactgcgc cagggacgtc 300
ggccacacca ccttctggta cttcgacgtc tggggcaggg gcacactagt gaccgtgtcc 360
agc                                                               363
```

<210> 56
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 56

```
Glu Met 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 Asn Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 57
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens and Mus musculus

<400> 57

gaggtgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc aactacgcca tgagctgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtggccacc atcagcgacg gcggcagctt cacctactat 180
ctggacaacg tgaggggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag ggccgaggat accgccgtgt actactgcgc cagggacgtc 300
ggccacacca ccttctggta cttcgacgtc tggggctccg gcacactagt gaccgtgtcc 360
agc 363

<210> 58
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 58
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 Asn Tyr
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50   55   60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100   105   110
Ser Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 59
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 59
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaagctg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgccgtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa ggtggagatc aag 333

<210> 60
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 60
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
            20   25   30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60

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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Leu His Ser Arg
85 90 95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 61
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 61
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaaggtg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgccgtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa ggtggagatc aag 333

<210> 62
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 62
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
20 25 30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Val Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Leu His Ser Arg
85 90 95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 63
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 63
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaagctg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgtggtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa ggtggagatc aag 333

<210> 64
<211> 111
<212> PRT

<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 64
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
            20   25   30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Ala Glu Asp Val Val Val Tyr Tyr Cys Leu His Ser Arg
                85   90   95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 65
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 65
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaagctg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgccgtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa cgtggagatc aag   333

<210> 66
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 66
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
            20   25   30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Leu His Ser Arg
                85   90   95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Asn Val Glu Ile Lys
            100   105   110

<210> 67
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 67
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaaggtg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgtggtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa cgtggagatc aag 333

<210> 68
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 68
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
            20   25   30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Val Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Ala Glu Asp Val Val Val Tyr Tyr Cys Leu His Ser Arg
                85   90   95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Asn Val Glu Ile Lys
            100   105   110

<210> 69
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 69
gaggtgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc aactacgcca tgagctgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtggccacc atcagcgacg gcggcagctt cacctactat 180
ctggacaacg tgaggggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag ggccgaggat accgccgtgt actactgcgc cagggacgtc 300
ggccacacca ccttctggta cttcgacgtc tggggcaggg gcacactagt gaccgtgtcc 360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgccctggg ctgcctggtg aaggactact tccccgaacc ggtgaccgtg 480
tcctggaaca gcggagccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc 540
agcggcctgt acagcctgag cagcgtggtg accgtgccca gcagcagcct gggcacccag 600
acctacatct gtaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gtgacaagac ccacacctgc ccccccctgcc ctgccccga gctgctggga 720
ggccccagcg tgttcctgtt ccccccaag cctaaggaca ccctgatgat cagcagaacc 780
cccgaggtga cctgtgtggt ggtggatgtg agccacgagg accctgaggt gaagttcaac 840
tggtacgtgg acggcgtgga ggtgcacaat gccaagacca agcccaggga ggagcagtac 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggattg gctgaacggc 960
aaggagtaca agtgtaaggt gtccaacaag gccctgcctg cccctatcga gaaaaccatc 1020
agcaaggcca agggccagcc cagagagccc caggtgtaca ccctgccccc tagcagagat 1080
gagctgacca agaaccaggt gtccctgacc tgcctggtga agggcttcta ccccagcgac 1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cacccccct 1200
gtgctggaca gcgatggcag cttcttcctg tacagcaagc tgaccgtgga caagagcaga 1260
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caatcactac 1320
acccagaaga gcctgagcct gtcccctggc aag 1353

<210> 70
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 70
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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 Asn Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

<210> 71
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 71
gacatcgtga tgactcagag ccccgatagc ctggccgtga gcctgggcga aagggccacc 60
atcaactgca gggccagcaa gagcgtgagc gctgccggct acaacttcat gcactggtac 120
cagcagaagc ccggccagcc ccccaaggtg ctgatctact acgcctccaa cctggagagc 180
ggcgtgccag acaggttcag cggatctggc agcggcaccg acttcaccct gaccatctca 240
agcctgcagg ccgaggacgt cgccgtgtac tactgcctgc acagcaggga gttccccttc 300
acctttggcg gcggcaccaa ggtggagatc aagcgtacgg tggccgcccc cagcgtgttc 360
atcttccccc ccagcgatga gcagctgaag agcggcaccg ccagcgtggt gtgtctgctg 420
aacaacttct acccccggga ggccaaggtg cagtggaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
acccaccagg gcctgtccag ccccgtgacc aagagcttca accggggcga gtgc 654

<210> 72
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 72
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Ala Ala
            20   25   30
Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Val Leu Ile Tyr Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Leu His Ser Arg
                85   90   95
Glu Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115   120   125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130   135   140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145   150   155   160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165   170   175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180   185   190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195   200   205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 73
<211> 360
<212> DNA
<213> Artificial Sequence

<220>

<223> Homo sapiens and Mus musculus

<400> 73
gaggtgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc tacgccatga gctgggtgag gcaggccccc 120
ggcaagggcc tggagtgggt ggccaccatc agcgacggcg gcagcttcac ctactatctg 180
gacaacgtga ggggcaggtt caccatcagc agggacaacg ccaagaacag cctgtacctg 240
cagatgaaca gcctgagggc cgaggatacc gccgtgtact actgcgccag ggacgtcggc 300
cacaccacct tctggtactt cgacgtctgg ggcaggggca cactagtgac cgtgtccagc 360

<210> 74
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 74
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
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50   55   60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100   105   110
Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 75
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 75
gaggtgcagc tggtggaaag cggcggcggc ctggtccagc ccggcgggag cctgagactc 60
tcttgcgccg ctagcggctt caccttcagc agctacgcca tgagctgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtggccacc atcagcgacg gcggcagctt cacctactat 180
ctggacaacg tgaggggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag ggccgaggat accgccgtgt actactgcgc cagggacgtc 300
ggccacacca ccttctggta cttcgacgtc tggggcaggg gcacactagt gaccgtgtcc 360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgccctggg ctgcctggtg aaggactact tccccgaacc ggtgaccgtg 480
tcctggaaca gcggagccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc 540
agcggcctgt acagcctgag cagcgtggtg accgtgccca gcagcagcct gggcacccag 600
acctacatct gtaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gtgacaagac ccacacctgc ccccccctgcc ctgccccga gctgctggga 720
ggccccagcg tgttcctgtt ccccccaag cctaaggaca ccctgatgat cagcagaacc 780
cccgaggtga cctgtgtggt ggtggatgtg agccacgagg accctgaggt gaagttcaac 840
tggtacgtgg acggcgtgga ggtgcacaat gccaagacca agcccaggga ggagcagtac 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggattg gctgaacggc 960
aaggagtaca agtgtaaggt gtccaacaag gccctgcctg cccctatcga gaaaaccatc 1020
agcaaggcca agggccagcc cagagagccc caggtgtaca ccctgccccc tagcagagat 1080
gagctgacca agaaccaggt gtccctgacc tgcctggtga agggcttcta ccccagcgac 1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cacccccct 1200
gtgctggaca gcgatggcag cttcttcctg tacagcaagc tgaccgtgga caagagcaga 1260

tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caatcactac 1320
acccagaaga gcctgagcct gtcccctggc aag 1353

<210> 76
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 76

```
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
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Asp Gly Gly Ser Phe Thr Tyr Tyr Leu Asp Asn Val
    50                  55                  60
Arg 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 Arg Asp Val Gly His Thr Thr Phe Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
```

Pro Gly Lys
450

<210> 77
<211> 5
<212> PRT
<213> Homo sapiens

<400> 77
Ser Tyr Ala Met Ser
1 5

<210> 78
<211> 7
<212> PRT
<213> Homo sapiens

<400> 78
Lys Ala Ser Ser Leu Glu Ser
1 5

<210> 79
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 79
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60
Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

```
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
```

<210> 80
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 80

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1                  5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
        35                  40                  45
Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65                  70                  75                  80
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Leu 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
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> 81
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 81
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
    50   55   60
Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 82
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens and Mus musculus

<400> 82
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
            20   25   30
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
        35   40   45
Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65   70   75   80
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 83
<211> 759
<212> DNA
<213> Homo sapiens

<400> 83
atgggggtac tgctcacaca gaggacgctg ctcagtctgg tccttgcact cctgtttcca 60
agcatggcga gcatggcggc tataggcagc tgctcgaaag agtaccgcgt gctccttggc 120
cagctccaga agcagacaga tctcatgcag gacaccagca gactcctgga cccctatata 180
cgtatccaag gcctggatgt tcctaaactg agagagcact gcagggagcg ccccggggcc 240
ttccccagtg aggagaccct gaggggctg ggcaggcggg gcttcctgca gaccctcaat 300
gccacactgg gctgcgtcct gcacagactg gccgacttag agcagcgcct ccccaaggcc 360
caggatttgg agaggtctgg gctgaacatc gaggacttgg agaagctgca gatggcgagg 420
ccgaacatcc tcgggctcag gaacaacatc tactgcatgg cccagctgct ggacaactca 480
gacacggctg agcccacgaa ggctggccgg ggggcctctc agccgcccac ccccacccct 540
gcctcggatg cttttcagcg caagctggag ggctgcaggt tcctgcatgg ctaccatcgc 600
ttcatgcact cagtggggcg ggtcttcagc aagtgggggg agagcccgaa ccggagccgg 660
agacacagcc cccaccaggc cctgaggaag ggggtgcgca ggaccagacc ctccaggaaa 720
ggcaagagac tcatgaccag gggacagctg ccccggtag 759

<210> 84
<211> 252
<212> PRT
<213> Homo sapiens

<400> 84

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