

SEQUENCE LISTING

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<120> ANTI-5T4 ANTIBODIES AND USES THEREOF

<130> SP9715A

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<150> 60/891,248

<151> 2007-02-23

<150> 60/781,346

<151> 2006-03-10

<160> 99

<170> PatentIn version 3.4

<210> 1

<211> 414

<212> DNA

<213> Mus musculus

<220>

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<222> (1)..(57)

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<222> (58)..(414)

<223> heavy chain variable region

<220>

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<222> (260)..(260)

<223> n is g or t

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atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt caagatctcc 120

tgcaaggctt ctggatatac cttcacaaac tttggaatga actgggtgaa gcagggtcca 180

ggagaggggtt taaagtggat gggctggata aacaccaaca ctggagagcc aagatatgct 240
 gaagagttca agggacggtn tgccttttct ttggaaacca ctgccagcac tgcctatttg 300
 cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgcaag agactgggac 360
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<210> 2
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<220>
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<220>
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<220>
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 <222> (69)..(85)
 <223> CDR2

<220>
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 <222> (87)..(87)
 <223> Xaa is cystein (C) or phenylalanine (F); this is position 67 with
 numbering according to Kabat

<220>
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 <222> (118)..(127)
 <223> CDR3

<400> 2

Met Asp Trp Leu Trp Asn Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1 5 10 15

Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Phe Gly Met Asn Trp Val Lys Gln Gly Pro Gly Glu Gly Leu
 50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala
 65 70 75 80

Glu Glu Phe Lys Gly Arg Xaa Ala Phe Ser Leu Glu Thr Thr Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Ala Arg Asp Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp
 115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 3
 <211> 381
 <212> DNA
 <213> Mus musculus

<220>
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 <222> (1)..(60)
 <223> leader sequence

<220>
 <221> misc_feature
 <222> (61)..(381)
 <223> light chain variable region

<400> 3
 atgaagtcac agaccaggt cttcgtatct ctactgctct gtgtgtctgg tgctcatggg 60
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 ataacctgca aggccagtca gagggtgagt aatgatgtag cttggtacca acagaagcca 180
 gggcagtcctc cttaaactgtt gataaacttt gcaaccaatc gctacactgg agtcacctaat 240
 cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 300
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<210> 4
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<220>
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<222> (21)..(127)
<223> light chain variable region

<220>
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<222> (44)..(54)
<223> CDR1

<220>
<221> MISC_FEATURE
<222> (70)..(76)
<223> CDR2

<220>
<221> MISC_FEATURE
<222> (109)..(117)
<223> CDR3

<400> 4

Met Lys Ser Gln Thr Gln Val Phe Val Phe Leu Leu Leu Cys Val Ser
1 5 10 15

Gly Ala His Gly Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu
20 25 30

Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser
35 40 45

Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

Lys Leu Leu Ile Asn Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Asn
65 70 75 80

Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser
85 90 95

Thr Val Gln Ala Glu Asp Leu Ala Leu Tyr Phe Cys Gln Gln Asp Tyr
100 105 110

Ser Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 5
<211> 405
<212> DNA
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<222> (1)..(54)
<223> leader sequence

<220>
<221> misc_feature
<222> (55)..(405)
<223> heavy chain variable region

<400> 5
atggaatgga ggatctttct cttcatcctg tcaggaactg caggtgtcca ctcccaggtt 60
cagctgcagc agtctagacc tgagctggtg aagcctgggg cttcagtga gatgtcctgc 120
aaggcttctg gatacacttt cactgactat gttataagct gggatgaagca gagaactgga 180
cagggccttg agtggattgg agagatttat cctggaagta atagtattta ttacaatgag 240
aagttcaagg gcagggccac actgactgca gacaaatcct ccagcacagc ctacatgcag 300
ctcagcagcc tgacatctga ggactctgcg gtctatttct gtgcaatggg gggtaactac 360
ggctttgact attggggcca aggcaccact ctcacagtct cctca 405

<210> 6
<211> 135
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(18)
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<220>
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<222> (19)..(135)
<223> heavy chain variable region

<220>
<221> MISC_FEATURE
<222> (44)..(53)
<223> CDR1

<220>
<221> MISC_FEATURE

<222> (68)..(84)
<223> CDR2

<220>
<221> MISC_FEATURE
<222> (117)..(124)
<223> CDR3
<400> 6

Met Glu Trp Arg Ile Phe Leu Phe Ile Leu Ser Gly Thr Ala Gly Val
1 5 10 15

His Ser Gln Val Gln Leu Gln Gln Ser Arg Pro Glu Leu Val Lys Pro
20 25 30

Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
35 40 45

Asp Tyr Val Ile Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Tyr Pro Gly Ser Asn Ser Ile Tyr Tyr Asn Glu
65 70 75 80

Lys Phe Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Met Gly Gly Asn Tyr Gly Phe Asp Tyr Trp Gly Gln Gly
115 120 125

Thr Thr Leu Thr Val Ser Ser
130 135

<210> 7
<211> 390
<212> DNA
<213> Mus musculus

<220>
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<222> (1)..(66)
<223> leader sequence

<220>
<221> misc_feature

<222> (67)..(390)

<223> light chain variable region

<400> 7

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agaggacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctct aggggaacgg 120
gtcaccttga cctgcactgc cagctcaagt gtaaattcca attacttaca ctggtaccag 180
cagaagccag gatcctcccc caaactctgg atttatagca catccaacct ggcttctgga 240
gtcccagctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagc 300
atggaggctg aagatgctgc cacttattac tgccaccagt atcatcgttc cccgctcacg 360
ttcggtgctg ggaccaagct ggagctgaaa 390
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<210> 8

<211> 130

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

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<220>

<221> MISC_FEATURE

<222> (23)..(130)

<223> light chain variable region

<220>

<221> MISC_FEATURE

<222> (46)..(56)

<223> CDR1

<220>

<221> MISC_FEATURE

<222> (73)..(79)

<223> CDR2

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<221> MISC_FEATURE

<222> (112)..(120)

<223> CDR3

<400> 8

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1           5           10           15
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Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
20           25           30
```

Met Ser Ala Ser Leu Gly Glu Arg Val Thr Leu Thr Cys Thr Ala Ser
 35 40 45

Ser Ser Val Asn Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

Ser Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 85 90 95

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
 100 105 110

Gln Tyr His Arg Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
 115 120 125

Leu Lys
 130

<210> 9
 <211> 423
 <212> DNA
 <213> Mus musculus

<220>
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 <222> (1)..(57)
 <223> leader sequence

<220>
 <221> misc_feature
 <222> (58)..(423)
 <223> heavy chain variable region

<220>
 <221> misc_difference
 <222> (347)..(347)
 <223> n is g or a

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 gtgcagcttg ttgagtctgg tggaggattg gtgcagccta aagggtcatt gaaactctca 120
 tgtgcagcct ctggattcac cttcaatacc tacgccatga actgggtccg ccagggtcca 180
 ggaaagggtt tggaatgggt tgctcgcata agaagtaaaa gtaataatta tgcaacatat 240

tatgccgatt cagtgaaga caggttcacc atctccagag atgattcaca aagcatgctc 300
 tatctgcaaa tgaacaactt gaaaactgaa gacacagcca tgtattnctg tgtgagacag 360
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 tca 423

<210> 10
 <211> 141
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 <213> Mus musculus

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 <223> leader sequence

<220>
 <221> MISC_FEATURE
 <222> (20)..(141)
 <223> heavy chain variable region

<220>
 <221> MISC_FEATURE
 <222> (45)..(54)
 <223> CDR1

<220>
 <221> MISC_FEATURE
 <222> (69)..(87)
 <223> CDR2

<220>
 <221> MUTAGEN
 <222> (116)..(116)
 <223> Xaa is cysteine (C) or tyrosine (Y); this is position 91 with
 numbering according to Kabat

<220>
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 <222> (120)..(130)
 <223> CDR3

<400> 10

Met Leu Leu Gly Leu Lys Trp Val Phe Phe Val Val Phe Tyr Gln Gly
 1 5 10 15

Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Lys Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Ser Met Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
100 105 110

Ala Met Tyr Xaa Cys Val Arg Gln Trp Asp Tyr Asp Val Arg Ala Met
115 120 125

Asn Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135 140

<210> 11
<211> 381
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(60)
<223> leader sequence

<220>
<221> misc_feature
<222> (61)..(381)
<223> light chain variable region

<400> 11
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gacattgtga tgaccagtc tcacatattc atgtccacat cagtaggaga cagggtcagc 120
atcacctgca aggcagtc g gatgtggat actgctgtag cctgggtatca acagaaacca 180
gggcaatctc ctaaactact gatttactgg gcatccaccc ggctcactgg agtccctgat 240
cgcttcacag gcagtggatc tgggacggat ttcactctca ccattagcaa tgtgcagtct 300
gaagacttgg cagattatct ctgtcagcaa tatagcagct atccgtacac gttcggaggg 360
gggaccaagc tggaaataaa a 381

<210> 12
<211> 127

<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(20)
<223> leader sequence

<220>
<221> MISC_FEATURE
<222> (21)..(127)
<223> light chain variable region

<220>
<221> MISC_FEATURE
<222> (44)..(54)
<223> CDR1

<220>
<221> MISC_FEATURE
<222> (70)..(76)
<223> CDR2

<220>
<221> MISC_FEATURE
<222> (109)..(117)
<223> CDR3

<400> 12

Met	Glu	Thr	His	Ser	Gln	Val	Phe	Val	Tyr	Met	Leu	Leu	Trp	Leu	Ser
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Gly	Val	Glu	Gly	Asp	Ile	Val	Met	Thr	Gln	Ser	His	Ile	Phe	Met	Ser
		20						25					30		

Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp
		35					40					45			

Val	Asp	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro
	50					55					60				

Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Leu	Thr	Gly	Val	Pro	Asp
65					70					75				80	

Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser
				85					90					95	

Asn	Val	Gln	Ser	Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Ser
				100				105					110		

Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 13
<211> 98
<212> PRT
<213> Homo sapiens
<400> 13

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

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

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

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

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

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

Ala Arg

<210> 14
<211> 98
<212> PRT
<213> Homo sapiens
<400> 14

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

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

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

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

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

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

Ala Arg

<210> 15
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 15

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

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

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

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

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

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

Ala Arg

<210> 16
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 16

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg

<210> 17
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 17

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

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

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

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

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

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

Ala Arg

<210> 18
<211> 98
<212> PRT
<213> Homo sapiens

<400> 18

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

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

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

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

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

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

Ala Thr

<210> 19
<211> 98
<212> PRT
<213> Homo sapiens

<400> 19

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

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

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

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

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

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

Ala Arg

<210> 20
<211> 98
<212> PRT
<213> Homo sapiens

<400> 20

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

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

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

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

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

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

Ala Arg

<210> 21
<211> 98
<212> PRT
<213> Homo sapiens

<400> 21

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

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

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

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

Gln Glu Arg Val Thr Ile Thr Arg Asp Met Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Ala

<210> 22
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 22

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg

<210> 23
<211> 98
<212> PRT
<213> Homo sapiens

<400> 23

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

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

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

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

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

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

Ala Arg

<210> 24
<211> 98
<212> PRT
<213> Homo sapiens

<400> 24

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

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

Gly Leu Val Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Glu Lys Phe
50 55 60

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

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

Ala Thr

<210> 25
<211> 30
<212> PRT
<213> artificial

<220>
<223> consensus sequence of human VH1 heavy chain variable region
framework 1

<400> 25

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

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

<210> 26
<211> 14
<212> PRT
<213> Artificial

<220>
<223> consensus sequence of human VH1 heavy chain variable region
framework 2

<400> 26

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 27
<211> 32
<212> PRT
<213> Artificial

<220>

<223> consensus sequence of human VH1 heavy chain variable region
framework 3

<400> 27

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 28

<211> 101

<212> PRT

<213> Homo sapiens

<400> 28

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 Pro
100

<210> 29

<211> 98

<212> PRT

<213> Homo sapiens

<400> 29

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

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

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

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

Thr Val

<210> 30
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 30

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

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

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

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

Thr Val

<210> 31
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 31

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

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

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

<210> 32
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 32

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 Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
85 90 95

<210> 33
<211> 96
<212> PRT
<213> Homo sapiens
<400> 33

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

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

Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Ser Ile Pro Ala Arg Phe Ser
50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp His Asn Leu Pro
85 90 95

<210> 34
<211> 96
<212> PRT
<213> Homo sapiens
<400> 34

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

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

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
50 55 60

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

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

<210> 35
<211> 95
<212> PRT
<213> Homo sapiens

<400> 35

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

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

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

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

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

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

<210> 36
<211> 95
<212> PRT
<213> Homo sapiens

<400> 36

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

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

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

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

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

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

<210> 37
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 37

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

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

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

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

<210> 38
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 38

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

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

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

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

<210> 39
<211> 95
<212> PRT
<213> Homo sapiens

<400> 39

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

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

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

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

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

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

<210> 40
<211> 95
<212> PRT
<213> Homo sapiens

<400> 40

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

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

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

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

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

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

<210> 41
<211> 95
<212> PRT
<213> Homo sapiens

<400> 41

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

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

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

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

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

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

<210> 42
<211> 95
<212> PRT
<213> Homo sapiens

<400> 42

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

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

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

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

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

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

<210> 43
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 43

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser
 85 90 95

<210> 44
 <211> 95

<212> PRT
<213> Homo sapiens

<400> 44

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser
85 90 95

<210> 45
<211> 327
<212> PRT
<213> Homo sapiens

<400> 45

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 Lys
 325

<210> 46
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 46

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 47
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 47

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 48
 <211> 357
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 48
 caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60
 tcctgcaagg cttctggata taccttcaca aactttggaa tgaactgggt gcgacaggcc 120
 cctggacaag ggcttaagtg gatgggatgg ataaacacca acactggaga gccaagatat 180
 gctgaagagt tcaagggacg gtttgtcttc tccttggaca cctctgtcag cactgcctat 240
 ctgcagatct ccagcctgaa ggctgaggac actgccgtgt attactgtgc cagagactgg 300
 gacggtgcct acttctttga ctactggggc caaggcacc cttgtcacagt ctctca 357

<210> 49
 <211> 119
 <212> PRT
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<220>
 <221> MISC_FEATURE
 <222> (23)..(35)
 <223> CDR1

<220>
 <221> MISC_FEATURE
 <222> (50)..(66)
 <223> CDR2

<220>

<221> MISC_FEATURE
 <222> (99)..(108)
 <223> CDR3

<400> 49

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala Glu Glu Phe
 50 55 60

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

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

Ala Arg Asp Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 50
 <211> 357
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 50
 caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60
 tcctgcaagg cttctggata taccttcaca aactttggaa tgaactgggt ggcacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg ataaacacca acactggaga gccaagatat 180
 gctgaagagt tcaagggacg gtttgtcttc tccttggaca cctctgtcag cactgcctat 240
 ctgcagatct ccagcctgaa ggctgaggac actgccgtgt attactgtgc cagagactgg 300

gacggtgcct acttctttga ctactggggc caaggcaccc ttgtcacagt ctctctca

357

<210> 51

<211> 119

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 51

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala Glu Glu Phe
50 55 60

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

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

Ala Arg Asp Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 52

<211> 119

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 52

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala Glu Glu Phe
50 55 60

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

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

Ala Arg Asp Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 53
<211> 357
<212> DNA
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 53
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggata taccttcaca aactttggaa tgaactgggt ccgccaggct 120
ccaggaagg ggctggagtg ggtggcctgg ataaacacca acaccggtga gccaagatat 180
gctgaagagt tcaagggacg attcaccatc tccagagaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac accgctgtgt attactgtgc cagagactgg 300
gacgggtgcct acttctttga ctactggggc caaggcaccc ttgtcacagt ctctca 357

<210> 54
<211> 119
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<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 Tyr Thr Phe Thr Asn Phe
20 25 30

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

Ala Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala Glu Glu Phe
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 Asp Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 55

<211> 357

<212> DNA

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 55

gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggata taccttcaca aactttggaa tgaactgggt ccgccaggct 120
ccaggggaagg ggctgaagtg gatgggctgg ataaacacca acaccggtga gccaagatat 180
gctgaagagt tcaagggacg attcaccatc tccttgaca acgccaagtc ctcagcctat 240
ctgcaaatga acagcctgag agccgaggac accgctgtgt attactgtgc cagagactgg 300
gacggtgcct acttctttga ctactggggc caaggcaccc ttgtcacagt ctctca 357

<210> 56
 <211> 119
 <212> PRT
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 56

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 Tyr Thr Phe Thr Asn Phe
 20 25 30

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

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Arg Tyr Ala Glu Glu Phe
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Leu Asp Asn Ala Lys Ser Ser Ala 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 Trp Asp Gly Ala Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 57
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 57

gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
 atcaactgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca gcagaaacca 120
 ggacagcctc ctaagctgct catttacttt gcaaccaatc gctacactgg agtccttgac 180

cgcttctccg gcagcggatc cggcacagat ttcactctca ccatcagcag cctgcaggct 240
gaagatgtgg cagtttatta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
ggcaccaagg tggaaatcaa a 321

<210> 58
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 58

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 Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Ser Ser Pro Trp
85 90 95

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

<210> 59
<211> 321
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 59

Gly Ala Cys Ala Thr Cys Gly Thr Gly Ala Thr Gly Ala Cys Cys Cys
1 5 10 15

Ala Gly Thr Cys Thr Cys Cys Ala Gly Ala Cys Thr Cys Cys Cys Thr
 20 25 30

Gly Gly Cys Thr Gly Thr Gly Thr Cys Thr Cys Thr Gly Gly Gly Cys
 35 40 45

Gly Ala Gly Ala Gly Gly Gly Cys Cys Ala Cys Cys Ala Thr Cys Ala
 50 55 60

Ala Cys Thr Gly Cys Ala Ala Gly Gly Cys Cys Ala Gly Thr Cys Ala
 65 70 75 80

Gly Ala Gly Thr Gly Thr Gly Ala Gly Thr Ala Ala Thr Gly Ala Thr
 85 90 95

Gly Thr Gly Gly Cys Thr Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys
 100 105 110

Ala Gly Ala Ala Ala Cys Cys Ala Gly Gly Ala Cys Ala Gly Cys Cys
 115 120 125

Thr Cys Cys Thr Ala Ala Gly Cys Thr Gly Cys Thr Cys Ala Thr Thr
 130 135 140

Thr Ala Cys Thr Thr Thr Gly Cys Ala Ala Cys Cys Ala Ala Thr Cys
 145 150 155 160

Gly Cys Thr Ala Cys Ala Cys Thr Gly Gly Ala Gly Thr Cys Cys Cys
 165 170 175

Thr Gly Ala Cys Cys Gly Cys Thr Thr Cys Thr Cys Cys Gly Gly Cys
 180 185 190

Ala Gly Cys Gly Gly Ala Thr Ala Cys Gly Gly Cys Ala Cys Ala Gly
 195 200 205

Ala Thr Thr Thr Cys Ala Cys Thr Cys Thr Cys Ala Cys Cys Ala Thr
 210 215 220

Cys Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala Gly Gly Cys Thr
 225 230 235 240

Gly Ala Ala Gly Ala Thr Gly Thr Gly Gly Cys Ala Gly Thr Thr Thr
245 250 255

Ala Thr Thr Ala Cys Thr Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala
260 265 270

Thr Thr Ala Thr Ala Gly Cys Thr Cys Thr Cys Cys Cys Thr Gly Gly
275 280 285

Ala Cys Cys Thr Thr Cys Gly Gly Thr Cys Ala Gly Gly Gly Cys Ala
290 295 300

Cys Cys Ala Ala Gly Gly Thr Gly Gly Ala Ala Ala Thr Cys Ala Ala
305 310 315 320

Ala

<210> 60
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<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 Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Ser Ser Pro Trp
85 90 95

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

<210> 61
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 61
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
 atcacttgca aggccagtca gagtgtgagt aatgatgtgg cttggtatca gcagaaacca 120
 ggcaaagccc ctaagctcct gatctatctt gcaaccaatc gctacactgg agtcccatcc 180
 cgcttcagcg gcagcggatc cggcacagat ttactctca ccatcagcag cctgcaacct 240
 gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
 ggcaccaagg tggaaatcaa a 321

<210> 62
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 62

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

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

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

Tyr Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> 63
<211> 321
<212> DNA
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 63
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
atcacttgca aggccagtca gagggtgagt aatgatgtgg cttggtatca gcagaaacca 120
ggcaaattccc ctaagctcct gatctatctt gcaaccaatc gctacactgg agtcccatcc 180
cgcttcagcg gcagcggatc cggcacagat ttcactctca ccatcagcag cctgcaacct 240
gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac cttcgggtcag 300
ggcaccaagg tggaaatcaa a 321

<210> 64
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 64

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

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

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

Tyr Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 65
<211> 321
<212> DNA
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 65
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
atcacttgca aggccagtca gagtgtgagt aatgatgtgg cttggtatca gcagaaacca 120
ggcaaagccc ctaagctcct gatcaatttt gcaaccaatc gctacactgg agtcccatcc 180
cgcttcagcg gcagcggatc cggcacagat ttactctca ccatcagcag cctgcaacct 240
gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac ctcgggtcag 300
ggcaccaagg tggaaatcaa a 321

<210> 66
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 66

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

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

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

Asn Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> 67

<211> 321

<212> DNA

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 67

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
 atcacttgca aggccagtca gagggtgagt aatgatgtgg cttggtatca gcagaaacca 120
 ggcaaagccc ctaagctcct gatctatttt gcaaccaatc gctacactgg agtcccaaac 180
 cgcttcagcg gcagcggatc cggcacagat ttcactctca ccatcagcag cctgcaacct 240
 gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
 ggcaccaagg tggaaatcaa a 321

<210> 68

<211> 107

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 68

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

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

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

Tyr Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Asn Arg Phe Ser Gly
 50 55 60

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

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

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

<210> 69
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 69
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
 atcacttgca aggccagtca gagggtgagt aatgatgtgg cttggtatca gcagaaacca 120
 ggcaaagccc ctaagctcct gatctatctt gcaaccaatc gctacactgg agtcccatcc 180
 cgcttcagcg gcagcggata cggcacagat ttcactctca ccatcagcag cctgcaacct 240
 gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac cttcgggtcag 300
 ggcaccaagg tggaaatcaa a 321

<210> 70
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 70

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

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

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

Tyr Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 71
<211> 321
<212> DNA
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 71
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
atcacttgca aggccagtca gagtgtgagt aatgatgtgg cttggtatca gcagaaacca 120
ggcaaagccc ctaagctcct gatctatctt gcaaccaatc gctacactgg agtcccatcc 180
cgcttcagcg gcagcggatc cggcacagat ttcactttca ccatcagcag cctgcaacct 240
gaagattttg caacttacta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
ggcaccaagg tggaaatcaa a 321

<210> 72
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 72

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

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

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

Tyr Phe Ala Thr Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> 73
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 73
 gaaattgtga tgacacagtc tccagccacc ctgtccctgt ctccaggcga aagagccacc 60
 ctctcctgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca gcagaaacct 120
 gggcaggctc ccaggctgct gatctatctt gcaaccaatc gctacactgg catcccagcc 180
 cgcttctccg gcagcggctc cggcacagac ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg cagtttatta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
 ggcaccaagg tggaaatcaa a 321

<210> 74
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> derived from human and mouse sequences

<400> 74

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

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Ser Ser Pro Trp
85 90 95

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

<210> 75

<211> 321

<212> DNA

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 75

gaaattgtga tgacacagtc tccagccacc ctgtccctgt ctccaggcga aagagccacc 60
ctctcctgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca gcagaaacct 120
gggcaggctc ccaggctgct gatctatattt gcaaccaatc gctacactgg catcccagcc 180
cgcttctccg gcagcggcta cggcacagac ttactctca ccatcagcag cctgcagcct 240
gaagattttg cagtttatta ctgtcagcag gattatagct ctccctggac cttcggtcag 300
ggcaccaagg tggaaatcaa a 321

<210> 76

<211> 107

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 76

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

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Ser Ser Pro Trp
85 90 95

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

<210> 77

<211> 117

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 77

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

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

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

Gly Glu Ile Tyr Pro Gly Ser Asn Ser Ile Tyr Tyr Asn Glu Lys Phe
50 55 60

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

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

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

Val Thr Val Ser Ser
115

<210> 78

<211> 117

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 78

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 Tyr Thr Phe Thr Asp Tyr
20 25 30

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

Ala Glu Ile Tyr Pro Gly Ser Asn Ser Ile Tyr Tyr Asn Glu Lys Phe
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 Gly Gly Asn Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 79
<211> 108
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 79

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 Thr Ala Ser Ser Ser Val Asn Ser Asn
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Leu Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 80
<211> 108
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 80

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

Asp Arg Val Thr Ile Thr Cys Thr Ala Ser Ser Ser Val Asn Ser Asn
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 81

<211> 122

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 81

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 Asn Thr Tyr
20 25 30

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

Gly Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

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

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

<210> 82
<211> 122
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 82

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 Asn Thr Tyr
20 25 30

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
65 70 75 80

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

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

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

<210> 83
<211> 107
<212> PRT
<213> Artificial

<220>
<223> derived from human and mouse sequences

<400> 83

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 Ala Ser Gln Asp Val Asp Thr Ala
 20 25 30

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 84

<211> 107

<212> PRT

<213> Artificial

<220>

<223> derived from human and mouse sequences

<400> 84

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 85
<211> 367
<212> PRT
<213> marmosets

<220>
<221> MISC_FEATURE
<222> (1)..(29)
<223> leader sequence

<220>
<221> mat_peptide
<222> (30)..(367)
<223> mature peptide - partial sequence

<220>
<221> MISC_FEATURE
<222> (30)..(356)
<223> ectodomain

<400> 85

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asn Gly Arg Leu
-25 -20 -15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
-10 -5 -1 1

Ser Pro Thr Ser Ser Ala Ser Ser Ser Ser Ser Ser Ala Pro Phe Leu
5 10 15

Ala Ser Ala Val Ser Ala Gln Pro Leu Leu Pro Gly Gln Cys Pro Ala
20 25 30 35

Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
40 45 50

Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Pro Tyr Val Arg Asn Leu
55 60 65

Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
70 75 80

Arg Val Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
 85 90 95

Arg Leu Glu Asp Val Gln Ala Gly Ala Phe Glu His Leu Pro Ser Leu
 100 105 110 115

Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Val Leu Ser Pro Phe
 120 125 130

Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
 135 140 145

Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Asn Asn
 150 155 160

Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Arg Ala Gly Gly Ala
 165 170 175

Leu His Gly Leu His Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
 180 185 190 195

Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
 200 205 210

Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
 215 220 225

Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
 230 235 240

Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Val Arg
 245 250 255

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
 260 265 270 275

Met Val Ala Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Tyr Gln
 280 285 290

Leu Thr Cys Ala Phe Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
 295 300 305

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
 310 315 320

Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly
 325 330 335

<210> 86
 <211> 420
 <212> PRT
 <213> Cynomologous monkey

<220>
 <221> MISC_FEATURE
 <222> (1)..(29)
 <223> leader sequence

<220>
 <221> mat_peptide
 <222> (30)..(420)

<220>
 <221> MISC_FEATURE
 <222> (30)..(356)
 <223> ectodomain

<400> 86

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
 -25 -20 -15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
 -10 -5 -1 1

Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
 5 10 15

Ala Ser Ala Ala Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
 20 25 30 35

Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
 40 45 50

Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Leu Tyr Val Arg Asn Leu
 55 60 65

Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
 70 75 80

Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
 85 90 95

Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu
 100 105 110 115

Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Tyr Leu Ser Pro Phe
 120 125 130

Ala Phe Ser Gly Ser Asn Ala Ser Ile Ser Ala Pro Ser Pro Leu Val
 135 140 145

Glu Leu Ile Leu Asn His Ile Val Pro Pro Asp Asp Lys Arg Gln Asn
 150 155 160

Arg Ser Phe Glu Gly Met Val Ala Ala Ala Leu Val Ala Gly Arg Ala
 165 170 175

Leu Gln Gly Leu His Leu Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
 180 185 190 195

Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg Tyr Leu Asp
 200 205 210

Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
 215 220 225

Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
 230 235 240

Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Val Arg
 245 250 255

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
 260 265 270 275

Met Val Thr Trp Leu Lys Gln Thr Glu Val Val Gln Gly Lys Asp Arg
 280 285 290

Leu Thr Cys Ala Phe Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
 295 300 305

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
 310 315 320

Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
 325 330 335

Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
 340 345 350 355

Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
 360 365 370

Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
 375 380 385

Asn Ser Asp Val
 390

<210> 87
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 87

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

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
 20 25 30

Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
 35 40 45

Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
 50 55 60

Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
 65 70 75 80

Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
 85 90 95

Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
 100 105 110

Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
 115 120 125

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

Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe
 145 150 155 160

Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
 165 170 175

Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
 180 185 190

Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala
 195 200 205

Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
 210 215 220

Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
 225 230 235 240

Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
 245 250 255

Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
 260 265 270

Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
 275 280 285

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
 290 295 300

Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
 305 310 315 320

Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
 325 330 335

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
 340 345 350

Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
 355 360 365

Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
 370 375 380

Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
 385 390 395 400

Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
 405 410 415

Asn Ser Asp Val
 420

<210> 88
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 88

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

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

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

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

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

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

Ala Arg Asp Ser Arg Gly Tyr Ser Tyr Asp Phe Trp Ser Gly Tyr Phe
 100 105 110

Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
 115 120 125

Ser Ser
 130

<210> 89
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 89

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> 90
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 90

Glu Val Gln Leu Leu 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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Lys

<210> 91
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 91

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 Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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> 92
 <211> 98

<212> PRT
<213> Homo sapiens

<400> 92

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 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
35 40 45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 93
<211> 97
<212> PRT
<213> Homo sapiens

<400> 93

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

Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
35 40 45

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

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

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

Arg

<210> 94
<211> 95
<212> PRT
<213> Homo sapiens

<400> 94

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

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

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

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

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

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

<210> 95
<211> 95
<212> PRT
<213> Homo sapiens

<400> 95

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

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

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

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

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

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

<210> 96
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 96

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

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

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

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

<210> 97
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 97

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

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

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
 35 40 45

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

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

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

<210> 98
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 98

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 Pro
 100

<210> 99
 <211> 96

<212> PRT

<213> Homo sapiens

<400> 99

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

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

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
50 55 60

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

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