

SEQUENCE LISTING

<110> GLAXO GROUP LIMITED
 BEMBRIDGE, Gary Peter
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 ELLIS, Jonathan Henry
 HAMBLIN, Paul, Andrew
 Lewis, Alan
 MCADAM, Ruth
 KOPSIDAS, George

<120> Immunoglobulins

<130> PB62663

<150> 60977841

<151> 2007-10-05

<160> 123

<170> FastSEQ for windows Version 4.0

<210> 1

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<212> PRT

<213> Mus Musculus

<400> 1

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<210> 2

<211> 17

<212> PRT

<213> Mus Musculus

<400> 2

Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys
 1 5 10 15
 Gly

<210> 3

<211> 17

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<213> Mus Musculus

<400> 3

Cys Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala Leu Asp
 1 5 10 15
 Tyr

<210> 4

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Mutated CDR

<400> 4

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 1 5 10 15

Tyr

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

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 Asn Gly Ala Lys Leu Glu Ser
 1 5

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<400> 7
 Leu Gln Asn Lys Glu Val Pro Tyr Thr
 1 5

<210> 8
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 <212> PRT
 <213> mus musculus

<400> 8
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 1 5 10 15
 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Cys Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 115 120 125

<210> 9
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 <212> DNA
 <213> mus musculus

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 actggacagg gccttgagtg gattggagag aattatccta gaagtggtaa tacttactac 180
 aatgagaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcgtac 240
 atggagctcc gcagcctgac atctgaggac tctgcggtct atttctgtgc aagatgcgaa 300

tttattagta cggtagtagc tccctattac tatgctctgg actactgggg tcaaggaacc 360
tcagtcaccg tctcctca 378

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<211> 119
<212> PRT
<213> mus musculus

<400> 10
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Lys Ala Thr Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
20 25 30
Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
35 40 45
Pro Lys Leu Ile Tyr Asn Gly Ala Lys Leu Glu Ser Gly Val Ser Ala
50 55 60
Arg Phe Ser Asp Ser Gly Ser Gln Asn Arg Ser Pro Phe Gly Asn Gln
65 70 75 80
Leu Ser Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
85 90 95
Thr Tyr Tyr Cys Leu Gln Asn Lys Glu Val Pro Tyr Thr Phe Gly Gly
100 105 110
Gly Thr Lys Leu Glu Ile Lys
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<211> 357
<212> DNA
<213> mus musculus

<400> 11
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taccaacaga aaccaggaca gccaccctata atggagccaa actagaatct 180
ggggtcagtg ccagggttcag tgacagtggg tctcagaacc gctcaccatt tggaaatcag 240
ctcagcttca cctcaccat tgatcctgtg gaggctgatg atgcagcaac ctattactgt 300
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<210> 12
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric sequence

<400> 12
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Gly Ile Thr Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Cys Glu Phe Ile Ser Thr Val Ala Pro Tyr Tyr Tyr Ala
100 105 110
Leu Asp Tyr Trp Gly Gln Gly Thr Ser Leu Val Thr Val Ser Ser Ala
115 120 125
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
130 135 140
Thr Ser Gly Gly Thr Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

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Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 Val His Thr Phe 165 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 Ile Cys Asn Val Asn His Lys 185 Pro Ser Asn Thr Lys Val Asp Lys Lys
 Val Glu Pro Lys Ser Cys 195 Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 Ala Pro Glu Leu Leu 200 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 Pro Lys Asp Thr 210 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 Val Asp Gly Val Glu Val His 220 Asn Ala Lys Thr Lys Pro Arg Glu Glu
 Gln Tyr Asn Ser Thr Tyr 235 Arg Val Val Ser Val Leu Thr Val Leu His
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 Ala Leu Pro Ala Pro Ile Glu Lys Thr 240 Ile Ser Lys Ala Lys Gly Gln
 Pro Arg Glu Pro Gln Val Tyr Thr 250 Leu Pro Pro Ser Arg Asp Glu Leu
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 Lys Ser Leu Ser Leu Ser Pro Gly Lys 445

<210> 13
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric sequence

<400> 13
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 actggacagg gccttgagtg gattggagag aattatccta gaagtggtaa tacttactac 180
 aatgagaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcgta 240
 atggagctcc gcagcctgac atctgaggac tctgcggtct atttctgtgc aagatgcaaa 300
 ttattagta cggtagtagc tccctattac tatgctctgg actactgggg tcaaggaacc 360
 tcaactagta ccgtgtccag cgccagcacc aagggcccca gcgtgttccc cctggccccc 420
 agcagcaaga gcaccagcgg cggcacagcc gccctgggct gcctggtgaa ggactacttc 480
 cccgaaccgg tgaccgtgtc ctggaacagc ggagccctga ccagcggcgt gcacaccttc 540
 cccgccgtgc tgcagagcag cggcctgtac agcctgagca gcgtggtgac cgtgcccagc 600
 agcagcctgg gcacccagac ctacatctgt aacgtgaacc acaagcccag caacaccaag 660
 gtggacaaga aggtggagcc caagagctgt gacaagaccc acacctgccc cccctgccc 720
 gccccgagc tgctgggagg cccagcgtg ttcctgttcc cccccaagcc taaggacacc 780
 ctgatgatca gcagaacccc cgaggtgagc tgtgtggtgg tggatgtgag ccacgaggac 840
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 cccagggagg agcagtacaa cagcacctac cgggtggtgt ccgtgctgac cgtgctgcac 960
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 ctgcccccta gcagagatga gctgaccaag aaccaggtgt ccctgacctg cctggtgaag 1140
 ggcttctacc ccagcgacat cgccgtggag tgggagagca acggccagcc cgagaacaac 1200

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 accgtggaca agagcagatg gcagcagggc aacgtgttca gctgctccgt gatgcacgag 1320
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<210> 14

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric sequence

<400> 14

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

<210> 15

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric sequence

<400> 15

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taccaacaga	aaccaggaca	gccacccaaa	ctcatctata	atggagccaa	actagaatct	180
ggggtcagtg	ccaggttcag	tgacagtggg	tctcagaacc	gctcaccatt	tggaatcag	240
ctcagcttca	ccctcaccat	tgatcctgtg	gaggctgatg	atgcagcaac	ctattactgt	300
ctgcaaaata	aagaggttcc	gtacacgttc	ggagggggga	ccaagctgga	aataaaacgt	360
acggtggccg	ccccagcgt	gttcattctt	ccccccagcg	atgagcagct	gaagagcggc	420
accgccagcg	tggtgtgtct	gctgaacaac	ttctaccccc	gggaggccaa	ggtgcagtgg	480
aaggtggaca	atgccctgca	gagcggcaac	agccaggaga	gcgtgaccga	gcaggacagc	540
aaggactcca	cctacagcct	gagcagcacc	ctgaccctga	gcaaggccga	ctacgagaag	600
cacaaggtgt	acgcctgtga	ggtgaccac	cagggcctgt	ccagccccgt	gaccaagagc	660
ttcaaccggg	gcgagtgc					678

<210> 16

<211> 126

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 16
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 17
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 17
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 agctgcaaag cctcaggcta cacccttcacc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgctgtgt actactgctc caggagcgag 300
 ttcacagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
 ctagtgaccg tgtccagc 378

<210> 18
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 18
 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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 19
 <211> 333

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 19
 Gly Ala Cys Ala Thr Cys Gly Thr Gly Ala Thr Gly Ala Cys Cys Cys
 1 5 10 15
 Ala Gly Ala Gly Cys Cys Cys Cys Gly Ala Thr Ala Gly Cys Cys Thr
 20 25 30
 Cys Gly Cys Thr Gly Thr Gly Ala Gly Cys Cys Thr 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 Cys Ala Ala
 65 70 75 80
 Gly Ala Ala Gly Gly Thr Cys Ala Cys Cys Ala Thr Cys Thr Thr Cys
 85 90 95
 Gly Gly Cys Ala Gly Cys Ala Thr Cys Thr Cys Cys Gly Cys Cys Cys
 100 105 110
 Thr Gly Cys Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys Ala
 115 120 125
 Gly Ala Ala Gly Cys Cys Cys Gly Gly Ala Cys Ala Gly Cys Cys Cys
 130 135 140
 Cys Cys Cys Ala Ala Gly Cys Thr Gly Ala Thr Cys Thr Ala Cys Ala
 145 150 155 160
 Ala Cys Gly Gly Cys Gly Cys Cys Ala Ala Gly Cys Thr Gly Gly Ala
 165 170 175
 Gly Ala Gly Cys Gly Gly Cys Gly Thr Gly Cys Cys Cys Gly Ala Cys
 180 185 190
 Ala Gly Gly Thr Thr Thr Ala Gly Cys Gly Gly Cys Ala Gly Cys Gly
 195 200 205
 Gly Cys Ala Gly Cys Gly Gly Cys Ala Cys Ala Gly Ala Cys Thr Thr
 210 215 220
 Cys Ala Cys Cys Cys Thr Gly Ala Cys Cys Ala Thr Thr Ala Gly Cys
 225 230 235 240
 Ala Gly Cys Cys Thr Gly Cys Ala Gly Gly Cys Cys Gly Ala Ala Gly
 245 250 255
 Ala Cys Gly Thr Gly Gly Cys Cys Gly Thr Gly Thr Ala Cys Thr Ala
 260 265 270
 Cys Thr Gly Cys Cys Thr Gly Cys Ala Gly Ala Ala Cys Ala Ala Gly
 275 280 285
 Gly Ala Gly Gly Thr Gly Cys Cys Cys Thr Ala Cys Ala Cys Cys Thr
 290 295 300
 Thr Cys Gly Gly Cys Gly Gly Gly Gly Cys Ala Cys Cys Ala Ala
 305 310 315 320
 Ala Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala Gly
 325 330

<210> 20
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

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

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<210> 21
<211> 357
<212> DNA
<213> Artificial Sequence
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<220>
<223> Humanised sequence

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tatcagcaga	aacccggaca	gccccccaag	ctgactctaca	acggcgccaa	gctggaaaagc	180	
ggcgtgagcg	acaggttcag	cgatagcggc	agccagaaca	ggagcccttt	cggcaaacag	240	
ctgagcttca	ccctgaccat	cagcagcctc	caggccgagg	acgtcgcagt	gtactactgc	300	
ctgcagaaca	aggaggtgcc	ctacaccttt	ggcggcggca	ccaaggtgga	gattaag	357	

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<210> 22
<211> 119
<212> PRT
<213> Artificial Sequence
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<220>
<223> Humanised sequence

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<210> 23
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanised sequence

<400> 23							
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tacctgcaga	aacccgggca	gcccccccag	ctgatctata	acggcgctaa	gctggagagc		180
ggcgtgtccg	acaggttcag	cgactctgga	agccagaaca	ggagccccct	cggaaccag		240
ctgagcttca	cctgaagatg	cagcagggtg	gaagccgagg	acgtggcggt	gtactactgc		300
ctgcagaaca	aggaggtgcc	ctacaccttc	ggaggcggca	ccaaggctca	gatcaag		357

<210> 24

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

<220>
 <223> Humanised sequence

<400> 24
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Gln Leu Ile Tyr Asn Gly Ala Lys Leu Glu Ser Gly Val Ser Asp
 50 55 60
 Arg Phe Ser Asp Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 65 70 75 80
 Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 25
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 25
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 tacctccaga agcccgggca gcccacacag ctgatctaca acggcgccaa gctggagagc 180
 ggcgtgagcg acaggttctc tgatagcggc agcggcaccg acttcaccct gaagattagc 240
 aggggtggagg ccgaggacgt gggcgtgtac tactgcctgc agaacaagga ggtgccctac 300
 accttcggcg gcggcaccaa agtcgagatc aag 333

<210> 26
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 26
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 115 120 125
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 130 135 140
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 145 150 155 160

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Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 165 170 175
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 180 185 190
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 195 200 205
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 210 215 220
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 225 230 235 240
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 275 280 285
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 290 295 300
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 305 310 315 320
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 340 345 350
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 355 360 365
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 405 410 415
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 420 425 430
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 27

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 27

caggtgcagc	tggtgcagag	cggcgccgaa	gtgaagaagc	ccggctccag	cgtgaagggtg	60
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cccggccagg	gactggagtg	gatgggagag	aactacccca	ggagcggcaa	cacctactac	180
aacgagaagt	tcaagggcag	ggtgaccatc	accgccgaca	agagcaccag	caccgcctac	240
atggagctga	gcagcctgag	gagcgaggac	accgctgtgt	actactgcgc	caggagcgag	300
ttcatcagca	ccgtcgtggc	cccctactac	tacgccctcg	actattgggg	ccagggcaca	360
ctagtgaccg	tgtccagcgc	cagcaccaag	ggccccagcg	tgttccccct	ggcccccagc	420
agcaagagca	ccagcggcgg	cacagccgcc	ctgggctgcc	tggtgaagga	ctacttcccc	480
gaaccggtga	ccgtgtcctg	gaacagcgga	gccctgacca	gcggcgtgca	caccttcccc	540
gccgtgctgc	agagcagcgg	cctgtacagc	ctgagcagcg	tggtgaccgt	gcccagcagc	600
agcctgggca	cccagaccta	catctgtaac	gtgaaccaca	agcccagcaa	caccaagggtg	660
gacaagaagg	tggagcccaa	gagctgtgac	aagaccacaca	cctgcccccc	ctgccctgcc	720
cccgagctgc	tgggaggccc	cagcgtgttc	ctgttcccc	ccaagcctaa	ggacaccctg	780
atgatcagca	gaacccccga	ggtgacctgt	gtgggtggtg	atgtgagcca	cgaggaccct	840
gaggtgaagt	tcaactggta	cgtggacggc	ctggaggtgc	acaatgccaa	gaccaagccc	900
agggaggagc	agtacaacag	cacctaccgg	gtggtgtccg	tgctgaccgt	gctgcaccag	960
gattggctga	acggcaagga	gtacaagtgt	aaggtgtcca	acaaggccct	gcctgccct	1020
atcgagaaaa	ccatcagcaa	ggccaagggc	cagcccagag	agccccaggt	gtacaccctg	1080
ccccctagca	gagatgagct	gaccaagaac	caggtgtccc	tgacctgcct	ggtgaagggc	1140
ttctacccca	gcgacatcgc	cgtggagttg	gagagcaacg	gccagcccga	gaacaactac	1200

PhoenixTemp3419.tmp.txt

```

aagaccaccc cccctgtgct ggacagcgat ggcagcttct tcctgtacag caagctgacc 1260
gtggacaaga gcagatggca gcagggcaac gtgttcagct gctccgtgat gcacgaggcc 1320
ctgcacaatc actacacca gaagagcctg agcctgtccc ctggcaag 1368

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<210> 28
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<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 Ala Ser Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr 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 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> 29
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 29
 gacatcgtga tgaccagag ccccgatagc ctcgctgtga gcctgggcga gagggccacc 60
 atcaactgca aggccagcaa gaaggtcacc atcttcggca gcatctccgc cctgcactgg 120
 taccagcaga agcccggaca gcccccaag ctgatctaca acggcgccaa gctggagagc 180
 ggcgtgcccg acaggtttag cggcagcggc agcggcacag acttcaccct gaccattagc 240
 agcctgcagg ccgaagacgt ggccgtgtac tactgcctgc agaacaagga ggtgccctac 300
 accttcggcg ggggcaccaa agtggagatc aagcgtacgg tggccgcccc cagcgtgttc 360
 atcttcccc ccagcgatga gcagctgaag agcggcaccc ccagcgtggt gtgtctgctg 420
 aacaacttct acccccggga ggccaaggtg cagtgggaagg tggacaatgc cctgcagagc 480
 ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
 agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
 acccaccagg gcctgtccag ccccgtagcc aagagcttca accggggcga gtgc 654

<210> 30
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 30

```

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

```

<210> 31

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 31

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gacatcgtga tgactcagtc tcccgcacagc ctggccgtga gcctgggcga gagggccacc 60
atcaactgca aggccagcaa gaaggtgacc atcttcggga gcatctccgc cctgcactgg 120
tatcagcaga aacccggaca gcccccaag ctgatctaca acggcgccaa gctggaaagc 180
ggcgtgagcg acaggttcag cgatagcggc agccagaaca ggagcccttt cggcaaccag 240
ctgagcttca ccctgacat cagcagcctc caggccgagg acgtcgcagt gtactactgc 300
ctgcagaaca aggaggtgcc ctacaccttt ggcgccggca ccaaggtgga gattaagcgt 360
acggtgcccg ccccagcgt gttcatcttc ccccagcg atgagcagct gaagagcggc 420
accgccagcg tgggtgtgtct gctgaacaac ttctaccccc gggaggccaa ggtgcagtgg 480
aaggtggaca atgccctgca gagcggcaac agccaggaga gcgtgaccga gcaggacagc 540
aaggactcca cctacagcct gagcagcacc ctgaccctga gcaaggccga ctacgagaag 600
cacaaggtgt acgcctgtga ggtgaccac cagggcctgt ccagccccgt gaccaagagc 660
ttcaaccggg gcgagtgc
678

```

<210> 32

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 32

```

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

```

PhoenixTemp3419.tmp.txt

Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
 20 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Pro
 35 45
 Pro Gln Leu Ile Tyr Asn Gly Ala Lys Leu Glu Ser Gly Val Ser Asp
 50 60
 Arg Phe Ser Asp Ser Gly Ser Gln Asn Arg Ser Pro Phe Gly Asn Gln
 65 75 80
 Leu Ser Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
 85 95
 Val Tyr Tyr Cys Leu Gln Asn Lys Glu Val Pro Tyr Thr Phe Gly Gly
 100 110
 Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Val Phe
 115 125
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 130 140
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 145 155 160
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 165 175
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 180 190
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 195 205
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 210 220
 Glu Cys
 225

<210> 33
 <211> 678
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 33
 gatatcgtga tgaccagac ccccctgagc ctgagcgtga ctccaggcca gcccgccagc 60
 atcagctgca aggccagcaa gaaggtgacc atcttcggca gcattagcgc cctccactgg 120
 tacctgcaga aacccgggca gcccccccag ctgatctata acggcgctaa gctggagagc 180
 ggctgtgccg acaggttcag cgactctgga agccagaaca ggagcccctt cggcaaccag 240
 ctgagcttca ccctgaagat cagcaggggtg gaagccgagg acgtgggctg gtactactgc 300
 ctgcagaaca aggaggtgcc ctacaccttc ggaggcggca ccaaggtcga gatcaagcgt 360
 acggtggccg cccccagcgt gttcatcttc cccccagcgc atgagcagct gaagagcggc 420
 accgccagcg tgggtgtgtc gctgaacaac ttctaccccc gggaggccaa ggtgcagtgg 480
 aaggtggaca atgccctgca gagcggcaac agccaggaga gcgtgaccga gcaggacagc 540
 aaggactcca cctacagcct gagcagcacc ctgaccctga gcaaggccga ctacgagaag 600
 cacaaggtgt acgcctgtga ggtgaccac cagggcctgt ccagcccctg gaccaagagc 660
 ttcaaccggg gcgagtgc 678

<210> 34
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 34
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Gln Leu Ile Tyr Asn Gly Ala Lys Leu Glu Ser Gly Val Ser Asp
 50 55 60

PhoenixTemp3419.tmp.txt

Arg Phe Ser Asp Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 65 70 75 80
 Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr 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> 35
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 35
 gacatcgtga tgaccagac tcccctgtcc ctgagcgtga ccccgagaca gcccgccagc 60
 atcagctgca aggccagcaa gaaggtgacc atcttcggca gcatcagcgc cctgcactgg 120
 tacctccaga agccggggca gcccacacag ctgatctaca acggcgccaa gctggagagc 180
 ggctgagcgc acaggttctc tgatagcggc agcggcaccg acttcaccct gaagattagc 240
 aggggtggagg ccgaggacgt gggcgtgtac tactgcctgc agaacaagga ggtgccctac 300
 accctcggcg gcggcaccaa agtcgagatc aagcgtacgg tggccgcccc cagcgtgttc 360
 atcttcccc ccagcgatga gcagctgaag agcggcaccg ccagcgtggg gtgtctgctg 420
 aacaacttct acccccgga ggccaaggtg cagtgggaagg tggacaatgc cctgcagagc 480
 ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
 agcaccctga cctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
 acccaccagg gcctgtccag ccccgtagacc aagagcttca accggggcga gtgc 654

<210> 36
 <211> 19
 <212> PRT
 <213> Homo Sapiens

<400> 36
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser

<210> 37
 <211> 189
 <212> PRT
 <213> Homo Sapiens

<400> 37
 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Pro Trp Thr
 1 5 10 15
 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
 20 25 30
 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
 35 40 45
 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
 50 55 60

PhoenixTemp3419.tmp.txt

Thr	Asn	Asp	Val	Pro	His	Ile	Gln	Cys	Gly	Asp	Gly	Cys	Asp	Pro	Gln
65					70					75					80
Gly	Leu	Arg	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	His	Gln	Gly
				85					90					95	
Leu	Ile	Phe	Tyr	Glu	Lys	Leu	Leu	Gly	Ser	Asp	Ile	Phe	Thr	Gly	Glu
			100					105					110		
Pro	Ser	Leu	Leu	Pro	Asp	Ser	Pro	Val	Gly	Gln	Leu	His	Ala	Ser	Leu
		115					120					125			
Leu	Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr
	130					135					140				
Gln	Gln	Ile	Pro	Ser	Leu	Ser	Pro	Ser	Gln	Pro	Trp	Gln	Arg	Leu	Leu
145					150					155					160
Leu	Arg	Phe	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala
				165					170					175	
Ala	Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Ser	Pro			
			180					185							

<210> 38
 <211> 567
 <212> DNA
 <213> Homo Sapiens

<400> 38
 atgctgggga gcagagctgt aatgctgctg ttgctgctgc cctggacagc tcagggcaga 60
 gctgtgccctg ggggcagcag ccctgcctgg actcagtgcc agcagctttc acagaagctc 120
 tgcacactgg cctggagtgc acatccacta gtgggacaca tggatctaag agaagaggga 180
 gatgaagaga ctacaaatga tgttcccat atccagtgtg gagatggctg tgacccccaa 240
 ggactcaggg acaacagtca gttctgcttg caaaggatcc accaggggtct gattttttat 300
 gagaagctgc taggatcgga tattttcaca ggggagcctt ctctgctccc tgatagccct 360
 gtggggccagc ttcatgcctc cctactgggc ctcagccaac tcctgcagcc tgagggtcac 420
 cactggggaga ctcagcagat tccaagcctc agtcccagcc agccatggca gcgtctcctt 480
 ctccgcttca aaatccttcg cagcctccag gcctttgtgg ctgtagccgc ccgggtcttt 540
 gccatggag cagcaaccct gagtccc 567

<210> 39
 <211> 328
 <212> PRT
 <213> Homo Sapiens

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

PhoenixTemp3419.tmp.txt

```

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235
Leu Gln Leu Lys Pro 245 Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
250 255
Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270
Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285
Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300
Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320
Glu Trp Ala Ser Val Pro Cys Ser
325

```

<210> 40
 <211> 984
 <212> DNA
 <213> Homo Sapiens

```

<400> 40
atgtgtcacc agcagttggt catctcttgg ttttccctgg tttttctggc atctcccctc 60
gtggccatat gggaactgaa gaaagatggt tatgtcgtag aattggattg gtatccggat 120
gccccctggag aaatgggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa 240
gagtttgag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatttt aaaggaccag 360
aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480
ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc 540
agagggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca 600
gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac 780
acctggagta ctccacattc ctacttctcc ctgacattct gcgttcagggt ccagggcaag 840
agcaagagag aaaagaaaga tagagtcttc acggacaaga cctcagccac ggtcatctgc 900
cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc 960
gaatgggcat ctgtgccctg cagt
984

```

<210> 41
 <211> 253
 <212> PRT
 <213> Homo Sapiens

```

<400> 41
Met Trp Pro Pro Gly Ser Ala Ser Gln Pro Pro Pro Ser Pro Ala Ala
1 5 10 15
Ala Thr Gly Leu His Pro Ala Ala Arg Pro Val Ser Leu Gln Cys Arg
20 25 30
Leu Ser Met Cys Pro Ala Arg Ser Leu Leu Val Ala Thr Leu Val
35 40 45
Leu Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro
50 55 60
Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
65 70 75 80
Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
85 90 95
Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
100 105 110
Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
115 120 125
Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
130 135 140
Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
145 150 155 160
Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn
165 170 175
Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn

```


PhoenixTemp3419.tmp.txt

Met	Leu	Ala	Val	Ile	Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser
		195					200					205			
Glu	Thr	Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys
	210					215					220				
Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala
225					230					235					240
Val	Thr	Ile	Asp	Arg	Val	Met	Ser	Tyr	Leu	Asn	Ala	Ser			
				245					250						

```
<210> 42
<211> 759
<212> DNA
<213> Homo Sapiens
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<400>	42						
atgtggcccc	ctgggtcagc	ctcccagcca	ccgccctcac	ctgccgcggc	cacaggtctg	60	
catccagcgg	ctcgccctgt	gtcccttcag	tgccggctca	gcattgtgtc	agcgcgcagc	120	
ctctctcttg	tggctacctt	ggtcctctgt	gaccacctca	gtttggccag	aaacctcccc	180	
gtggccactc	cagaccacag	aatgttccca	tgcttcacc	actcccaaaa	cctgctgagg	240	
gccgtcagca	acatgctcca	gaaggccaga	caaactctag	aattttaccc	ttgcacttct	300	
gaagagattg	atcatgaaga	tatcacaaaa	gataaaaacca	gcacagtggg	ggcctgttta	360	
ccatttgaat	taaccaagaa	tgagagtgtc	ctaaattcca	gagagacctc	tttcataact	420	
aatggggagt	gcctggcctc	cagaaagacc	ctttttatga	tggccctgtg	ccctagtagt	480	
atztatgaag	acttgaagat	gtaccaggtg	gagttcaaga	ccatgaatgc	aaagcttctg	540	
atggatccta	agaggcagat	ctttctagat	caaaacatgc	tggcagttat	tgatgagctg	600	
atgcaggccc	tgaatttcaa	cagtgcagct	gtgccacaaa	aatcctccct	tgaagaaccg	660	
gatttttata	aaactaaaa	caagctctgc	atacttcttc	atgccttcag	aattcgggca	720	
gtgactattg	atagagtgat	gagctatctg	aatgccttcc			759	

<210> 43
<211> 189
<212> PRT
<213> Macaca fascicularis

<400>	43															
Met	Leu	Gly	Ser	Arg	Ala	Val	Met	Leu	Leu	Leu	Leu	Leu	Ser	Trp	Thr	
1				5				10					15			
Ala	Gln	Gly	Arg	Ala	Val	Pro	Gly	Gly	Ser	Ser	Pro	Ala	Trp	Ala	Gln	
			20					25					30			
Cys	Gln	Gln	Leu	Ser	Gln	Lys	Leu	Cys	Thr	Leu	Ala	Trp	Ser	Ala	His	
		35					40					45				
Pro	Leu	Val	Gly	His	Met	Asp	Leu	Arg	Glu	Glu	Gly	Asp	Glu	Glu	Thr	
	50					55					60					
Thr	Asn	Asp	Val	Pro	His	Ile	Gln	Cys	Gly	Asp	Gly	Cys	Asp	Pro	Gln	
65					70					75					80	
Gly	Leu	Arg	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	Arg	Gln	Gly	
				85					90					95		
Leu	Ile	Phe	Tyr	Glu	Lys	Leu	Leu	Gly	Ser	Asp	Ile	Phe	Thr	Gly	Glu	
			100					105					110			
Pro	Ser	Leu	Leu	Pro	Asp	Ser	Pro	Val	Gly	Gln	Leu	His	Ala	Ser	Leu	
		115					120					125				
Leu	Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr	
	130					135					140					
Gln	Gln	Ile	Pro	Ser	Pro	Ser	Pro	Ser	Gln	Pro	Trp	Gln	Arg	Leu	Leu	
145					150					155					160	
Leu	Arg	Phe	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala	
				165					170					175		
Ala	Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Ser	Pro				
			180					185								

```
<210> 44
<211> 567
<212> DNA
<213> Macaca fascicularis
```

<400> 44

PhoenixTemp3419.tmp.txt

```

atgctgggga gcagagctgt aatgctgctg ttgctgctgt cctggacagc tcagggcagg 60
gctgtgcctg ggggcagcag ccctgcctgg gctcagtgcc agcagctttc acagaagctc 120
tgacactgg cctggagtg acatccacta gtgggacaca tggatctaag agaagaggga 180
gatgaagaga ctacaaatga tgttcccat atccagtgtg gagatggctg tgaccccaa 240
ggactcaggg acaacagtca gttctgcttg caaaggattc gccaggggtct gattttttac 300
gagaagctac tgggatcgga tattttcaca ggggagcctt ctctgctgcc tgatagccct 360
gtgggccagc ttcatgcctc cctactgggc ctcagccaac tcctgcagcc tgaggggtcac 420
cactgggaga ctcagcagat tccaagcccc agtcccagcc agccatggca gcgcctcctt 480
ctccgcttca aaatccttcg cagcctccag gcctttgtgg ctgtagctgc ccgggtcttt 540
gcccatggag cagcaaccct gagtccc 567

```

<210> 45
 <211> 328
 <212> PRT
 <213> Macaca fascicularis

```

<400> 45
Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
1      5      10      15
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20     25     30
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35     40     45
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
50     55     60
Ser Gly Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65     70     75     80
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Ala
85     90     95
Leu Ser His Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100    105    110
Ser Thr Asp Val Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115    120    125
Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130    135    140
Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
145    150    155    160
Gly Ser Ser Asn Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165    170    175
Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180    185    190
Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Arg Leu Pro Ile
195    200    205
Glu Val Met Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr
210    215    220
Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225    230    235    240
Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245    250    255
Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260    265    270
Phe Cys Ile Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275    280    285
Ile Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290    295    300
Ser Phe Ser Val Gln Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305    310    315    320
Glu Trp Ala Ser Val Pro Cys Ser
325

```

<210> 46
 <211> 984
 <212> DNA
 <213> Macaca fascicularis

```

<400> 46
atgtgtcacc agcagctggg catctcttgg ttttcctgg tttttctggc atctcccctc 60
atggccatat gggaactgaa gaaagacgtt tatgtttag aattggactg gtaccgcat 120

```

PhoenixTemp3419.tmp.txt

```

gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttggacc agagtgggtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggctct aagccattca 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatgtttt aaaggaccag 360
aaagaaccca aaaataagac ctttctaaga tgcgaggcca aaaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatctgacat tcagtgtcaa aagcagcaga 480
ggctcttcta acccccaagg ggtgacgtgt ggagccgtta cactctctgc agagaggggtc 540
agaggggaca ataaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca 600
gccgctgagg agaggctgcc cattgaggtc atgggtgatg ccattcacia gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacccgaccc acccaagaac 720
ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac 780
acctggagta ctccacattc ctacttctcc ctgacattct gcattccagg ccagggcaag 840
agcaagagag aaaagaaaaga tagaatcttc acagacaaga cctcagccac ggtcatctgc 900
cgcaaaaatg ccagcttttag cgtgcaggcc caggaccgct actatagctc atcttggagc 960
gaatgggcat ctgtgccctg cagt

```

<210> 47

<211> 629

<212> PRT

<213> Homo Sapiens

<400> 47

```

Met Asn Gln Val Thr Ile Gln Trp Asp Ala Val Ile Ala Leu Tyr Ile
1      5      10      15
Leu Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly
20     25     30
His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile
35     40     45
Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu
50     55     60
His Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile
65     70     75     80
Asn Lys Thr Thr Ala Arg Leu Trp Tyr Lys Asn Phe Leu Glu Pro His
85     90     95
Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Lys His Phe Gln Glu Thr
100    105    110
Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ile Pro
115    120    125
Asp Glu Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys
130    135    140
Thr Trp Asn Ala Gly Lys Leu Thr Tyr Ile Asp Thr Lys Tyr Val Val
145    150    155    160
His Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Thr Ser
165    170    175
Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Tyr
180    185    190
Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Glu Ser Lys
195    200    205
Gln Leu Gln Ile His Leu Asp Asp Ile Val Ile Pro Ser Ala Ala Val
210    215    220
Ile Ser Arg Ala Glu Thr Ile Asn Ala Thr Val Pro Lys Thr Ile Ile
225    230    235    240
Tyr Trp Asp Ser Gln Thr Thr Ile Glu Lys Val Ser Cys Glu Met Arg
245    250    255
Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr
260    265    270
Asn Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ile
275    280    285
Lys Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp
290    295    300
Gln Pro Trp Ser Ser Leu Phe Phe His Lys Thr Pro Glu Thr Val Pro
305    310    315    320
Gln Val Thr Ser Lys Ala Phe Gln His Asp Thr Trp Asn Ser Gly Leu
325    330    335
Thr Val Ala Ser Ile Ser Thr Gly His Leu Thr Ser Asp Asn Arg Gly
340    345    350
Asp Ile Gly Leu Leu Leu Gly Met Ile Val Phe Ala Val Met Leu Ser
355    360    365
Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Phe Arg Thr Gly Ile

```

PhoenixTemp3419.tmp.txt

370 375 380
 Lys Arg Arg Ile Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp Ile
 385 390 395 400
 Pro Asn Met Lys Asn Ser Asn Val Val Lys Met Leu Gln Glu Asn Ser
 405 410 415
 Glu Leu Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp Pro
 420 425 430
 Met Ile Thr Glu Ile Lys Glu Ile Phe Ile Pro Glu His Lys Pro Thr
 435 440 445
 Asp Tyr Lys Lys Glu Asn Thr Gly Pro Leu Glu Thr Arg Asp Tyr Pro
 450 455 460
 Gln Asn Ser Leu Phe Asp Asn Thr Thr Val Val Tyr Ile Pro Asp Leu
 465 470 475 480
 Asn Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Pro Glu Gly Ser
 485 490 495
 His Leu Ser Asn Asn Asn Glu Ile Thr Ser Leu Thr Leu Lys Pro Pro
 500 505 510
 Val Asp Ser Leu Asp Ser Gly Asn Asn Pro Arg Leu Gln Lys His Pro
 515 520 525
 Asn Phe Ala Phe Ser Val Ser Ser Val Asn Ser Leu Ser Asn Thr Ile
 530 535 540
 Phe Leu Gly Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Cys Ser Ser
 545 550 555 560
 Pro Asp Ile Gln Asn Ser Val Glu Glu Glu Thr Thr Met Leu Leu Glu
 565 570 575
 Asn Asp Ser Pro Ser Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro Asp
 580 585 590
 Glu Phe Val Ser Cys Leu Gly Ile Val Asn Glu Glu Leu Pro Ser Ile
 595 600 605
 Asn Thr Tyr Phe Pro Gln Asn Ile Leu Glu Ser His Phe Asn Arg Ile
 610 615 620
 Ser Leu Leu Glu Lys
 625

<210> 48
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 48
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 49
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

```

<400> 49
caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccgggtccag cgtgaagggtg 60
agctgcaaag cctcaggcta caccttcacc agctacggca tcacttgggt gaggcaggcc 120
cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggagctga gcagcctgag gagcgaggac accgctgtgt actactgcg cagggctgag 300
ttcatcagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
ctagtgaccg tgtccagc 378

```

```

<210> 50
<211> 126
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Humanised sequence

```

```

<400> 50
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 Tyr Thr Phe Thr Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
          50          55          60
Lys 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 Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100          105          110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115          120          125

```

```

<210> 51
<211> 378
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Humanised sequence

```

```

<400> 51
caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccgggtccag cgtgaagggtg 60
agctgcaaag cctcaggcta caccttcacc agctacggca tcacttgggt gaggcaggcc 120
cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggagctga gcagcctgag gagcgaggac accgctgtgt actactgcg caggggtggag 300
ttcatcagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
ctagtgaccg tgtccagc 378

```

```

<210> 52
<211> 126
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Humanised sequence

```

```

<400> 52
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 Tyr Thr Phe Thr Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45

```

PhoenixTemp3419.tmp.txt

Gly	Glu	Asp	Tyr	Pro	Arg	Ser	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Lys	Phe
	50					55					60				
Lys	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	Ser	Glu	Phe	Ile	Ser	Thr	Val	Val	Ala	Pro	Tyr	Tyr	Tyr	Ala
			100					105					110		
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

<210> 53
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 53
 cagggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccgggtccag cgtgaagggtg 60
 agctgcaaag cctcaggcta caccttcacc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagtg gatgggagag gactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgctgtgt actactgctc caggagcgag 300
 ttcacagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
 ctagtgaccg tgtccagc 378

<210> 54
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

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	Tyr	Thr	Phe	Ala	Ser	Tyr
			20					25					30		
Gly	Ile	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Glu	Asn	Tyr	Pro	Arg	Ser	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Lys	Phe
	50					55					60				
Lys	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	Met	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Ser	Glu	Phe	Ile	Ser	Thr	Val	Val	Ala	Pro	Tyr	Tyr	Tyr	Ala
			100					105					110		
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

<210> 55
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 55
 cagggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccgggtccag cgtgaagggtg 60
 agctgcaaag cctcaggcta caccttcgcc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240

PhoenixTemp3419.tmp.txt

atggagctga gcagcctgag gagcgaggac accgctatgt actactgctg caggagcgag 300
 ttcatcagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccaggggcaca 360
 ctagtgaccg tgtccagc 378

<210> 56
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 56
 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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 57
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 57
 gacatcgtga tgaccagag ccccgatagc ctcgctgtga gcctgggcca gagggccacc 60
 atcaactgca aggccagcaa gaaggtcacc atcttcggca gcacctccgc cctgcactgg 120
 taccagcaga agcccgaca gcccccaag ctgatctaca acggcgccaa gctggagagc 180
 ggcgtgcccc acagggttag cggcagcggc agcggcacag acttcaccct gaccattagc 240
 agcctgcagg ccgaagacgt ggccgtgtac tactgcctgc agaacaagga ggtgccctac 300
 accttcggcg ggggcaccaa agtgagatc aag 333

<210> 58
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys Pro 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

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

<220>
 <223> Humanised sequence

<400> 59
 gacatcgtga tgaccagag ccccgatagc ctcgctgtga gcctgggcga gagggccacc 60
 atcaactgca aggccagcaa gaaggtcacc atcttcggca gcacctccgc cctgcactgg 120
 taccagcaga agcccgaca gcccccaag ctgacttaca acggcgccaa gcccgagagc 180
 ggctgtgccc acaggtttag cggcagcggc agcggcacag acttcaccct gaccattagc 240
 agcctgcagg ccgaagacgt ggccgtgtac tactgcctgc agaacaagga ggtgcctac 300
 accttcggcg ggggcacaa agtgagatc aag 333

<210> 60
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 60
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 115 120 125
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 130 135 140
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 145 150 155 160
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 165 170 175
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 180 185 190
 Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 195 200 205
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 210 215 220
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 225 230 235 240
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 275 280 285
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 290 295 300
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 305 310 315 320
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

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```

          340          345          350
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
          355          360          365
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
          370          375          380
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385          390          395          400
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
          405          410          415
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
          420          425          430
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
          435          440          445
Ser Leu Ser Leu Ser Pro Gly Lys
          450          455

```

<210> 61

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 61

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caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccggctccag cgtgaagggtg 60
agctgcaaag cctcaggcta caccttcacc agctacggca tcacttgggt gaggcaggcc 120
cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
atggagctga gcagcctgag gagcgaggac accgctgtgt actactgcgc cagggctgag 300
ttcatcagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
ctagtgaccg tgtccagcgc cagcaccaag ggccccagcg tgttccccct ggcccccagc 420
agcaagagca ccagcggcgg cacagccgcc ctgggctgcc tgggtgaagga ctacttcccc 480
gaaccggtga ccgtgtcctg gaacagcggg gccctgacca gcggcgtgca caccttcccc 540
gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tggtgaccgt gccagcagc 600
agcctgggca cccagaccta catctgtaac gtgaaccaca agcccagcaa caccaagggtg 660
gacaagaagg tggagcccaa gagctgtgac aagaccaca cctgcccccc ctgccctgcc 720
cccgagctgc tgggaggccc cagcgtgttc ctgttcccc ccaagcctaa ggacaccctg 780
atgatcagca gaacccccga ggtgacctgt gtggtggtgg atgtgagcca cgaggacctt 840
gaggtgaagt tcaactggta cgtggacggc gtggaggtgc acaatgccaa gaccaagccc 900
agggaggagc agtacaacag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 960
gattggctga acggcaagga gtacaagtgt aaggtgtcca acaaggccct gcctgcccct 1020
atcgagaaaa ccatcagcaa ggccaagggc cagcccagag agccccaggt gtacaccctg 1080
ccccctagca gagatgagct gaccaagaac caggtgtccc tgacctgcct ggtgaagggc 1140
ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1200
aagaccaccc cccctgtgct ggacagcgat ggcagcttct tcctgtacag caagctgacc 1260
gtggacaaga gcagatggca gcagggcaac gtgttcagct gctccgtgat gcacgaggcc 1320
ctgcacaatc actacacca gaagagcctg agcctgtccc ctggcaag 1368

```

<210> 62

<211> 456

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 62

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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 Tyr Thr Phe Thr Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
          50          55          60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65          70          75          80

```

PhoenixTemp3419.tmp.txt

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 115 120 125
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Lys Ser Thr
 130 135 140
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 145 150 155 160
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 165 170 175
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 180 185 190
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 195 200 205
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 210 215 220
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 225 230 235 240
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 275 280 285
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 290 295 300
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 305 310 315 320
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 340 345 350
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 355 360 365
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 405 410 415
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 420 425 430
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 63

<211> 1368

<212> DNA

<213> Artificial sequence

<220>

<223> Humanised sequence

<400> 63

cagggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ccgggtccag cgtgaagggtg 60
 agctgcaaag cctcaggcta caccttcacc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagt gatgggagag aactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgctgtgt actactgcgc cagggtggag 300
 ttcacagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
 ctagtaccg tgtccagcgc cagcaccaag ggccccagcg tgttccccct ggccccagc 420
 agcaagagca ccagcggcgg cacagccgcc ctgggctgcc tgggtgaagga ctacttcccc 480
 gaaccggtga ccgtgtcctg gaacagcgga gccctgacca gcggcgtgca caccctcccc 540
 gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tggtgaccgt gccacgagc 600

PhoenixTemp3419.tmp.txt

```

agcctgggca cccagaccta catctgtaac gtgaaccaca agcccagcaa caccaaggtg 660
gacaagaagg tggagcccaa gagctgtgac aagaccaca cctgcccccc ctgccctgcc 720
cccgagctgc tgggaggccc cagcgtgttc ctgttcccc ccaagcctaa ggacaccctg 780
atgatcagca gaacccccga ggtgacctgt gtggtggtgg atgtgagcca cgaggacctt 840
gaggtgaagt tcaactggta cgtggacggc gtggaggtgc acaatgccaa gaccaagccc 900
agggaggagc agtacaacag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 960
gattggctga acggcaagga gtacaagtgt aaggtgtcca acaaggccct gcctgcccct 1020
atcgagaaaa ccatacagcaa ggccaagggc cagcccagag agccccaggt gtacaccctg 1080
ccccctagca gagatgagct gaccaagaac caggtgtccc tgacctgcct ggtgaagggc 1140
ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1200
aagaccacc cccctgtgct ggacagcgat ggcagcttct tcctgtacag caagctgacc 1260
gtggacaaga gcagatggca gcagggaac gtgttcagct gctccgtgat gcacgaggcc 1320
ctgcacaatc actacacca gaagagcctg agcctgtccc ctggcaag 1368

```

<210> 64

<211> 456

<212> PRT

<213> QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYGITWVRQAPGQGLEWMGP

<220>

<223> Humanised sequence

<400> 64

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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 Tyr Thr Phe Thr Ser Tyr
20     25     30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35     40     45
Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50     55     60
Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100    105    110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115    120    125
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Lys Ser Thr
130    135    140
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145    150    155    160
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
165    170    175
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180    185    190
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
195    200    205
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
210    215    220
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225    230    235    240
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
245    250    255
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
260    265    270
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
275    280    285
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
290    295    300
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305    310    315    320
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
325    330    335
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
340    345    350
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
355    360    365

```

PhoenixTemp3419.tmp.txt

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 405 410 415
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 420 425 430
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 65
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 65
 caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc cgggctccag cgtgaagggtg 60
 agctgcaaag cctcaggcta caccctcacc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagtg gatgggagag gactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgcccaga agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgctgtgt actactgctc caggagcgag 300
 ttcatcagca ccgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
 ctagtgaccg tgtccagcgc cagcaccaag ggccccagc ggccccagc 420
 agcaagagca ccagcggcgg cacagccgcc ctgggctgcc tgggtgaagga ctacttcccc 480
 gaaccggtga ccgtgtcctg gaacagcgga gccctgacca gcggcgtgca caccctcccc 540
 gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tggtgaccgt gccagcagc 600
 agcctgggca cccagaccta catctgtaac gtgaaccaca agcccagcaa caccaagggtg 660
 gacaagaag tggagcccaa gagctgtgac aagaccaca cctgcccccc ctgcccctgcc 720
 cccgagctgc tgggaggccc cagcgtgttc ctgttcccc ccaagcctaa ggacaccctg 780
 atgatcagca gaacccccga ggtgacctgt gtgggtggtg atgtgagcca cgaggacctt 840
 gaggtgaagt tcaactggta cgtggacggc gtggaggtgc acaatgccaa gaccaagccc 900
 agggaggagc agtacaacag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 960
 gattggctga acggcaagga gtacaagtgt aaggtgtcca acaaggccct gcctgcccct 1020
 ctcgagaaaa ccacagcaa ggccaagggc cagcccagag agcccagggt gtacaccctg 1080
 ccccctagca gagatgagct gaccaagaac caggtgtccc tgacctgcct ggtgaagggc 1140
 ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1200
 aagaccacc cccctgtgct ggacagcgat ggcagcttct tcctgtacag caagctgacc 1260
 gtggacaaga gcagatggca gcagggcaac gtgttcagct gctccgtgat gcacgaggcc 1320
 ctgcacaatc actacacca gaagagcctg agcctgtccc ctggcaag 1368

<210> 66
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 66
 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 Tyr Thr Phe Ala Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Met Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala

PhoenixTemp3419.tmp.txt

100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser
 115 120 125
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 130 135 140
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 145 150 155 160
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 165 170 175
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 180 185 190
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 195 200 205
 Cys Asn Val Asn His Lys Pro Asn Thr Lys Val Asp Lys Lys Val
 210 215 220
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 225 230 235 240
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 275 280 285
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 290 295 300
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 305 310 315 320
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 340 345 350
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 355 360 365
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 405 410 415
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 420 425 430
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 67

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 67

caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc cgggctccag cgtgaagggtg 60
 agctgcaaag cctcaggcta caccctcgcc agctacggca tcacttgggt gaggcaggcc 120
 cccggccagg gactggagtg gatgggagag aactacccca ggagcggcaa cacctactac 180
 aacgagaagt tcaagggcag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgctatgt actactgctc caggagcgag 300
 ttcacagca cgtcgtggc cccctactac tacgccctcg actattgggg ccagggcaca 360
 ctagtaccg tgtccagcg cagcaccaag ggccccagc tggtccccct ggccccagc 420
 agcaagagca ccagcggcgg cacagccgcc ctgggctgcc tgggtgaagga ctacttcccc 480
 gaaccggtga ccgtgtcctg gaacagcgga gccctgacca gcggcgtgca caccttcccc 540
 gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tgggtgaccgt gccagcagc 600
 agcctgggca cccagaccta catctgtaac gtgaaccaca agcccagcaa caccaagggtg 660
 gacaagaagg tggagcccaa gagctgtgac aagaccaca cctgcccccc ctgccctgcc 720
 cccgagctgc tgggaggccc cagcgtgttc ctgttcccc ccaagcctaa ggacaccctg 780

PhoenixTemp3419.tmp.txt

```

atgatcagca gaacccccga ggtgacctgt gtggtggtgg atgtgagcca cgaggaccct 840
gaggtgaagt tcaactggta cgtggacggc gtggaggtgc acaatgccaa gaccaagccc 900
agggaggagc agtacaacag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 960
gattggctga acggcaagga gtacaagtgt aaggtgtcca acaaggccct gcctgccctt 1020
atcgagaaaa ccatcagcaa ggccaagggc cagcccagag agccccaggt gtacaccctg 1080
ccccctagca gagatgagct gaccaagaac caggtgtccc tgacctgcct ggtgaagggc 1140
ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1200
aagaccaccc cccctgtgct ggacagcgat ggcagcttct tcctgtacag caagctgacc 1260
gtggacaaga gcagatggca gcagggaac gtgttcagct gctccgtgat gcacgaggcc 1320
ctgcacaatc actacaccca gaagagcctg agcctgtccc ctggcaag 1368

```

<210> 68
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<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	Lys	Ala	Ser	Lys	Lys	Val	Thr	Ile	Phe
		20						25				30			
Gly	Ser	Thr	Ser	Ala	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Lys	Leu	Ile	Tyr	Asn	Gly	Ala	Lys	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	Gln	Asn	Lys
			85					90						95	
Glu	Val	Pro	Tyr	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> 69
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 69

gacatcgtga	tgaccagag	ccccgatagc	ctcgctgtga	gcctgggcca	gagggccacc	60
atcaactgca	aggccagcaa	gaaggtcacc	atcttcggca	gcacctccgc	cctgcactgg	120
taccagcaga	agcccgga	gcccccaag	ctgatctaca	acggcgccaa	gctggagagc	180
ggcgtgccc	acaggtttag	cggcagcggc	agcggcacag	acttcaccct	gaccattagc	240
agcctgcagg	ccgaagacgt	ggccgtgtac	tactgcctgc	agaacaagga	ggtgcccctac	300
accttcggcg	ggggcaccaa	agtggagatc	aagcgtacgg	tggccgcccc	cagcgtgttc	360
atcttcccc	ccagcgatga	gcagctgaag	agcggcaccg	ccagcgtggg	gtgtctgctg	420
aacaacttct	acccccggga	ggccaaggtg	cagtgggaag	tggacaatgc	cctgcagagc	480
ggcaacagcc	aggagagcgt	gaccgagcag	gacagcaagg	actccaccta	cagcctgagc	540
agcacctga	ccctgagcaa	ggccgactac	gagaagcaca	aggtgtacgc	ctgtgaggtg	600

accaccagg gcctgtccag cccgtgacc aagagcttca accggggcga gtgc

654

<210> 70

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 70

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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 Lys Lys Val Thr Ile Phe
20     25     30
Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
35     40     45
Pro Lys Leu Ile Tyr Asn Gly Ala Lys Pro 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 Gln Asn Lys
85     90     95
Glu Val Pro Tyr 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 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> 71

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 71

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gacatcgtga tgaccagag ccccgatagc ctcgctgtga gcctgggcga gagggccacc 60
atcaactgca aggccagcaa gaaggtcacc atcttcggca gcacctccgc cctgcactgg 120
taccagcaga agcccggaca gcccccaag ctgatctaca acggcgccaa gcccgagagc 180
ggcgtgcccc acaggtttag cggcagcggc agcggcacag acttcaccct gaccattagc 240
agcctgcagg ccgaagacgt ggccgtgtac tactgcctgc agaacaagga ggtgccctac 300
accttcggcg ggggcaccaa agtggagatc aagcgtacgg tggccgcccc cagcgtgttc 360
atcttcccc ccagcgatga gcagctgaag agcggcaccg ccagcgtggg gtgtctgctg 420
aacaacttct acccccggga ggccaagggt cagtgggaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600
accaccagg gcctgtccag ccccgtagc aagagcttca accggggcga gtgc 654

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<210> 72

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 72

Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys
 1 5 10 15
 Gly

<210> 73

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 73

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

<210> 74

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 74

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

<210> 75

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 75

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

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 76

Asn Gly Ala Lys Pro Glu Ser
 1 5

<210> 77

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 77

Asp Gly Ala Lys Leu Glu Ser
 1 5

<210> 78

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 78

Gln Gly Ala Lys Leu Glu Ser
 1 5

<210> 79

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 79

Asp Gly Ala Lys Pro Glu Ser
 1 5

<210> 80

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated CDR

<400> 80

Gln Gly Ala Lys Pro Glu Ser
 1 5

<210> 81

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 81

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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala

100
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125 110

<210> 82
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 82
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 83
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 83
 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 Tyr Thr Phe Ala Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Met Tyr Tyr Cys
 85 90 95
 Ala Arg Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 84
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 84
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

PhoenixTemp3419.tmp.txt

```

1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Ser Tyr
20
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85
Ala Arg Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115
120
125

```

<210> 85
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

```

<400> 85
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 Tyr Thr Phe Ala Ser Tyr
20
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85
Ala Arg Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115
120
125

```

<210> 86
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

```

<400> 86
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 Tyr Thr Phe Ala Ser Tyr
20
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85
Ala Arg Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115
120
125

```

<210> 87
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 87
 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 Tyr Thr Phe Ala Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 88
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 88
 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 Tyr Thr Phe Ala Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 89
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 89
 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 Tyr Thr Phe Ala Ser Tyr
 20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ala Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 90

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 90

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 Tyr Thr Phe Ala Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asp Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Val Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 91

<211> 107

<212> PRT

<213> Homo Sapiens

<400> 91

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

<210> 92

<211> 330

<212> PRT

<213> Homo Sapiens

<400> 92

PhoenixTemp3419.tmp.txt

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	Ser	Val	Leu	Thr	Val	Leu	
			180					185					190		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195					200					205			
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
		210				215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
225					230					235					240
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			245						250					255	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			260					265					270		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		275					280					285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
		290				295					300				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
				325					330						

<210> 93

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 93

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	Lys	Lys	Val	Thr	Ile	Phe
			20					25					30		
Gly	Ser	Ile	Ser	Ala	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Lys	Leu	Ile	Tyr	Asp	Gly	Ala	Lys	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	Gln	Asn	Lys
			85						90					95	
Glu	Val	Pro	Tyr	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			

PhoenixTemp3419.tmp.txt

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 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> 94

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 94

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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Gln Gly Ala Lys 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 Cys Leu Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr 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 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> 95

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated CDR

<400> 95

Ser Glu Phe Ile Ser Thr Val Met Ala Pro Tyr Tyr Tyr Ala Leu Asp
 1 5 10 15
 Tyr

<210> 96

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

<220>
 <223> Humanised sequence

<400> 96
 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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asp Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 97
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 97
 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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Gln Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 98
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutated CDR

<400> 98
 Glu Asn Tyr Pro Arg Ser Gly Asn Ile Tyr Tyr Asn Glu Lys Phe Lys
 1 5 10 15
 Gly

<210> 99
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mutated CDR

<400> 99

Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Arg
 1 5 10 15
 Gly

<210> 100

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated CDR

<400> 100

Ser Glu Phe Thr Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala Leu Asp
 1 5 10 15
 Tyr

<210> 101

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated CDR

<400> 101

Lys Ala Ser Lys Lys Val Thr Ile Tyr Gly Ser Thr Ser Ala Leu His
 1 5 10 15

<210> 102

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated CDR

<400> 102

Asn Ser Ala Lys Leu Glu Ser
 1 5

<210> 103

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 103

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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr

PhoenixTemp3419.tmp.txt

65	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	80	Cys
				85	Phe	Ile	Ser	Thr	Val	90	Met	Ala	Pro	Tyr	Tyr	95	
Ala	Arg	Ser	Glu	100	Trp	Gly	Gln	Gly	Thr	105	Leu	Val	Thr	Val	Ser	110	Ala
Leu	Asp	Tyr	115						120						125		

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<210> 104
<211> 126
<212> PRT
<213> Artificial Sequence
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<220>
<223> Humanised sequence

<400>	104														
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	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Gly	Ile	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Glu	Asp	Tyr	Pro	Arg	Ser	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Lys	Phe
	50					55				60					
Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Gly	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Ser	Glu	Phe	Ile	Ser	Thr	Val	Val	Ala	Pro	Tyr	Tyr	Tyr	Ala
			100					105					110		
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

```
<210> 105
<211> 126
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Humanised sequence

<400>	105														
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Arg	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Gly	Ile	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Glu	Asn	Tyr	Pro	Arg	Ser	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Lys	Phe
			50			55					60				
Lys	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	Ser	Glu	Phe	Ile	Ser	Thr	Val	Val	Ala	Pro	Tyr	Tyr	Tyr	Ala
			100					105					110		
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
			115				120					125			

```
<210> 106
<211> 126
<212> PRT
<213> Artificial Sequence
```

$\langle 220 \rangle$

<223> Humanised sequence

<400> 106

```

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 Tyr Thr Phe Ala Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
          50          55          60
Lys 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 Ala Tyr Tyr Cys
          85          90          95
Ala Arg Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
          100          105          110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120          125

```

<210> 107

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 107

```

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 Glu Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
          50          55          60
Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
          100          105          110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120          125

```

<210> 108

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 108

```

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 Tyr Thr Phe Thr Ser Tyr
          20          25          30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
          50          55          60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 109
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 109
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Asn Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 110
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 110
 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 Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Arg 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
 100 105 110
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 111
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 111

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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 Tyr Thr Phe Thr Ser Tyr
20      25      30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35      40      45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Ile Tyr Tyr Asn Glu Lys Phe
50      55      60
Lys 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100      105      110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115      120      125

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<210> 112

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 112

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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 Tyr Thr Phe Thr Ser Tyr
20      25      30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35      40      45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50      55      60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65      70      75      80
Met Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85      90      95
Ala Arg Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100      105      110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115      120      125

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<210> 113

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 113

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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 Tyr Thr Phe Ala Ser Tyr
20      25      30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35      40      45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50      55      60
Arg 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100      105      110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115      120      125

```

115

<210> 114
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised sequence

<400> 114
Gln Val Gln Leu Val Gln Ser Ser Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Ser Tyr
20 25 30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys 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 Ser Glu Phe Thr Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100 105 110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 115
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised sequence

<400> 115
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 Tyr Thr Phe Ala Ser Tyr
20 25 30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Asn Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Gly 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 Ser Glu Phe Ile Ser Thr Val Val Ala Pro Tyr Tyr Tyr Ala
100 105 110
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 116
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanised sequence

<400> 116
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Val Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Lys Lys Val Thr Ile Phe

PhoenixTemp3419.tmp.txt

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

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<210> 117
<211> 111
<212> PRT
<213> Artificial Sequence
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<220>
<223> Humanised sequence

<400>	117															
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	Lys	Lys	Val	Thr	Ile	Phe	
			20					25					30			
Gly	Ser	Ile	Ser	Ala	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	
		35					40					45				
Pro	Lys	Leu	Val	Tyr	Asn	Gly	Ala	Lys	Leu	Glu	Ser	Gly	Val	Pro	Asp	
	50					55					60					
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Ala	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
65					70					75					80	
Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Leu	Gln	Asn	Lys	
				85					90					95		
Glu	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys		
			100					105					110			

```
<210> 118
<211> 111
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Humanised sequence

<400>	118															
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	Lys	Lys	Val	Thr	Ile	Phe	
			20					25					30			
Gly	Ser	Ile	Ser	Ala	Leu	His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Pro	
		35					40					45				
Pro	Lys	Leu	Ile	Tyr	Asn	Gly	Ala	Lys	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	Gln	Asn	Lys	
				85					90					95		
Glu	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys		
			100					105					110			

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<210> 119
<211> 111
<212> PRT
<213> Artificial Sequence
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 $\langle 220 \rangle$

<223> Humanised sequence

<400> 119

```

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 Lys Lys Val Thr Ile Phe
          20           25           30
Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
          35           40           45
Pro Lys Leu Ile Tyr Asn Gly Ala Lys Leu Glu Ser Gly Val Pro Gly
          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 Gln Asn Lys
          85           90           95
Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110

```

<210> 120

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 120

```

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 Lys Lys Val Thr Ile Phe
          20           25           30
Gly Ser Ile Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
          35           40           45
Pro Lys Leu Ile Tyr Asn Ser Ala Lys 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 Gln Asn Lys
          85           90           95
Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110

```

<210> 121

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised sequence

<400> 121

```

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 Lys Lys Val Thr Ile Tyr
          20           25           30
Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
          35           40           45
Pro Lys Leu Ile Tyr Asn Gly Ala Lys Pro 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 Gln Asn Lys
          85           90           95
Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110

```


<210> 122
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 122
 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 Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys Pro 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 123
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanised sequence

<400> 123
 Gly 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 Lys Lys Val Thr Ile Phe
 20 25 30
 Gly Ser Thr Ser Ala Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 35 40 45
 Pro Lys Leu Ile Tyr Asn Gly Ala Lys 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 Gln Asn Lys
 85 90 95
 Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110