

SEQUENCE LISTING

<110> Omeros Corporation
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Dudler, Tom
Schwaeble, Hans-Wilhelm

<120> Methods for Reducing Proteinuria in a Human Subject
Suffering from Immunoglobulin A Nephropathy

<130> MP.1.0269.PCT

<150> 62/527,926

<151> 2017-06-30

<150> 15/470,647

<151> 2017-03-27

<150> 15/399,524

<151> 2017-01-05

<150> 62/407,979

<151> 2016-10-13

<160> 85

<170> PatentIn version 3.5

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<222> (27)..(584)

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Asp Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu	
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cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag	245
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu	
60 65 70	
tac gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg	293
Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu	
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Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr	
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ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac	389
Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr	
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Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu	
125 130 135	
gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac	485
Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp	
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His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala	
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ggc tac gtc ctg cac cgt aac aag cgc acc tgc tca gag cag agc ctc	581
Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu	
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
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Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
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Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
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Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
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Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
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Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
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Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
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Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val	
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Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp	
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cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg cgc	195
Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg	
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Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly	
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Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro	
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cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc atc agc ctg gag	675
Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu	
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gag ggg ttc agt gtc att ctg gac ttt gtg gag tcc ttc gat gtg gag	723
Glu Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu	
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Tyr Ile Thr Gly Pro Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr	
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Leu Pro Val Cys Glu Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly	
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Gly Arg Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp	
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Gln Val Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr	
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Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His	
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gat gca tcc gcc ctg gac att cga atg ggc acc ctg aaa aga cta tca	1539
Asp Ala Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser	
495 500 505	
cct cat tat aca caa gcc tgg tct gaa gct gtt ttt ata cat gaa ggt	1587
Pro His Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly	
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tat act cat gat gct ggc ttt gac aat gac ata gca ctg att aaa ttg	1635
Tyr Thr His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu	
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
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Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
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Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
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Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn

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Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
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Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
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Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
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Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
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Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
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Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
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Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
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Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
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Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
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Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
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Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
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Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
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Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
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Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
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Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr

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Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
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Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
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Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
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Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
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Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
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Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
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Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
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Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
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Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
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Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
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Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
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Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
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Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
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Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
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Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
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Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
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Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
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Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
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Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
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tcctgcagca tggccccac cacgttcccg tcaccctcgg tgacccacc tcttcagggtg	4140

ctctatggag gtcaaggctg gggcttcgag tacaagtgtg ggaggcagag tggggagggg	4200
cacccaatc catggcctgg gttggcctca ttggctgtcc ctgaaatgct gaggaggtgg	4260
gttacttccc tccgcccagg ccagacccag gcagctgctc cccagctttc atgagcttct	4320
ttctcagatt caaacagaca gagaagaaca tggcccatc tgtgggaaga cattgcccc	4380
caggattgaa acaaaaagca acacggtgac catcacctt gtcacagatg aatcaggaga	4440
ccacacaggc tggaagatcc actacacgag cacagtgagc aagtgggctc agatccttgg	4500
tggaagcgca gagctgcctc tctctggagt gcaaggagct gtagagtgtg gggctcttct	4560
gggcaggact aggaaggac accaggttta gtggtgctga ggtctgaggc agcagcttct	4620
aaggggaagc acccgtgccc tcctcagcag caccacagcat cttcaccact cattcttcaa	4680
ccaccattc acccatcact catcttttac ccaccaccc ttgcccactc atccttctgt	4740
ccctcatcct tccaaccatt catcaatcac ccaccatcc atccttggcc acacaaccat	4800
ccaccattc ttctacctac ccacccatc catccatcct tctatcagca tccttctacc	4860
acccatcctt cgttcgggtca tccatcatca tccatccatc	4900

<210> 8
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Arg	Leu	Leu	Thr	Leu	Leu	Gly	Leu	Leu	Cys	Gly	Ser	Val	Ala	Thr
1				5				10						15	

Pro	Leu	Gly	Pro	Lys	Trp	Pro	Glu	Pro	Val	Phe	Gly	Arg	Leu	Ala	Ser
			20					25					30		

Pro	Gly	Phe	Pro	Gly	Glu	Tyr	Ala	Asn	Asp	Gln	Glu	Arg	Arg	Trp	Thr
		35					40					45			

Leu	Thr	Ala	Pro	Pro	Gly	Tyr	Arg	Leu	Arg	Leu	Tyr	Phe	Thr	His	Phe
	50					55					60				

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala
130 135

<210> 9
<211> 181
<212> PRT
<213> Homo sapiens

<400> 9

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser
180

<210> 10
<211> 293
<212> PRT
<213> Homo sapiens

<400> 10

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
180 185 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
225 230 235 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
275 280 285

Trp Lys Ile His Tyr
290

<210> 11
<211> 41
<212> PRT
<213> Homo sapiens

<400> 11

Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
1 5 10 15

Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
20 25 30

Ala Gly Tyr Val Leu His Arg Asn Lys
35 40

<210> 12
<211> 242
<212> PRT
<213> Homo sapiens

<400> 12

Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val
1 5 10 15

Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn
20 25 30

Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala
35 40 45

Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His
50 55 60

Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr
65 70 75 80

His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn
85 90 95

Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys
100 105 110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
115 120 125

Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val
130 135 140

Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys
145 150 155 160

Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly
165 170 175

Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala
180 185 190

Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile
195 200 205

Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val
210 215 220

Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
225 230 235 240

Asp Phe

<210> 13

<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13

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

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
1 5 10 15

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
1 5 10 15

Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser
20 25 30

Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
35 40

<210> 16
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16

Thr Phe Arg Ser Asp Tyr Ser Asn
1 5

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17

Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
1 5 10 15

Ser Asn Glu Lys Pro Phe Thr Gly Phe
20 25

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18

Ile Asp Glu Cys Gln Val Ala Pro Gly
1 5

<210> 19
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19

Ala	Asn	Met	Leu	Cys	Ala	Gly	Leu	Glu	Ser	Gly	Gly	Lys	Asp	Ser	Cys
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Arg	Gly	Asp	Ser	Gly	Gly	Ala	Leu	Val
			20					25

<210> 20

<211> 960

<212> DNA

<213> Homo sapiens

<220>

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<222> (51)..(797)

<400> 20

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ctg	ttt	cca	tca	ctc	cct	ctc	ctt	ctc	ctg	agt	atg	gtg	gca	gcg	tct	104
Leu	Phe	Pro	Ser	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Met	Val	Ala	Ala	Ser	
		5						10					15			

tac	tca	gaa	act	gtg	acc	tgt	gag	gat	gcc	caa	aag	acc	tgc	cct	gca	152
Tyr	Ser	Glu	Thr	Val	Thr	Cys	Glu	Asp	Ala	Gln	Lys	Thr	Cys	Pro	Ala	
		20				25					30					

gtg	att	gcc	tgt	agc	tct	cca	ggc	atc	aac	ggc	ttc	cca	ggc	aaa	gat	200
Val	Ile	Ala	Cys	Ser	Ser	Pro	Gly	Ile	Asn	Gly	Phe	Pro	Gly	Lys	Asp	
35					40				45					50		

ggg	cgt	gat	ggc	acc	aag	gga	gaa	aag	ggg	gaa	cca	ggc	caa	ggg	ctc	248
Gly	Arg	Asp	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Glu	Pro	Gly	Gln	Gly	Leu	
				55					60					65		

aga	ggc	tta	cag	ggc	ccc	cct	gga	aag	ttg	ggg	cct	cca	gga	aat	cca	296
Arg	Gly	Leu	Gln	Gly	Pro	Pro	Gly	Lys	Leu	Gly	Pro	Pro	Gly	Asn	Pro	
			70					75					80			

ggg	cct	tct	ggg	tca	cca	gga	cca	aag	ggc	caa	aaa	gga	gac	cct	gga	344
Gly	Pro	Ser	Gly	Ser	Pro	Gly	Pro	Lys	Gly	Gln	Lys	Gly	Asp	Pro	Gly	
		85					90					95				

aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa aga aaa gct Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala 100 105 110	392
ctg caa aca gaa atg gca cgt atc aaa aag tgg ctc acc ttc tct ctg Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe Ser Leu 115 120 125 130	440
ggc aaa caa gtt ggg aac aag ttc ttc ctg acc aat ggt gaa ata atg Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu Ile Met 135 140 145	488
acc ttt gaa aaa gtg aag gcc ttg tgt gtc aag ttc cag gcc tct gtg Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala Ser Val 150 155 160	536
gcc acc ccc agg aat gct gca gag aat gga gcc att cag aat ctc atc Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn Leu Ile 165 170 175	584
aag gag gaa gcc ttc ctg ggc atc act gat gag aag aca gaa ggg cag Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu Gly Gln 180 185 190	632
ttt gtg gat ctg aca gga aat aga ctg acc tac aca aac tgg aac gag Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp Asn Glu 195 200 205 210	680
ggt gaa ccc aac aat gct ggt tct gat gaa gat tgt gta ttg cta ctg Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu Leu Leu 215 220 225	728
aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc cat ctg gcc Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His Leu Ala 230 235 240	776
gtc tgt gag ttc cct atc tga agggatcatat cactcaggcc ctccttgtct Val Cys Glu Phe Pro Ile 245	827
ttttactgca acccacaggc ccacagtatg cttgaaaaga taaattatat caatttcctc	887
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aagcaataat agt	960

<210> 21
<211> 248

<212> PRT

<213> Homo sapiens

<400> 21

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
115 120 125

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

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu

180

185

190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X at position 1 represents hydroxyproline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein X at position 4 represents hydrophobic residue

<400> 22

Xaa Gly Lys Xaa Gly Pro
1 5

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Wherein X represents hydroxyproline

<400> 23

Xaa Gly Lys Leu Gly

1 5

<210> 24

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (9)..(15)

<223> Wherein X at positions 9 and 15 represents hydroxyproline

<400> 24

Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa Gly

1 5 10 15

<210> 25

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (3)..(27)

<223> Wherein X at positions 3, 6, 15, 21, 24, 27 represents hydroxyproline

<400> 25

Gly Pro Xaa Gly Pro Xaa Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly
1 5 10 15

Lys Leu Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa
20 25

<210> 26
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (32)..(32)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (35)..(35)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<400> 26

Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
1 5 10 15

Gln Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa

20

25

30

Gly Asn Xaa Gly Pro Ser Gly Ser Xaa Gly Pro Lys Gly Gln Lys Gly
35 40 45

Asp Xaa Gly Lys Ser
50

<210> 27
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(33)
<223> Wherein X at positions 3, 6, 12, 18, 21, 30, 33 represents
hydroxyproline

<400> 27

Gly Ala Xaa Gly Ser Xaa Gly Glu Lys Gly Ala Xaa Gly Pro Gln Gly
1 5 10 15

Pro Xaa Gly Pro Xaa Gly Lys Met Gly Pro Lys Gly Glu Xaa Gly Asp
20 25 30

Xaa

<210> 28
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<221> MISC_FEATURE
<222> (3)..(45)
<223> Wherein X at positions 3, 6, 9, 27, 30, 36, 42, 45 represents
hydroxyproline

<400> 28

Gly Cys Xaa Gly Leu Xaa Gly Ala Xaa Gly Asp Lys Gly Glu Ala Gly
1 5 10 15

Thr Asn Gly Lys Arg Gly Glu Arg Gly Pro Xaa Gly Pro Xaa Gly Lys
20 25 30

Ala Gly Pro Xaa Gly Pro Asn Gly Ala Xaa Gly Glu Xaa
35 40 45

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29

Leu Gln Arg Ala Leu Glu Ile Leu Pro Asn Arg Val Thr Ile Lys Ala
1 5 10 15

Asn Arg Pro Phe Leu Val Phe Ile
20

<210> 30
<211> 559
<212> DNA
<213> Homo sapiens

<400> 30
atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg 60
aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120
aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240

tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggccc	300
cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac	360
tactccaacg agaagccggtt cacgggggttc gaggccttct atgcagccga ggacattgac	420
gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg	480
ggcggtttct actgctcctg ccgcgaggc tacgtcctgc accgtaacaa gcgcacctgc	540
tcagccctgt gctccggcc	559

<210> 31
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 31	
cgggcacacc atgaggctgc tgaccctcct gggc	34

<210> 32
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 32	
gacattacct tccgctccga ctccaacgag aag	33

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

<220>
 <223> Synthetic

<400> 33	
agcagccctg aatacccacg gccgtatccc aaa	33

<210> 34
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34
cgggatccat gaggctgctg accctc

26

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 35
ggaattccta ggctgcata

19

<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36
ggaattccta cagggcgct

19

<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37
ggaattccta gtagtggat

19

<210> 38
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
tgcggccgct gtaggtgctg tcttt 25

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
ggaattcact cgttattctc gga 23

<210> 40
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
tccgagaata acgagtg 17

<210> 41
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
cattgaaagc tttggggtag aagttgttc 29

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42
cgcggccgca gctgctcaga gtgtaga 27

<210> 43
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
cggtaagctt cactggctca gggaaata 28

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44
aagaagcttg ccgccaccat ggattggctg tggaact 37

<210> 45
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45
cgggatcctc aaactttctt gtccaccttg g 31

<210> 46
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 46

aagaaagctt gccgccacca tgttctcact agctct 36

<210> 47

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 47

cgggatcctt ctccctctaa cactct 26

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48

Glu Pro Lys Ser Cys Asp Lys Thr His

1 5

<210> 49

<211> 4960

<212> DNA

<213> Homo Sapiens

<400> 49

ccggacgtgg tggcgcatgc ctgtaatccc agctactcgg gaggctgagg caggagaatt 60

gctcgaaccc cggaggcaga ggtttggtgg ctcacacctg taatcccagc actttgagag 120

gctgaggcag gtgcatcgct ttggctcagg agttcaagac cagcctgggc aacacaggga 180

gacccccatc tctacaaaaa acaaaaaaca atataaaggg gataaaaaaa aaaaaaagac 240

aagacatgaa tccatgagga cagagtgtgg aagaggaagc agcagcctca aagttctgga 300

agctggaaga acagataaac aggtgtgaaa taactgcctg gaaagcaact tctttttttt 360

tttttttttt tttgaggtgg agtctcactc tgtcgtccag gctggagtgc agtgggtgcga	420
tctcggatca ctgcaacctc cgcctcccag gctcaagcaa ttctcctgcc tcagcctccc	480
gagtagctgg gattataagt gcgcgctgcc acacctggat gattttttgta ttttttagtag	540
agatgggatt tcaccatggt ggtcaggctg gtctcaaact cccaacctcg tgatccaccc	600
accttggcct cccaaagtgc tgggattaca ggtataagcc accgagccca gccaaaagcg	660
acttctaagc ctgcaaggga atcgggaatt ggtggcacca ggtccttctg acagggttta	720
agaaattagc cagcctgagg ctgggcacgg tggctcacac ctgtaatccc agcactttgg	780
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cttgccagtt taattccagc cttaccatt gactcaaggg gacataaacc acgagagtga	4800
cagtcattct tgcccacca gtgtaatgtc actgctcaaa ttacatttca ttaccttaaa	4860

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Gly Leu Leu Trp Ser Leu Val Ala Thr Leu Leu Gly Ser Lys Trp Pro
10 15 20

gaa cct gta ttc ggg cgc ctg gtg tcc cct ggc ttc cca gag aag tat 149
Glu Pro Val Phe Gly Arg Leu Val Ser Pro Gly Phe Pro Glu Lys Tyr
25 30 35

gct gac cat caa gat cga tcc tgg aca ctg act gca ccc cct ggc tac 197
Ala Asp His Gln Asp Arg Ser Trp Thr Leu Thr Ala Pro Pro Gly Tyr
40 45 50 55

cgc ctg cgc ctc tac ttc acc cac ttt gac ctg gaa ctc tct tac cgc 245
Arg Leu Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser Tyr Arg
60 65 70

tgc gag tat gac ttt gtc aag ttg agc tca ggg acc aag gtg ctg gcc 293
Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser Gly Thr Lys Val Leu Ala
75 80 85

aca ctg tgt ggg cag gag agt aca gac act gag cag gca cct ggc aat 341
Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Gln Ala Pro Gly Asn
90 95 100

gac acc ttc tac tca ctg ggt ccc agc cta aag gtc acc ttc cac tcc 389
Asp Thr Phe Tyr Ser Leu Gly Pro Ser Leu Lys Val Thr Phe His Ser
105 110 115

gac tac tcc aat gag aag ccg ttc aca ggg ttt gag gcc ttc tat gca 437
Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala

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gcg gag gat gtg gat gaa tgc aga gtg tct ctg gga gac tca gtc cct				485
Ala Glu Asp Val Asp Glu Cys Arg Val Ser Leu Gly Asp Ser Val Pro				
	140	145	150	
tgt gac cat tat tgc cac aac tac ttg ggc ggc tac tat tgc tcc tgc				533
Cys Asp His Tyr Cys His Asn Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys				
	155	160	165	
aga gcg ggc tac att ctc cac cag aac aag cac acg tgc tca gcc ctt				581
Arg Ala Gly Tyr Ile Leu His Gln Asn Lys His Thr Cys Ser Ala Leu				
	170	175	180	
tgt tca ggc cag gtg ttc aca gga aga tct ggg tat ctc agt agc cct				629
Cys Ser Gly Gln Val Phe Thr Gly Arg Ser Gly Tyr Leu Ser Ser Pro				
	185	190	195	
gag tac ccg cag cca tac ccc aag ctc tcc agc tgc acc tac agc atc				677
Glu Tyr Pro Gln Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile				
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cgc ctg gag gac ggc ttc agt gtc atc ctg gac ttc gtg gag tcc ttc				725
Arg Leu Glu Asp Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe				
	220	225	230	
gat gtg gag acg cac cct gaa gcc cag tgc ccc tat gac tcc ctc aag				773
Asp Val Glu Thr His Pro Glu Ala Gln Cys Pro Tyr Asp Ser Leu Lys				
	235	240	245	
att caa aca gac aag ggg gaa cac ggc cca ttt tgt ggg aag acg ctg				821
Ile Gln Thr Asp Lys Gly Glu His Gly Pro Phe Cys Gly Lys Thr Leu				
	250	255	260	
cct ccc agg att gaa act gac agc cac aag gtg acc atc acc ttt gcc				869
Pro Pro Arg Ile Glu Thr Asp Ser His Lys Val Thr Ile Thr Phe Ala				
	265	270	275	
act gac gag tcg ggg aac cac aca ggc tgg aag ata cac tac aca agc				917
Thr Asp Glu Ser Gly Asn His Thr Gly Trp Lys Ile His Tyr Thr Ser				
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aca gca cgg ccc tgc cct gat cca acg gcg cca cct aat ggc agc att				965
Thr Ala Arg Pro Cys Pro Asp Pro Thr Ala Pro Pro Asn Gly Ser Ile				
	300	305	310	
tca cct gtg caa gcc acg tat gtc ctg aag gac agg ttt tct gtc ttc				1013
Ser Pro Val Gln Ala Thr Tyr Val Leu Lys Asp Arg Phe Ser Val Phe				
	315	320	325	

tgc aag aca ggc ttc gag ctt ctg caa ggt tct gtc ccc ctg aaa tca	1061
Cys Lys Thr Gly Phe Glu Leu Leu Gln Gly Ser Val Pro Leu Lys Ser	
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ttc act gct gtc tgt cag aaa gat gga tct tgg gac cgg ccg atg cca	1109
Phe Thr Ala Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met Pro	
345 350 355	
gag tgc agc att att gat tgt ggc cct ccc gat gac cta ccc aat ggc	1157
Glu Cys Ser Ile Ile Asp Cys Gly Pro Pro Asp Asp Leu Pro Asn Gly	
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cat gtg gac tat atc aca ggc cct caa gtg act acc tac aaa gct gtg	1205
His Val Asp Tyr Ile Thr Gly Pro Gln Val Thr Thr Tyr Lys Ala Val	
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Ile Gln Tyr Ser Cys Glu Glu Thr Phe Tyr Thr Met Ser Ser Asn Gly	
395 400 405	
aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa	1301
Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu	
410 415 420	
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Lys Leu Pro Pro Val Cys Glu Pro Val Cys Gly Leu Ser Thr His Thr	
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Ile Gly Gly Arg Ile Val Gly Gly Gln Pro Ala Lys Pro Gly Asp Phe	
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Pro Trp Gln Val Leu Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala	
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Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu	
475 480 485	
aaa aga atg gca gcg tcc tcc ctg aac atc cga atg ggc atc ctc aaa	1541
Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys	
490 495 500	
agg ctc tca cct cat tac act caa gcc tgg ccc gag gaa atc ttt ata	1589
Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Pro Glu Glu Ile Phe Ile	
505 510 515	
cat gaa ggc tac act cac ggt gct ggt ttt gac aat gat ata gca ttg	1637
His Glu Gly Tyr Thr His Gly Ala Gly Phe Asp Asn Asp Ile Ala Leu	

520	525	530	535	
att aaa ctc aag aac aaa gtc aca atc aac gga agc atc atg cct gtt				1685
Ile Lys Leu Lys Asn Lys Val Thr Ile Asn Gly Ser Ile Met Pro Val				
	540	545	550	
tgc cta ccg cga aaa gaa gct gca tcc tta atg aga aca gac ttc act				1733
Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu Met Arg Thr Asp Phe Thr				
	555	560	565	
gga act gtg gct ggc tgg ggg tta acc cag aag ggg ctt ctt gct aga				1781
Gly Thr Val Ala Gly Trp Gly Leu Thr Gln Lys Gly Leu Leu Ala Arg				
	570	575	580	
aac cta atg ttt gtg gac ata cca att gct gac cac caa aaa tgt acc				1829
Asn Leu Met Phe Val Asp Ile Pro Ile Ala Asp His Gln Lys Cys Thr				
	585	590	595	
acc gtg tat gaa aag ctc tat cca gga gta aga gta agc gct aac atg				1877
Thr Val Tyr Glu Lys Leu Tyr Pro Gly Val Arg Val Ser Ala Asn Met				
	600	605	610	615
ctc tgt gct ggc tta gag act ggt ggc aag gac agc tgc aga ggt gac				1925
Leu Cys Ala Gly Leu Glu Thr Gly Gly Lys Asp Ser Cys Arg Gly Asp				
	620	625	630	
agt ggg ggg gca tta gtg ttt cta gat aat gag aca cag cga tgg ttt				1973
Ser Gly Gly Ala Leu Val Phe Leu Asp Asn Glu Thr Gln Arg Trp Phe				
	635	640	645	
gtg gga gga ata gtt tcc tgg ggt tcc att aat tgt ggg gcg gca ggc				2021
Val Gly Gly Ile Val Ser Trp Gly Ser Ile Asn Cys Gly Ala Ala Gly				
	650	655	660	
cag tat ggg gtc tac aca aaa gtc atc aac tat att ccc tgg aat gag				2069
Gln Tyr Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Asn Glu				
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aac ata ata agt aat ttc taa				2090
Asn Ile Ile Ser Asn Phe				
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Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp Thr
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

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

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Val
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln Asn
165 170 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
180 185 190

Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala Gln
225 230 235 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser His
260 265 270

Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
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Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
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Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Gln
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Gln
450 455 460

Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu Thr
465 470 475 480

Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu Asn
485 490 495

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
500 505 510

Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
515 520 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
530 535 540

Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala Ser
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Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu Thr
565 570 575

Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
580 585 590

Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro Gly
595 600 605

Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

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660 665 670

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35 40 45

Phe Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro

85

90

95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
 100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
 115 120 125

Val Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
 130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln
 145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
 165 170 175

Arg Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
 180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val
 195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala
 210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His
 225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
 245 250 255

His Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr
 260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro
 275 280 285

Thr Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

Gly Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly
340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
355 360 365

Gln Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro
405 410 415

Val Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly
420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

Gln Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu
450 455 460

Thr Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu
465 470 475 480

Asn Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln

485

490

495

Ala Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala
 500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
 515 520 525

Ile Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala
 530 535 540

Ser Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu
 545 550 555 560

Thr Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
 565 570 575

Ile Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro
 580 585 590

Gly Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly
 595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
 610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
 625 630 635 640

Ser Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
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Ala	Thr	Leu	Leu	Gly	Ser	Lys	Trp	Pro	Glu	Pro	Val	Phe	Gly	Arg	Leu	
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gtg	tcc	ctg	gcc	ttc	cca	gag	aag	tat	ggc	aac	cat	cag	gat	cga	tcc	147
Val	Ser	Leu	Ala	Phe	Pro	Glu	Lys	Tyr	Gly	Asn	His	Gln	Asp	Arg	Ser	
				35					40					45		

tgg	acg	ctg	act	gca	ccc	cct	ggc	ttc	cgc	ctg	cgc	ctc	tac	ttc	acc	195
Trp	Thr	Leu	Thr	Ala	Pro	Pro	Gly	Phe	Arg	Leu	Arg	Leu	Tyr	Phe	Thr	
			50					55					60			

cac	ttc	aac	ctg	gaa	ctc	tct	tac	cgc	tgc	gag	tat	gac	ttt	gtc	aag	243
His	Phe	Asn	Leu	Glu	Leu	Ser	Tyr	Arg	Cys	Glu	Tyr	Asp	Phe	Val	Lys	
		65					70					75				

ttg	acc	tca	ggg	acc	aag	gtg	cta	gcc	acg	ctg	tgt	ggg	cag	gag	agt	291
Leu	Thr	Ser	Gly	Thr	Lys	Val	Leu	Ala	Thr	Leu	Cys	Gly	Gln	Glu	Ser	
	80					85					90					

aca	gat	act	gag	cgg	gca	cct	ggc	aat	gac	acc	ttc	tac	tca	ctg	ggc	339
Thr	Asp	Thr	Glu	Arg	Ala	Pro	Gly	Asn	Asp	Thr	Phe	Tyr	Ser	Leu	Gly	
95					100					105					110	

ccc	agc	cta	aag	gtc	acc	ttc	cac	tcc	gac	tac	tcc	aat	gag	aag	cca	387
Pro	Ser	Leu	Lys	Val	Thr	Phe	His	Ser	Asp	Tyr	Ser	Asn	Glu	Lys	Pro	
				115					120					125		

ttc	aca	gga	ttt	gag	gcc	ttc	tat	gca	gcg	gag	gat	gtg	gat	gaa	tgc	435
Phe	Thr	Gly	Phe	Glu	Ala	Phe	Tyr	Ala	Ala	Glu	Asp	Val	Asp	Glu	Cys	
			130					135					140			

aga	aca	tcc	ctg	gga	gac	tca	gtc	cct	tgt	gac	cat	tat	tgc	cac	aac	483
Arg	Thr	Ser	Leu	Gly	Asp	Ser	Val	Pro	Cys	Asp	His	Tyr	Cys	His	Asn	
		145					150					155				

tac	ctg	ggc	ggc	tac	tac	tgc	tcc	tgc	cga	gtg	ggc	tac	att	ctg	cac	531
Tyr	Leu	Gly	Gly	Tyr	Tyr	Cys	Ser	Cys	Arg	Val	Gly	Tyr	Ile	Leu	His	

160	165	170	
cag aac aag cat acc tgc tca gcc ctt tgt tca ggc cag gtg ttc act			579
Gln Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr			
175	180	185	190
ggg agg tct ggc ttt ctc agt agc cct gag tac cca cag cca tac ccc			627
Gly Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro			
	195	200	205
aaa ctc tcc agc tgc gcc tac aac atc cgc ctg gag gaa ggc ttc agt			675
Lys Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser			
	210	215	220
atc acc ctg gac ttc gtg gag tcc ttt gat gtg gag atg cac cct gaa			723
Ile Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu			
	225	230	235
gcc cag tgc ccc tac gac tcc ctc aag att caa aca gac aag agg gaa			771
Ala Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu			
	240	245	250
tac ggc ccg ttt tgt ggg aag acg ctg ccc ccc agg att gaa act gac			819
Tyr Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp			
255	260	265	270
agc aac aag gtg acc att acc ttt acc acc gac gag tca ggg aac cac			867
Ser Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His			
	275	280	285
aca ggc tgg aag ata cac tac aca agc aca gca cag ccc tgc cct gat			915
Thr Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp			
	290	295	300
cca acg gcg cca cct aat ggt cac att tca cct gtg caa gcc acg tat			963
Pro Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr			
	305	310	315
gtc ctg aag gac agc ttt tct gtc ttc tgc aag act ggc ttc gag ctt			1011
Val Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu			
	320	325	330
ctg caa ggt tct gtc ccc ctg aag tca ttc act gct gtc tgt cag aaa			1059
Leu Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys			
335	340	345	350
gat gga tct tgg gac cgg ccg ata cca gag tgc agc att att gac tgt			1107
Asp Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys			
	355	360	365

ggc cct ccc gat gac cta ccc aat ggc cac gtg gac tat atc aca ggc Gly Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly 370 375 380	1155
cct gaa gtg acc acc tac aaa gct gtg att cag tac agc tgt gaa gag Pro Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu 385 390 395	1203
act ttc tac aca atg agc agc aat ggt aaa tat gtg tgt gag gct gat Thr Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp 400 405 410	1251
gga ttc tgg acg agc tcc aaa gga gaa aaa tcc ctc ccg gtt tgc aag Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys 415 420 425 430	1299
cct gtc tgt gga ctg tcc aca cac act tca gga ggc cgt ata att gga Pro Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly 435 440 445	1347
gga cag cct gca aag cct ggt gac ttt cct tgg caa gtc ttg tta ctg Gly Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu 450 455 460	1395
ggt gaa act aca gca gca ggt gct ctt ata cat gac gac tgg gtc cta Gly Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu 465 470 475	1443
aca gcg gct cat gct gta tat ggg aaa aca gag gcg atg tcc tcc ctg Thr Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu 480 485 490	1491
gac atc cgc atg ggc atc ctc aaa agg ctc tcc ctc att tac act caa Asp Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln 495 500 505 510	1539
gcc tgg cca gag gct gtc ttt atc cat gaa ggc tac act cac gga gct Ala Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala 515 520 525	1587
ggt ttt gac aat gat ata gca ctg att aaa ctc aag aac aaa gtc aca Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr 530 535 540	1635
atc aac aga aac atc atg ccg att tgt cta cca aga aaa gaa gct gca Ile Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala 545 550 555	1683
tcc tta atg aaa aca gac ttc gtt gga act gtg gct ggc tgg ggg tta Ser Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu	1731

Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Thr
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
100 105 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Thr
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln Asn
165 170 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
180 185 190

Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile Thr
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala Gln
225 230 235 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser Asn
260 265 270

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Glu
450 455 460

Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr Ala
465 470 475 480

Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp Ile
485 490 495

Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala Trp
500 505 510

Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly Phe
515 520 525

Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile Asn
530 535 540

Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu
545 550 555 560

Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr Gln
565 570 575

Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile Val
580 585 590

Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro Gly
595 600 605

Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr
660 665 670

Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
675 680 685

<210> 55
<211> 670
<212> PRT
<213> Rat

<400> 55

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
165 170 175

Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile
195 200 205

Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
245 250 255

Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro
275 280 285

Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp

325

330

335

Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly
 340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
 355 360 365

Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
 370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
 385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro
 405 410 415

Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly
 420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
 435 440 445

Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr
 450 455 460

Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp
 465 470 475 480

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala
 485 490 495

Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
 500 505 510

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
 515 520 525

Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser
530 535 540

Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr
545 550 555 560

Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
565 570 575

Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro
580 585 590

Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
660 665 670

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 56
atgaggctgc tgaccctcct gggccttc

<210> 57

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

<220>
<223> Homo Sapiens

<400> 57
gtgcccctcc tgcgtcacct ctg 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 58
cagaggtgac gcaggagggg cac 23

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 59
ttaaaatcac taattatggt ctcgatc 27

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 60
atgaggctac tcatcttcct gg 22

<210> 61
<211> 23
<212> DNA

<213> Artificial Sequence

<220>

<223> Murine

<400> 61

ctgcagaggt gacgcagggg ggg

23

<210> 62

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine

<400> 62

ccccccctgc gtcacctctg cag

23

<210> 63

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine

<400> 63

ttagaaatta cttattatgt tctcaatcc

29

<210> 64

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat

<400> 64

gaggtgacgc aggaggggca ttagtgttt

29

<210> 65

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat

<400> 65

ctagaaacac taatgcccct cctgcgtcac ctctgca

37

<210> 66

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60

acctgcaccg tctctggggtt ctactcagc aggggtaaaa tgggtgtgag ctggatccgt 120

cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180

tacaggacat cgctgaagag caggctcacc atctccaagg acacctcaa aaaccaggtg 240

gtccttacia tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300

cgacgtggag gaattgacta ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> 67

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 67

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
20 25 30

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

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 68
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68

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

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
20 25 30

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

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

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

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

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 69
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69

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

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

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

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

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

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

<210> 70
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 70
tcctatgagc tgatacagcc accctcgggtg tcagtggccc caggacagac ggccaccatt 60
acctgtgcgg gagacaacct tgggaagaaa cgtgtgcact ggtaccagca gaggccaggc 120
caggccccctg tgttgggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga 180
ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg 240
gatgaggccg actattattg tcagggtgtgg gacattgcta ctgatcatgt ggtcttcggc 300
ggagggacca agctcaccgt ccta 324

<210> 71
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71

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

Thr Ala Thr Ile Thr Cys Ala Gly Asp Asn Leu Gly Lys Lys Arg Val
20 25 30

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

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

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Gly Glu Ala Gly

65		70		75		80									
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ile	Ala	Thr	Asp	His
			85						90					95	

Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ala	Ala	Ala	Gly
			100					105					110		

Ser	Glu	Gln	Lys	Leu	Ile	Ser	Glu
		115					120

<210> 72
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 72

Leu	Glu	Val	Thr	Cys	Glu	Pro	Gly	Thr	Thr	Phe	Lys	Asp	Lys	Cys	Asn
1				5				10						15	

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

Trp	Cys	Asn	Gln
		35	

<210> 73
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 73

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

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

Gln

<210> 74
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74

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

Trp Cys Asn Gln
20

<210> 75
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Val
35 40 45

Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu Thr Leu

50

55

60

Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly Lys Met
 65 70 75 80

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
 85 90 95

Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser Leu Lys
 100 105 110

Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
 115 120 125

Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
 130 135 140

Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
 145 150 155 160

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 165 170 175

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 180 185 190

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 195 200 205

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 210 215 220

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 225 230 235 240

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
 245 250 255

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
260 265 270

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
275 280 285

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
305 310 315 320

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
355 360 365

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
385 390 395 400

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
435 440 445

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly

450

455

460

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 465 470 475 480

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 485 490

<210> 76
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 76

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
 50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro

115

120

125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

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

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ala Ala Gly
435 440 445

Gly Ser Gly Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp
450 455 460

Lys Cys Asn Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys
465 470 475 480

Thr Lys Leu Trp Cys Asn Gln Gly Ser Gly Ala
485 490

<210> 77

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Pro
35 40 45

Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln Thr Ala
50 55 60

Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala Tyr Trp
65 70 75 80

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr Gln Asp
85 90 95

Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
100 105 110

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
115 120 125

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val Phe Gly
130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser
145 150 155 160

Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
165 170 175

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val

180

185

190

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
 195 200 205

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
 210 215 220

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln
 225 230 235 240

Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu
 245 250 255

Cys Ser

<210> 78
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 78

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

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

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

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met

65					70					75					80
Asp	Glu	Ala	Asp	Tyr 85	Tyr	Cys	Gln	Ala	Trp 90	Asp	Ser	Ser	Thr	Ala 95	Val
Phe	Gly	Gly	Gly 100	Thr	Lys	Leu	Thr	Val 105	Leu	Gly	Gln	Pro	Lys 110	Ala	Ala
Pro	Ser	Val 115	Thr	Leu	Phe	Pro	Pro 120	Ser	Ser	Glu	Glu	Leu 125	Gln	Ala	Asn
Lys	Ala 130	Thr	Leu	Val	Cys	Leu 135	Ile	Ser	Asp	Phe	Tyr 140	Pro	Gly	Ala	Val
Thr 145	Val	Ala	Trp	Lys 150	Ala	Asp	Ser	Ser	Pro	Val 155	Lys	Ala	Gly	Val	Glu 160
Thr	Thr	Thr	Pro	Ser 165	Lys	Gln	Ser	Asn	Asn 170	Lys	Tyr	Ala	Ala	Ser 175	Ser
Tyr	Leu	Ser 180	Leu	Thr	Pro	Glu	Gln	Trp 185	Lys	Ser	His	Arg	Ser 190	Tyr	Ser
Cys	Gln 195	Val	Thr	His	Glu	Gly	Ser 200	Thr	Val	Glu	Lys	Thr 205	Val	Ala	Pro
Thr 210	Glu	Cys	Ser	Ala	Ala	Gly 215	Gly	Ser	Gly	Leu	Glu 220	Val	Thr	Cys	Glu
Pro 225	Gly	Thr	Thr	Phe	Lys 230	Asp	Lys	Cys	Asn	Thr 235	Cys	Arg	Cys	Gly	Ser 240
Asp	Gly	Lys	Ser	Ala 245	Val	Cys	Thr	Lys	Leu 250	Trp	Cys	Asn	Gln	Gly 255	Ser
Gly	Ala														

<210> 79
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser
1 5 10

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80

Ala Ala Gly Gly Ser Gly
1 5

<210> 81
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81

Gly Ser Gly Ala
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<210> 82
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82

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tcagatggga aatcggcggt ctgcacaaag ctctggtgta accagggcac cgggtggaggg	180
tcgggatcca gctcacaggt caccttgaag gagtctggtc ctgtgctggt gaaaccacaca	240
gagaccctca cgctgacctg caccgtctct gggttctcac tcagcagggg taaaatgggt	300
gtgagctgga tccgtcagcc cccaggggaag gccctggagt ggcttgcaca cattttttcg	360
agtgacgaaa aatcctacag gacatcgctg aagagcaggc tcaccatctc caaggacacc	420
tccaaaaacc aggtggtcct tacaatgacc aacatggacc ctgtggacac agccacgtat	480
tactgtgcac ggatacgacg tggaggaatt gactactggg gccaggggaac cctggtcact	540
gtctcctcag cctccaccaa gggcccatcc gtcttcccc tggcgccctg ctccaggagc	600
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	780
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gttgagtcca aatatgggtcc cccatgccc ccatgcccag cacctgagtt cctgggggga	900
ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggaccct	960
gaggtcacgt gcgtggtggt ggacgtgagc caggaagacc ccgaggtcca gttcaactgg	1020
tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac	1080
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1380
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<210> 83
 <211> 1533
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 83	
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tgcaccgtct ctgggttctc actcagcagg ggtaaaatgg gtgtgagctg gatccgtcag	180
cccccaggga aggccctgga gtggcttgca cacatTTTTT cgagtgcga aaaatcctac	240
aggacatcgc tgaagagcag gtcaccatc tccaaggaca cctccaaaaa ccagggtggtc	300
cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc acggatacga	360
cgtggaggaa ttgactactg gggccaggga accctgggtca ctgtctcctc agcctccacc	420
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
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<210> 84
 <211> 834
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 84	
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tcagatggga aatcggcggt ctgcacaaag ctctgggtgta accagggcac cggtagggg	180
tcgggatcca gtcacagcc agtgctgact cagccccct cactgtccgt gtccccagga	240
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cagcagaagc caggccagtc ccctgtgttg gtcattgtatc aagataaaca gcggccctca	360
gggatccctg agcgattctc tggctccaac tctgggaaca cagccactct gaccatcagc	420
gggacccagg ctatggatga ggctgactat tactgtcagg cgtgggacag cagcactgcg	480
gtattcggcg gagggaccaa gctgaccgtc ctaggccagc ctaaggcggc gccctcggtc	540
accctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	600
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc	660
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	720

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc	780
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc atag	834

<210> 85
 <211> 834
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 85	
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cctgagcagt ggaagtcca cagaagctac agctgccagg tcacgcatga agggagcacc	660
gtggagaaga cagtggcccc tacagaatgt tcagccgctg gtggtagtgg tttggaagtg	720
acgtgtgagc ccggaacgac attcaaagac aagtgaata cttgtcgggtg cggttcagat	780
gggaaatcgg cggctctgcac aaagctctgg tgtaaccagg gtagtggtgc ttag	834