

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
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 Ma, Dangshe
 Olson, William
 Thurston, Gavin

<120> RADIOLABELED ANTI-LAG3 ANTIBODIES FOR IMMUNO-PET IMAGING

<130> 10329W001

<140> TBD

<141> 2018-02-09

<150> 62/457,287

<151> 2017-02-10

<160> 589

<170> PatentIn version 3.5

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

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

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

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

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

Ala Lys Glu Ser Val Thr Gly Thr Ser Ser Tyr Tyr Tyr Gly Val Asp
 100 105 110

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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ccaggcaagg ggctggagtg ggtggcactt atatggtatg atggaactaa taaaaagtat 180

ggagactccg tgaagggccg attcaccatt tccagagaca attccaagaa cacggtgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagattgt 300

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
20 25 30

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

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

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

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

Ala Arg Asp Cys Gly His Ser Gly Asn Asp Arg Gly Thr Tyr Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
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Gly Phe Thr Phe Ser Trp Tyr Gly
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Ala Arg Asp Cys Gly His Ser Gly Asn Asp Arg Gly Thr Tyr Tyr Tyr
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Tyr Tyr Gly Met Asp Val
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		20						25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Pro
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Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys				
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Gln	Ser	Ile	Ser	Ser	Tyr
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Ala Ala Ser
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Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
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ccaggggaagg ggctggagtg ggttggggaa atcagtcata gaggaaccac caactacaac	180
ccgtccctca agagtcgagt caccatatca ctggacacgt ccaagaacca gttctccctg	240
aaactgacct ctgtgaccgc cgcggacacg gctgtgtatt actgttcgag agacgaggaa	300
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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr	
20 25 30	
Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Gly Glu Ile Ser His Arg Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys	
50 55 60	
Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu	
65 70 75 80	
Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ser	
85 90 95	
Arg Asp Glu Glu Leu Glu Phe Arg Phe Phe Asp Tyr Trp Gly Gln Gly	
100 105 110	

Thr Leu Val Thr Val Ser Ser
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Gly Gly Ser Phe Ser Gly Tyr Tyr
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Ile Ser His Arg Gly Thr Thr
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Ser Arg Asp Glu Glu Leu Glu Phe Arg Phe Phe Asp Tyr
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 ggccaggctc ccaggctcct cgtctatggc gcatccaaca gggccactgg catcccagcc 180
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

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

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

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Gln Ser Val Ser Ser Tyr

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 cagccccag ggaaggggct ggagtggatt ggcaatttct ttatatactgg ggccacctac 180
 tacaacccgt ccctcaagag tcgagtcacc atatccgctg acacgtccaa gaatcagttc 240
 tccctgaagc tgagctctgt gaccgccgca gacacggctc tgtattattg tgcgagttat 300
 aataggaatt accggttcga cccctggggc cagggaaccc tggtcaccgt ctcctca 357

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

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

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

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Tyr
 85 90 95

Cys Ala Ser Tyr Asn Arg Asn Tyr Arg Phe Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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Gly Asp Ser Ile Ile Ser Asn Ser Tyr Tyr
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Phe Phe Tyr Thr Gly Ala Thr
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Ala Ser Tyr Asn Arg Asn Tyr Arg Phe Asp Pro
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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caagggacac gactggagat taaa 324

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

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

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

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

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

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

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18

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<400> 60

Gln Ser Ile Ser Ser Tyr
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Ala Ala Ser
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Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
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 ccaggggaagg ggctggagtg gattggagag atcaatcata gtggaaacgc cgactacaac 180
 ccgtcccctca agagtcgagt ctccatatca gtggacacgt ccaagaacca gttctccctg 240
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Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Thr Tyr
 20 25 30

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

Gly Glu Ile Asn His Ser Gly Asn Ala Asp Tyr Asn Pro Ser Leu Lys
 50 55 60

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

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

Arg Ala Gly Tyr Cys Ser Ser Pro Thr Cys Tyr Ser Tyr Tyr Tyr Phe
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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24

<210> 68
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Gly Gly Ser Phe Ser Thr Tyr Tyr
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Ile Asn His Ser Gly Asn Ala
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gtc 63

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Ala Arg Ala Gly Tyr Cys Ser Ser Pro Thr Cys Tyr Ser Tyr Tyr Tyr
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Phe Gly Met Asp Val
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcttccca	180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatccg cagactggag	240
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<400> 74

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			20					25					30		

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

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

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

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

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

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<400> 76

Gln Ser Val Ile Ser Ser Phe
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<220>
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<400> 78

Gly Ala Ser
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<210> 80
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Gln Gln Tyr Gly Asn Ser Pro Trp Thr
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cagccccctg ggaaggccct ggagtggctt gcacacattt tttcgaatga cgagaagtcc 180
tacagcacat ctctgaggac cagactcacc atctccaagg acacctcaa aagccaggtg 240
gtccttaccg tgaccaactt ggaccctgtg gacacagcca catatttctg tgcacggata 300
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caagggacca cggtcacctg ctcctca 387

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<400> 82

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 Asn Ala
20 25 30

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

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

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

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

Cys Ala Arg Ile Pro Glu Phe Thr Ser Ser Ser Trp Ala Leu Tyr Tyr
100 105 110

Phe Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

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<212> DNA
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<210> 84
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<400> 84

Gly Phe Ser Leu Ser Asn Ala Gly Met Gly
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<210> 85
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<212> DNA
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<220>
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<400> 85
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<210> 86
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<220>
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<400> 86

Ile Phe Ser Asn Asp Glu Lys
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<210> 87
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Ala Arg Ile Pro Glu Phe Thr Ser Ser Ser Trp Ala Leu Tyr Tyr Phe

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Tyr Gly Met Asp Val
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cctggccagg ctcccaggct cctcatctat gctacatcca gcagggccac tggcgtccca 180
gacaggttca gtggcagtgg gtctgggacg gacttcactc tcaccatcag cagactggag 240
cctgatgatt ttgcagtgta ttactgtcag caatatggta ggtcaccttg gacgttcggc 300
caagggacca aggtggaagt caaa 324

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<400> 90

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

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

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

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

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

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

<210> 91
<211> 21
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<400> 91
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21

<210> 92
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<220>
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<400> 92

Gln Ser Ile Thr Ser Thr Tyr
1 5

<210> 93
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<400> 93
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9

<210> 94
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<400> 94

Ala Thr Ser
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cagcaatatg gtaggtcacc ttggacg 27

<210> 96
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<400> 96

Gln Gln Tyr Gly Arg Ser Pro Trp Thr
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<210> 97
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<220>
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<400> 97
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cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatgataa cacaaactat 180
gcacagaagc tccagggcag agtcaccatg accgcagaca catccacgaa tacagcctac 240
atggagctaa ggagcctgag atctgacgac acggccattt attactgtgt gcgatggaat 300
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 <212> PRT
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<400> 98

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 1 5 10 15

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

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

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

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

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

Val Arg Trp Asn Trp Gly Ser Val Tyr Trp Tyr Phe Asp Leu Trp Gly
 100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 99
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 <212> DNA
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<220>
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<400> 99

ggttacacct ttaccagtta tggt

24

<210> 100
<211> 8
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<220>
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<400> 100

Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 101
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<400> 101
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24

<210> 102
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<400> 102

Ile Ser Ala Tyr Asn Asp Asn Thr
1 5

<210> 103
<211> 42
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42

<210> 104
<211> 14
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<400> 104

Val Arg Trp Asn Trp Gly Ser Val Tyr Trp Tyr Phe Asp Leu
1 5 10

<210> 105
<211> 324
<212> DNA
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<400> 105

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cctggccagg ctcccaggct cctcatctat ggtgcgtcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcaatgta tttctgtcag cagtatggta actcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 106
<211> 108
<212> PRT
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<220>
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<400> 106

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1 5 10 15

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

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

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

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

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

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

<210> 107
 <211> 21
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<400> 107
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21

<210> 108
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<400> 108

Gln Ile Ile Ser Ser Ser Tyr
 1 5

<210> 109
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<400> 109
 ggtgcgtcc

9

<210> 110
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Gly Ala Ser
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<400> 111
cagcagtatg gtaactcacc ttggacg

27

<210> 112
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Gln Gln Tyr Gly Asn Ser Pro Trp Thr
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acttgcacct tctctgggtt ctactcaac actcatagag tgggtgtagg ctggatccgg

120

cagccccag gaaaggccct ggagtggctt gcactcattt atgggaatga tgттааgааc 180
 tacagcccat ctctggagac caggctcacc atcgccaagg acacctcaa aaaccaggtg 240
 gtccttacaа tgaccaacat ggaccctgtg gacacagcca catatttctg ttcgtacata 300
 acggggggaag gaatgtactg gggccaggga accctgggtca ccgtctcctc a 351

<210> 114
 <211> 117
 <212> PRT
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<220>
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<400> 114

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Asn Thr His
 20 25 30

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

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

Leu Glu Thr Arg Leu Thr Ile Ala 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 Phe
 85 90 95

Cys Ser Tyr Ile Thr Gly Glu Gly Met Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

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<400> 115

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30

<210> 116

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<212> PRT

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<223> synthetic

<400> 116

Gly Phe Ser Leu Asn Thr His Arg Val Gly

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10

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<211> 21

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<400> 117

atttatggga atgatgttaa g

21

<210> 118

<211> 7

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<400> 118

Ile Tyr Gly Asn Asp Val Lys

1

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<210> 119

<211> 27

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<400> 119
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<210> 120
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<400> 120
Ser Tyr Ile Thr Gly Glu Gly Met Tyr
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<210> 121
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<400> 121
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tttcaccaga ggccaggcca atctccaagg cgtctaattt ataaggtttc taaccgggac 180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240
agcagggtgg aggctgagga tgttgggggtt tattactgca tgcaaggtag acactggtag 300
acatttggcc aggggaccaa gctggagatc aaa 333

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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Met Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe His Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 123
<211> 33
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<400> 123
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33

<210> 124
<211> 11
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<400> 124

Gln Asn Leu Met Tyr Ser Asp Gly Asn Thr Tyr
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<210> 125
<211> 9
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<400> 125
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9

<210> 126
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Lys Val Ser
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<400> 127
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24

<210> 128
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Met Gln Gly Thr His Trp Tyr Thr
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<210> 129
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acctgcgctg tctatggtgg gtctttcagt ggttattact ggagctggat ccgccagccc 120
ccagggaagg gtctggaatg gattggggaa atcaatcata gaggaaacac caactacaac 180
ccgtccctca agagtcgagt caccatatca ctcgacacgt ccaagaaaca gttctccctg 240
aacctgagtt ctgtgaccgc cgcggacacg gctatgtatt actgtacgag agacgaagaa 300
caggaactac gtttccttga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 130
<211> 119
<212> PRT
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<400> 130

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1 5 10 15

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

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

Gly Glu Ile Asn His Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Asp Glu Glu Gln Glu Leu Arg Phe Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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24

<210> 132
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<400> 132

Gly Gly Ser Phe Ser Gly Tyr Tyr
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<210> 133
<211> 21
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21

<210> 134
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Ile Asn His Arg Gly Asn Thr
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<210> 135
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39

<210> 136
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Thr Arg Asp Glu Glu Gln Glu Leu Arg Phe Leu Asp Tyr
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ggccaggctc ccaggctcct catctatggg gcttccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cattttatta ctgtcaacag cgcagcaact ggccgctcac tttcggcgga 300
gggaccgagg tggagatcaa a 321

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<400> 138

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1 5 10 15

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

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

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

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

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

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

<210> 139
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<400> 139
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18

<210> 140
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Gln Asp Ile Ser Thr Tyr
1 5

<210> 141
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<212> DNA
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<400> 141
ggtgcttcc

9

<210> 142
<211> 3
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<400> 142

Gly Ala Ser
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<210> 143
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caacagcgca gcaactggcc gctcact

27

<210> 144
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Gln Gln Arg Ser Asn Trp Pro Leu Thr
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<210> 145
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<220>

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<400> 145

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ccagggaagg ggctggagtg gattggggaa atcaatcata gaggaaacac caactacaac      180
ccgtccctca agagtcgagt caccgtatca gaagacacgt ccaagaacca gttctccctg      240
aagctgagct ctttgaccgc cgcggacacg gctgtgtatt actgtgtgag aggagaggat      300
tacgattttt ggagtgatta ttataatgac tactggggcc agggaaccct ggtcaccgtc      360
tcctca                                     366
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<211> 122

<212> PRT

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<220>

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<400> 146

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

```
Thr Leu Ser Leu Thr Cys Val Val His Gly Gly Ser Phe Ser Gly Tyr
          20              25              30
```

```
Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35              40              45
```

```
Gly Glu Ile Asn His Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
          50              55              60
```

```
Ser Arg Val Thr Val Ser Glu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65              70              75              80
```

```
Lys Leu Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
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Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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Gly Gly Ser Phe Ser Gly Tyr Tyr
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21

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Val Arg Gly Glu Asp Tyr Asp Phe Trp Ser Asp Tyr Tyr Asn Asp Tyr
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ggccaggctc ccaggctcct catctatgat gcatcAAAA gggccacggg catcccagcc 180
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser Ser Tyr
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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Gln Thr Ile Ser Ser Tyr
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ccaggaagg ggctggagtg gattggggaa atcaatcata gaggaagcac caactacaac 180
ccgtcccctca agagtcgagc caccatatca gttgacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgttcgag aggcgaggat 300
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Thr Leu Ser Leu Ile Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

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

Gly Glu Ile Asn His Arg Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
Page 53

65		70		75		80
Lys	Leu	Ser	Ser	Val	Thr	Ala
				85		Ala
					Thr	Ala
					90	Val
						Tyr
						Tyr
						Cys
						95
						Ser
Arg	Gly	Glu	Asp	Tyr	Tyr	Asp
			100			Ser
						105
					Gly	Tyr
					Ser	Tyr
						110
						Tyr
						Phe
						Asp
Tyr	Trp	Gly	Gln	Gly	Thr	Leu
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						Thr
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24

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21

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Asp Tyr

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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

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

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

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

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

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

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<210> 172
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Gln Ser Val Ser Ser Tyr
1 5

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Asp Ala Ser
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Gln Gln Arg Ser Asn Trp Pro Leu Thr
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20 25 30

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

Gly Glu Ile Asn His Arg Gly Asn Ile Asn Phe Asn Pro Ser Leu Lys
 50 55 60

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

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

Arg Gly Glu Asp Tyr Asp Ile Trp Ser Gly Tyr Tyr Arg Glu Tyr Trp
 100 105 110

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

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Gly Gly Ser Phe Ser Gly Tyr Tyr
 1 5

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21

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Ile Asn His Arg Gly Asn Ile
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Ala Arg Gly Glu Asp Tyr Asp Ile Trp Ser Gly Tyr Tyr Arg Glu Tyr
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ggccaggctc ccaggctcct catctatgat gcatccaaga gggccactgg catcccagcc      180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct      240
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1              5              10              15
```

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

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

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

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

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
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```

```
Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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ccagagaagg gcctggagtg gattggggaa atcaatcatc gtggaaacac caactacaac 180

ccgtccctca agagtcgagt caccatatca gtagacatgt ccaagaacca gttctccctg 240

cagctgaact ctgtgaccgt cgcggacacg gctctgtatt actgtgcgtt tggctacgat 300

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 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Glu Phe
 20 25 30
 Tyr Trp Asn Trp Ile Arg Gln Pro Pro Glu Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Met Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Gln Leu Asn Ser Val Thr Val Ala Asp Thr Ala Leu Tyr Tyr Cys Ala
 85 90 95
 Phe Gly Tyr Asp Phe Arg Ser Ser Tyr Glu Asp Val Trp Gly Gln Gly
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 Thr Thr Val Thr Val Ser Ser
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Gly Gly Ser Phe Ser Glu Phe Tyr
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aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
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gggaccaagg tggagatcaa a 321

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

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

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

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

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

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

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18

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Gly Ser Ser
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27

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Gln Gln Arg Ser Asn Trp Pro Leu Thr
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 acagactccg tgaagggccg gttcaccatc tccagagaca attccaagag catgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccattt attactgtgc gaaagagagg 300
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20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Met Leu Tyr
65 70 75 80

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

Ala Lys Glu Arg Val Thr Gly Ile Asp His Tyr Tyr Tyr Gly Val Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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24

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Gly Phe Thr Phe Arg Ser Tyr Ala
1 5

<210> 213

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attagtggtag gtggtagtag gaca

24

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Ala Lys Glu Arg Val Thr Gly Ile Asp His Tyr Tyr Tyr Gly Val Asp
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Val

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gggaaagccc ctaagctcct gatctatgct acatccagtt tgcaaagtgg ggtcccatca 180
cggttcagtg gcagtgcac tggaacagat ttcactctcg ccatcagcag tctgcaacct 240
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gggaccaagg tggagatcaa a 321

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

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

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

55

60

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

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

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

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<220>
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<400> 219
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18

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<400> 220

Gln Ser Ile Ser Ser Tyr
 1 5

<210> 221
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<400> 221
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9

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<400> 222

Ala Thr Ser
1

<210> 223
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<220>
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<400> 223
caacagagtt acactacccc cctcact

27

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<400> 224

Gln Gln Ser Tyr Thr Thr Pro Leu Thr
1 5

<210> 225
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<212> DNA
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<400> 225
gaggtgcagc tgggtggagtc tggggggaggc ttggtacaac ctggagggtc cctgagactt 60
tcctgtgcag cctctggatt tacattcagc agttatgaaa tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatat atcagtagta gtggtataac caaagactac 180
gcaggctctg tgaagggccg agtcaccatc tccagagaca acgccaagaa cttactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt atcactgtgc gagagatgga 300
 gggcattacg atattttgac tggttccatg tcctactact actacgcttt ggacgtctgg 360
 ggccaaggga ccacgggtcac cgtctcctca 390

<210> 226
 <211> 130
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<220>
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<400> 226

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Asp Gly Gly His Tyr Asp Ile Leu Thr Gly Ser Met Ser Tyr
 100 105 110

Tyr Tyr Tyr Ala Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
 115 120 125

Ser Ser
 130

<210> 227
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
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<400> 227
ggatttacat tcagcagtta tgaa

24

<210> 228
<211> 8
<212> PRT
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<220>
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<400> 228

Gly Phe Thr Phe Ser Ser Tyr Glu
1 5

<210> 229
<211> 24
<212> DNA
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<220>
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<400> 229
atcagtagta gtggtaatac caaa

24

<210> 230
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 230

Ile Ser Ser Ser Gly Asn Thr Lys
1 5

<210> 231
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
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<400> 231
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 ttggacgtc 69

<210> 232
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<400> 232

Ala	Arg	Asp	Gly	Gly	His	Tyr	Asp	Ile	Leu	Thr	Gly	Ser	Met	Ser	Tyr
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Tyr	Tyr	Tyr	Ala	Leu	Asp	Val
			20			

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<220>
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<400> 233

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gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tgcaaagtgg	ggtcccgtca	180
aggttcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagattttg	caacttacta	ctgtcaacag	agttacagta	cccctccgat	caccttcggc	300
caagggacac	gactggagat	taaa				324

<210> 234
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 234

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

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

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

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

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

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

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

<210> 235

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 235

cagagcatta gcagctat

18

<210> 236

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 236

Gln Ser Ile Ser Ser Tyr

1

5

<210> 237
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 237
gctgcatcc

9

<210> 238
<211> 3
<212> PRT
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<220>
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<400> 238

Ala Ala Ser
1

<210> 239
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 239
caacagagtt acagtacccc tccgatacc

30

<210> 240
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 240

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 241
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<220>
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<400> 241
gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaaa acctatgcc a tgagctgggt ccgccaggct 120
ccagggaggg ggctggagtg ggtctcaggt attagtggta gtggtagtac ctcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attacaagaa gacgctgtct 240
ctgcaaatga acagtctgag agccgaggac acggccgttt attactgtgc gctggatata 300
atggcaacgg taggaggtct cttaacaac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 242
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 242
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Thr Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Ser Gly Ser Thr Ser Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Tyr Lys Lys Thr Leu Ser
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Leu Asp Ile Met Ala Thr Val Gly Gly Leu Phe Asn Asn Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 243
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 243
 ggattcacct ttaaaaccta tgcc

24

<210> 244
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 244

Gly Phe Thr Phe Lys Thr Tyr Ala
 1 5

<210> 245
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 245
 attagtggtgta gtggtagtagtac ctca

24

<210> 246
 <211> 8
 <212> PRT
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<220>

<223> synthetic

<400> 246

Ile Ser Gly Ser Gly Ser Thr Ser
1 5

<210> 247

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 247

gcgctggata taatggcaac ggtaggaggt ctctttaaca ac

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<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 248

Ala Leu Asp Ile Met Ala Thr Val Gly Gly Leu Phe Asn Asn
1 5 10

<210> 249

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 249

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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccttg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 250
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 250

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

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

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

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

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

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

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

<210> 251
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 251

cagagtgtta gcagcagcta c

21

<210> 252
 <211> 7
 <212> PRT
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<220>

<223> synthetic

<400> 252

Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 253

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 253

ggtgcatcc

9

<210> 254

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 254

Gly Ala Ser
1

<210> 255

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 255

cagcagtatg gtagctcacc ttggacg

27

<210> 256

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 256

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 257

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 257

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tcctgcaagg cttctggagg caccttcagc agacatacta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacacaagt tccagggcag agtcacgatt accacggacg aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtat attattgtgc gagagcccct 300
tatacccgac aggggtactt cgatctctgg ggccgtggca ccctggtcac cgtctcctca 360

<210> 258

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 258

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 259
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 259
ggaggcacct tcagcagaca tact 24

<210> 260
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 260
Gly Gly Thr Phe Ser Arg His Thr
1 5

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 261
atcatcccta tcttttgtac agca 24

<210> 262

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 262

Ile Ile Pro Ile Phe Gly Thr Ala
1 5

<210> 263
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
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<400> 263
gcgagagccc cttatacccg acaggggtac ttcgatctc

39

<210> 264
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 264

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

<210> 265
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
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<400> 265
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atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctactca ttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaaga ttatagtact 300
 ccgtggacgt tcggccaagg gaccaagggtg gaaatcaaa 339

<210> 266
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 266

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

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

Asp Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

<210> 267
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 267
cagagtgttt tatacagctc caacaataag aactac

36

<210> 268
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 268

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 269
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 269
tgggcatct

9

<210> 270
<211> 3
<212> PRT
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<220>
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<400> 270

Trp Ala Ser
1

<210> 271
<211> 27
<212> DNA
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<220>
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<400> 271
cagcaagatt atagtactcc gtggacg

27

<210> 272
 <211> 9
 <212> PRT
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<220>
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<400> 272

Gln Gln Asp Tyr Ser Thr Pro Trp Thr
 1 5

<210> 273
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 273

caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt	60
tcctgcaagg catctggata caccttcacc aactactata tacactgggt gcgacaggcc	120
cctggacaag ggcttgactg gatgggaatt atcaaccctg gtggtggtaa cacaaactac	180
gcacagaagt tcctgggcag agtcaccatg accagggaca cgtccacgac cacagtctac	240
atggagctga gcagcctgag atctgaggac acggccatat attactgtgc gagagaaaac	300
tggaactctt actttgacaa ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> 274
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 274

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 275
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 275
ggatacacct tcaccaacta ctat

24

<210> 276
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 276

Gly Tyr Thr Phe Thr Asn Tyr Tyr
1 5

<210> 277
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
 <223> synthetic

 <400> 277
 atcaaccctg gtggtggtaa caca 24

<210> 278
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 278

Ile Asn Pro Gly Gly Gly Asn Thr
 1 5

<210> 279
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 279
 gcgagagaaa actggaactc ttactttgac aac 33

<210> 280
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<220>
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<400> 280

Ala Arg Glu Asn Trp Asn Ser Tyr Phe Asp Asn
 1 5 10

<210> 281
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 281
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 tgggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctaccgg 180
 gaatccggggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcaggctga agatgtggca ctttattact gtcagcaata ttatgggtgct 300
 ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 282
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 282
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Gly Ala Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 Lys

<210> 283
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 283
cagagtgttt tatacagctc caacaataag aacttc

36

<210> 284
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 284

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Phe
1 5 10

<210> 285
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 285
tgggcatct

9

<210> 286
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 286

Trp Ala Ser
1

<210> 287

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

<220>
<223> synthetic

<400> 287
cagcaatatt atggtgctcc gtggacg

27

<210> 288
<211> 9
<212> PRT
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<220>
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<400> 288

Gln Gln Tyr Tyr Gly Ala Pro Trp Thr
1 5

<210> 289
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
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<400> 289
cagggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc agctatacta tcaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtat agcaaactac 180
gcacagaagt tccagggcag agtcacgatt accacggacg aatccacgaa cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccattt attactgtgc gagagcgaga 300
tatggttcgg ggagttatga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 290
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<400> 290

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 291

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 291

ggaggcacct tcagcagcta tact

24

<210> 292

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 292

Gly Gly Thr Phe Ser Ser Tyr Thr
1 5

<210> 293
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 293
atcatcccta tctttggtat agca

24

<210> 294
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 294

Ile Ile Pro Ile Phe Gly Ile Ala
1 5

<210> 295
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 295
gcgagagcga gatatggttc ggggagttat gactac

36

<210> 296
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 296

Ala Arg Ala Arg Tyr Gly Ser Gly Ser Tyr Asp Tyr
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tggtaccagc agaaaccagg acagcctcct aagctgctca ttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttataatact 300
ccatggacgt tcggccaagg gaccaaggtg gaaatcaaa 339

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<400> 298

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

85

90

95

Tyr Tyr Asn Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

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cagccccag gaaaggccct ggagtggctt ggaatcattt attggaatga tgataagcgc 180

tacagcccat ctctgaggag cagactcacc atcaccaagg acacctcaa aaaccaggtg 240

gtccttacia tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga 300

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 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Asn
 20 25 30

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

Trp Leu Gly Ile Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

Leu Arg Ser Arg Leu Thr Ile Thr 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 His Arg Gly Leu Phe Gly Gly Trp Phe Asp Pro Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

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Gly Phe Ser Leu Ser Thr Asn Gly Val Gly
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Ile Tyr Trp Asn Asp Asp Lys
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gggaaagccc ctaacctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

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

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

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

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

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

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18

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Gln Ser Ile Ser Arg Tyr
1 5

<210> 317
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gctgcatcc

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Ala Ala Ser
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caacagagtt acaataacccc gctcact

27

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<400> 320

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

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ccagggaagg cgctggagtg ggtctcagtt attagtggta gcggtggtaa cacatactac 180
gcagactccg tgaagggccg gttcacgctc tccagagaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat atttctgttc gaaagttgca 300
gcagctaata attactatta cgctttggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca 366

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<400> 322

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Ser Leu Arg Leu Ser Cys Ala Ile Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

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

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

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

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

Ser Lys Val Ala Ala Ala Asn Asn Tyr Tyr Tyr Ala Leu Asp Val Trp
100 105 110

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

<210> 323
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<212> DNA
<213> Artificial Sequence

<220>
 <223> synthetic

 <400> 323
 ggattcacct ttaggagtta tgcc

24

<210> 324
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<220>
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<400> 324

Gly Phe Thr Phe Arg Ser Tyr Ala
 1 5

<210> 325
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<220>
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<400> 325
 attagtggta gcggtggtaa caca

24

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<400> 326

Ile Ser Gly Ser Gly Gly Asn Thr
 1 5

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<400> 327
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<400> 328
Ser Lys Val Ala Ala Ala Asn Asn Tyr Tyr Tyr Ala Leu Asp Val
1 5 10 15

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<212> DNA
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<400> 329
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tacctgcaga agccagggca gtctccacaa ctctgatct atttggtttc taatcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgggggt tattattgca tgcaagctct acaaactccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

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<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 330
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
Page 107

20

25

30

Asn Gly Tyr Lys Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95

Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 331
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33

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Gln Ser Leu Leu His Ser Asn Gly Tyr Lys Tyr
 1 5 10

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Leu Val Ser
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27

<210> 336
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Met Gln Ala Leu Gln Thr Pro Tyr Thr
1 5

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ccaggcaagg ggctggagtg ggtggcagtt atatggaatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctccaagtga gcagcctgag agccgatgac acggctgtat attactgtgc gagggacgga	300
gaggtcgaat atagcagctc gaattacaac tactacggtc tggatgtctg gggccaaggg	360
accacggtca ccgtctcctc a	381

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

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

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

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

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

Ala Arg Asp Gly Glu Val Glu Tyr Ser Ser Ser Asn Tyr Asn Tyr Tyr	
100 105 110	

Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

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24

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<400> 340

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

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24

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<400> 342

Ile Trp Asn Asp Gly Ser Asn Lys
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<400> 344

Ala Arg Asp Gly Glu Val Glu Tyr Ser Ser Ser Asn Tyr Asn Tyr Tyr
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Gly Leu Asp Val
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gggaaagccc ctaaactcct gatctacgat gcatccaatt tggaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
gaagatattg taacatatta ctgtcaacag tatgatgatc tcccgatcac cttcggccaa 300
gggacacgac tggagattaa a 321

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<220>

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<400> 346

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

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

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

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

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

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

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<400> 347

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18

<210> 348

<211> 6

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<220>

<223> synthetic

<400> 348

Gln Asp Ile Ser Asn Tyr
1 5

<210> 349
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<212> DNA
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<400> 349
gatgcatcc

9

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<400> 350

Asp Ala Ser
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<211> 27
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caacagtatg atgatctccc gatcacc

27

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Gln Gln Tyr Asp Asp Leu Pro Ile Thr
1 5

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 ccagggaagg ggctggagtg ggtctcagtt attactggta gtggtactag cacacactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa aacgctatat 240
 ctgcaaatga atagcctgag agccgaggac acggccgtat attactgtgc gaaagatcgg 300
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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe His Asn Phe
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Thr Gly Ser Gly Thr Ser Thr His Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
 65 70 75 80

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

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

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

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24

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<211> 8
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<220>
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<400> 356

Gly Phe Ser Phe His Asn Phe Ala
1 5

<210> 357
<211> 24
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<400> 357
attactggta gtggtactag caca

24

<210> 358
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<400> 358

Ile Thr Gly Ser Gly Thr Ser Thr
1 5

<210> 359

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gcgaaagatc ggggctatga ttatagtggt tcttactaca actggttcga cccc 54

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Ala Lys Asp Arg Gly Tyr Asp Tyr Ser Gly Ser Tyr Tyr Asn Trp Phe
1 5 10 15

Asp Pro

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<211> 327

<212> DNA

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<220>

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<400> 361

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gggaaagccc ctaaactcct gatctttgct gcatcaaatt tgcaaagtgg ggtcccatca 180

aggttcagtgcagtggtgatctgggacagattcactctcacatcagtagtctgcaacct240
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<220>
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<400> 362

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1 5 10 15

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

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

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

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

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

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 363
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<400> 363

cagagtatta gcagctat

<210> 364
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<213> Artificial Sequence

<220>
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<400> 364

Gln Ser Ile Ser Ser Tyr
1 5

<210> 365
<211> 9
<212> DNA
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<220>
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<400> 365
gctgcatca

9

<210> 366
<211> 3
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Ala Ala Ser
1

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<211> 33
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<220>
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<400> 367
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33

<210> 368

<211> 11
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<220>
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<400> 368

Gln Gln Ser Tyr Ser Thr Pro Ser Leu Phe Thr
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ccagggaagg ggctggaatg ggtttcacac attagtagta gtggaagtac catatactac 180
gcagactctg tgaagggccg attcaccatg tccagagaca acgccaagaa ctactgtat 240
ctgcaaataa acagcctgag agccgaggac acggctgttt attactgtgc gagagatggg 300
aatatctgga gtggttatta tgccgcctac tacttctacg gtatggacgt ctggggccaa 360
gggaccacgg tcaccgtctc ctca 384

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<400> 370

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

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

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

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

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

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

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

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

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<400> 372

Gly Phe Thr Phe Ser Ser Tyr Glu
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Ile Ser Ser Ser Gly Ser Thr Ile
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Ala Arg Asp Gly Asn Ile Trp Ser Gly Tyr Tyr Ala Ala Tyr Tyr Phe
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Tyr Gly Met Asp Val
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cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccggttc 180
tctgggggtcc cagacagaat cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtg aagctgagga tgtcgggggtt tattactgca tgcaagctgt acaatttcct 300
cggacgttcg gccaaaggac caaggtggaa atcaaa 336

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<400> 378

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Val Gln Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
Page 123

100

105

110

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33

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Gln Ser Leu Val His Ser Asp Gly Lys Thr Tyr
 1 5 10

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Lys Ile Ser
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Met Gln Ala Val Gln Phe Pro Arg Thr
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 ccagggaagg ggctggagtg gattggggaa atcaatcatc gcggaagcac caactacaac 180
 ccgtccctca agagtcgtgt caccatttca gttgacacgt ccaagaacca gttctccctg 240
 aggatgagct ctgtgaccgc cgcggacgcg gctgtgtatt actgtgagag aggagaggat 300
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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ala Phe Ser Asp Tyr
20 25 30

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

Gly Glu Ile Asn His Arg Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Gly Glu Asp Tyr Asp Ile Trp Asn Gly Tyr Tyr Gln Glu Lys Trp
100 105 110

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

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Gly Gly Ala Phe Ser Asp Tyr Tyr
1 5

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21

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Ile Asn His Arg Gly Ser Thr
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Ala Arg Gly Glu Asp Tyr Asp Ile Trp Asn Gly Tyr Tyr Gln Glu Lys
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 ggccaggctc ccaggctcct catctatgat gcatccaaga gggccactgg catcccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
 gaagattttg tagtttatta ctgtcaccag cgtagcaact ggcctctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

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<400> 394

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

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

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

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

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

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

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cagagtatta gcacctac

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Gln Ser Ile Ser Thr Tyr
1 5

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Asp Ala Ser
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<211> 27

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<223> synthetic

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caccagcgta gcaactggcc tctcact

27

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His Gln Arg Ser Asn Trp Pro Leu Thr
1 5

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<212> DNA

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ccaggaaagg ggctggagtg gattggatat atctttttaca gtgggagtac cgactacaac 180

ccctccctca agagtcgagt caccatttca gtagacacgt ccaagaagca gttctccctg 240

aagctgacct ctgtgaccgc tgcggacacg gccgtctatt actgtgcgcg aacaataagt 300

acgtggtggt tcgccccctg gggccaggga accctggtca ccgtctcctc a 351

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

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

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

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

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

Arg Thr Ile Ser Thr Trp Trp Phe Ala Pro Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

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<400> 403

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24

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Gly Gly Ser Phe Ser Ser Tyr Tyr
1 5

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21

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Ile Phe Tyr Ser Gly Ser Thr
1 5

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Ala Arg Thr Ile Ser Thr Trp Trp Phe Ala Pro
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<211> 318

<212> DNA

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccaggc 180
aggttcagtg gcagtgggtc tggaacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagttttattc ctgtcagcag tataataact ggctcacttt cggcggaggg 300
accaaggtgg agatcaaa 318

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<400> 410

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

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

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Gly Arg Phe Ser Gly
Page 133

50

55

60

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

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

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

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18

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<220>
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Gln Ser Val Ser Asn Asn
1 5

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Gly Ala Ser
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24

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Gln Gln Tyr Asn Asn Trp Leu Thr
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ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccata tccagagaca attccaagaa cacacagtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gtcagtagct 300
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1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Gln Tyr
65 70 75 80

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

Ala Ser Val Ala Thr Ser Gly Asp Phe Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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24

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Gly Phe Thr Phe Ser Ser Tyr Gly

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<400> 422

Ile Trp Tyr Asp Gly Ser Asn Lys

1 5

<210> 423

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48

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<400> 424

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ggccaggctc	ccaggctcct	catctatgat	gcatccaaaa	gggccactgg	catcccagcc	180
aggttcagtg	gtagtgggtc	tgggacaggc	ttcactctca	ccatcagcag	cctagagcct	240
gaagattttg	cagtttatta	ctgtcagcag	cgtagtaact	ggcctctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	a				321

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<400> 426

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Glu	Arg	Thr	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Arg	Ile	Ser	Thr	Tyr
			20					25					30		

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

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

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

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

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

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18

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<400> 428

Gln Arg Ile Ser Thr Tyr
1 5

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Asp Ala Ser
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<220>
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27

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Gln Gln Arg Ser Asn Trp Pro Leu Thr
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cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac	180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagacgggat	300
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Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Asn	Tyr
			20					25					30		

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

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

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

Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	

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

Thr	Leu	Val	Thr	Val	Ser	Ser
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Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 439
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<212> DNA
<213> Artificial Sequence

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<223> synthetic

<400> 439

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<223> synthetic

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Ala Arg Arg Asp Thr Ile Phe Pro Ser Tyr Pro Leu

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10

<210> 441

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120

tacctgcaga agccagggca gtctccacaa ctctgatct atttggtttc taatcgggcc

180

tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc

240

agcagagtgg aggctgagga tattgggggt tattactgca tgcaagctct ccaaactccg

300

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336

<210> 442

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<220>

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<400> 442

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30
 Asn Gly Tyr Asn Phe Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Ile Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
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gtccttacaa tgaccaactt ggaccctgtg gacacagcca cttattactg tgtacacagg 300

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

Trp Leu Thr Leu Ile Tyr Trp Asn Glu Asn Lys His Tyr Ser Pro Ser
50 55 60

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

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

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ser Tyr
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Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65 70 75 80

Leu Gln Met Asn Ile Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Gly Thr Gly Gln Gln Val Asp Leu Tyr Asn Tyr Tyr Tyr Ala
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
20 25 30

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

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

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

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

Ala Arg Asp Lys Gly Ile Ser Gly Ile Lys Gly Gly Ser Tyr Tyr Tyr
 100 105 110

Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
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Ser

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Tyr Tyr Ala Met Asp Val
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20 25 30

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

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

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

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

Tyr Cys Ser Thr Val Asp Tyr Asn Trp Tyr Phe Asp Phe Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr
 1 5 10

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

Ala Leu Ile Trp Tyr Asp Gly Thr Asn Glu Asn Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Arg Gly Val Ala Thr Phe Thr Arg Gly Asn Tyr Tyr Tyr
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115 120 125

Ser

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ccaggcaagg ggctggaggg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccata tccagagaca attccaagaa catgctgtat 240
ctacaaatga ccagcctgag agccgaggac acggctgtgt attactgtgc gagagattcg 300
ggtaaaactg gaactgggat aactgggtac tcctactact acggtatgga cgtctggggc 360
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		Ala	Ala
		25	Ser
		Gly	Phe
		Thr	Phe
			30
		Ser	Phe
			Tyr
Gly	Met	His	Trp
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		Gln	Ala
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		Gly	Leu
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		Glu	Gly
			Val
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		Gly	Ser
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			Asp
			Ser
			Val
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		70	Ser
		Arg	Asp
		Asn	Ser
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		Met	Leu
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		85	Ser
		Leu	Arg
		Ala	Glu
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		Asp	Thr
		Ala	Val
			95
		Tyr	Tyr
			Cys
Ala	Arg	Asp	Ser
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		Thr	Gly
		105	Thr
		Gly	Ile
		Thr	Gly
			110
		Tyr	Ser
			Tyr
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Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Arg Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

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

Cys Ala Arg Glu Gly Asp Pro Ser Leu Asp Pro Trp Gly Gln Gly Thr
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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

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

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

Ser Leu Asp Ile Met Ala Thr Val Gly Gly Leu Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgg gagagatcaa 300
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Gly Phe Ile Phe Ser Phe Tyr Gly
1 5

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Ile Trp Tyr Asp Gly Ser Asn Glu
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ggtgtggacg tc

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Asn Tyr Tyr Tyr Gly Val Asp Val
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 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
 caagggacac gactggagat taaa 324

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

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

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

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

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

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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Gln Ser Ile Ser Ser Tyr
1 5

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Ala Ala Ser
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Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacagggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240

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

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

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

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

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

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

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

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21

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Gln Ser Val Ser Ser Ser Tyr
1 5

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ggtgcatcc

9

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Gly Ala Ser
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Gln Gln Tyr Gly Ser Ser Pro Trp Thr
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ccaggggaagg ggctggagtg ggttggggaa atcagtcata gaggaagcac caactacaac 180
ccgtccctca agagtcgagt caccatatca ctggacacgt ccaagaacca gttctccctg 240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgttcgag agacgaggaa 300
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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

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

Gly Glu Ile Ser His Arg Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
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50

55

60

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

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

Arg Asp Glu Glu Leu Glu Phe Arg Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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24

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Gly Gly Ser Phe Ser Gly Tyr Tyr
1 5

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21

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Ile Ser His Arg Gly Ser Thr
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ctctcctgca gggccagtca gagtgttagc agctatttag cctggtacca acaaaaacct

120

ggccaggctc ccaggctcct cgtctatggg gcatccaaca gggccactgg catcccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
 gaagattttg cattttatta ctgtcagcag cgtagcaact ggccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

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

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

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

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

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

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

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cagagtgtta gcagctat

18

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Gln Ser Val Ser Ser Tyr
1 5

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ggtgcatcc

9

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Gly Ala Ser
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cagcagcgta gcaactggcc gctcact

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Gln Gln Arg Ser Asn Trp Pro Leu Thr
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ccagggaagg ggctggaatg ggtctcaact attagtggta gtggtggtgg cacatactac	180
acagactccg ttaagggccg gttcaccatc tccagagaca attccaagaa cacactgtat	240
ctgcaaataa acagcctgag agccgacgac acggccgttt ttactgtac gaaagagagt	300
acaactggaa cttactccta cttctacggt atggacgtct ggggccaagg gaccacggtc	360
accgtctcct ca	372

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<400> 554

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

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

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

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

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

Thr Lys Glu Ser Thr Thr Gly Thr Tyr Ser Tyr Phe Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Gly Phe Thr Phe Ser Leu Tyr Ala
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attagtggta gtggtggtgg caca

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Ile Ser Gly Ser Gly Gly Thr
1 5

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acgaaagaga gtacaactgg aacttactcc tacttctacg gtatggacgt c

51

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Thr Lys Glu Ser Thr Thr Gly Thr Tyr Ser Tyr Phe Tyr Gly Met Asp
1 5 10 15

Val

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccctcagcgg tctccaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

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1 5 10 15

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

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

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

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

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

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

105

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18

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Gln Thr Ile Ser Ser Tyr
 1 5

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 gctgcatcc

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Ala Ala Ser
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caacagagtt acagtacccc gctcact

27

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Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

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<212> PRT
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<400> 569

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

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

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

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
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<400> 570

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 1 5 10 15

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 115 120 125

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

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 195 200 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
 225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 260 265 270

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
 290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 305 310 315 320

Ser Leu Ser Leu Gly Lys
 325

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<400> 571

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

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

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1 5 10 15

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Leu Gly Lys
325

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

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 574
 <211> 450
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> aa 1-478: Human Lag3 (aa 29 through 450 of NP_002277.4) aa
 451-478: myc-myc-hexahistidine tag

 <400> 574

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys
 1 5 10 15

Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
 20 25 30

Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
 35 40 45

Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
 50 55 60

Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
 65 70 75 80

Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
 85 90 95

Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
 100 105 110

Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
 115 120 125

Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
 130 135 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
 145 150 155 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
 165 170 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
180 185 190

Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser
195 200 205

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
210 215 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
225 230 235 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
245 250 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
325 330 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
340 345 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
355 360 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
370 375 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
385 390 395 400

Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
405 410 415

Leu Pro Ala Gly His Leu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
420 425 430

Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu His His His His
435 440 445

His His
450

<210> 575
<211> 655
<212> PRT
<213> Artificial Sequence

<220>
<223> aa 1-683: Human Lag3 (aa 29 through 450 of NP_002277.4) aa
451-683: mIgG2aFc

<400> 575

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys
1 5 10 15

Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
20 25 30

Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
35 40 45

Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
50 55 60

Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
65 70 75 80

Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
85 90 95

Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
100 105 110

Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
115 120 125

Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
130 135 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
145 150 155 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
165 170 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
180 185 190

Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser
195 200 205

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
210 215 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
225 230 235 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
245 250 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
Page 197

325																330																335															
Gly	Lys	Leu	Leu	Cys	Glu	Val	Thr	Pro	Val	Ser	Gly	Gln	Glu	Arg	Phe																																
340																345																350															
Val	Trp	Ser	Ser	Leu	Asp	Thr	Pro	Ser	Gln	Arg	Ser	Phe	Ser	Gly	Pro																																
355																360																365															
Trp	Leu	Glu	Ala	Gln	Glu	Ala	Gln	Leu	Leu	Ser	Gln	Pro	Trp	Gln	Cys																																
370																375																380															
Gln	Leu	Tyr	Gln	Gly	Glu	Arg	Leu	Leu	Gly	Ala	Ala	Val	Tyr	Phe	Thr																																
385																390																395															
Glu	Leu	Ser	Ser	Pro	Gly	Ala	Gln	Arg	Ser	Gly	Arg	Ala	Pro	Gly	Ala																																
405																410																415															
Leu	Pro	Ala	Gly	His	Leu	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys																																
420																425																430															
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val																																
435																440																445															
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser																																
450																455																460															
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp																																
465																470																475															
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln																																
485																490																495															
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser																																
500																505																510															
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys																																
515																520																525															
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile																																
530																535																540															

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
 545 550 555 560

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
 565 570 575

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
 580 585 590

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
 595 600 605

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
 610 615 620

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
 625 630 635 640

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 645 650 655

<210> 576
 <211> 516
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> aa 1-533 (aa 18 through 533 of cynomolgus XP_005570011.1 modified
 to replace amino acid at position 74 with a P based on Rhesus
 macaque XP_001108923.1

<400> 576

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

Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile Pro
 20 25 30

Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln His
 35 40 45

Gln Pro Asp Ser Gly Pro Pro Ala Pro Ala Pro Gly His Pro Pro Val
 50 55 60

Pro Gly His Arg Pro Ala Ala Pro Tyr Ser Trp Gly Pro Arg Pro Arg
65 70 75 80

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

Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln Arg
100 105 110

Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala Gly
115 120 125

Glu Tyr Arg Ala Thr Val His Leu Arg Asp Arg Ala Leu Ser Cys Arg
130 135 140

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

Ser Leu Arg Thr Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser Arg
165 170 175

Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Ser Arg Gly Gln Gly
180 185 190

Arg Val Pro Val Gln Gly Ser Pro His His His Leu Ala Glu Ser Phe
195 200 205

Leu Phe Leu Pro His Val Gly Pro Met Asp Ser Gly Leu Trp Gly Cys
210 215 220

Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn Leu
225 230 235 240

Thr Val Leu Gly Leu Glu Pro Ala Thr Pro Leu Thr Val Tyr Ala Gly
245 250 255

Ala Gly Ser Arg Val Glu Leu Pro Cys Arg Leu Pro Pro Ala Val Gly
260 265 270

Thr Gln Ser Phe Leu Thr Ala Lys Trp Ala Pro Pro Gly Gly Gly Pro
275 280 285

Asp Leu Leu Val Ala Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu Glu
290 295 300

Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Ile Cys His Ile Arg Leu
305 310 315 320

Gln Gly Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr Val
325 330 335

Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu Cys
340 345 350

Glu Val Thr Pro Ala Ser Gly Gln Glu His Phe Val Trp Ser Pro Leu
355 360 365

Asn Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala Gln
370 375 380

Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu His Gln Gly
385 390 395 400

Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser Pro
405 410 415

Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Arg Ala Gly His
420 425 430

Leu Pro Leu Phe Leu Ile Leu Gly Val Leu Phe Leu Leu Leu Val
435 440 445

Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg Gln Trp Arg Pro Arg
450 455 460

Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro Pro Gln Ala Gln Ser
465 470 475 480

Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Leu Glu Pro Glu Pro Glu
485 490 495

Leu Glu Arg Glu Leu Gly Pro Glu Pro Glu Pro Gly Pro Glu Pro Glu
Page 201

500

505

510

Pro Glu Gln Leu
515

<210> 577
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 577

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Gln Tyr
65 70 75 80

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

Ala Ser Val Ala Thr Ser Gly Asp Phe Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225 230 235 240

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

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

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

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

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

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

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

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
Page 203

370

375

380

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

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

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

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

Lys

<210> 578

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 578

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

Glu Arg Thr Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Thr Tyr
 20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 579
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 579

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Gln Tyr
65 70 75 80

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

Ala Ser Val Ala Thr Ser Gly Asp Phe Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225 230 235 240

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

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

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 580
<211> 445
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 580

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

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

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

Gly Glu Ile Ser His Arg Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Asp Glu Glu Leu Glu Phe Arg Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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
Page 209

420

425

430

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

<210> 581

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 581

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 582
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 582

Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
1 5 10 15

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

Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
35 40 45

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

His Gln Pro Asp Ser Gly Pro Pro Ala Ala Pro Gly His Pro Leu
65 70 75 80

Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
85 90 95

Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
100 105 110

Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
115 120 125

Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
130 135 140

Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145 150 155 160

Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
165 170 175

Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
180 185 190

Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
195 200 205

Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
210 215 220

Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225 230 235 240

Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
245 250 255

Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
260 265 270

Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
275 280 285

Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
290 295 300

Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305 310 315 320

Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
325 330 335

Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
340 345 350

Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
355 360 365

Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
370 375 380

Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385 390 395 400

Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
405 410 415

Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
420 425 430

Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
435 440 445

His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser Leu Leu Leu Leu
450 455 460

Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg Gln Trp Arg Pro
465 470 475 480

Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro Pro Gln Ala Gln
485 490 495

Ser Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Pro Glu Pro Glu Pro
500 505 510

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln Leu
515 520 525

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<211> 15
<212> PRT
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 Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
 1 5 10 15

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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 584
 agcagctctg ccctcat 17

<210> 585
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 <212> DNA
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<400> 585
 gctctggctg gtcttcagta tg 22

<210> 586
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 <212> DNA
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<400> 586
 ttgccgtatg gttggtttga ac 22

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<400> 587

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

Asp Gly Phe Asn Val Ser Ile Met Tyr Asn Leu Thr Val Leu Gly Leu
 225 230 235 240

Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala Gly Ala Gly Ser Arg Val
 245 250 255

Gly Leu Pro Cys Arg Leu Pro Ala Gly Val Gly Thr Arg Ser Phe Leu
 260 265 270

Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Asp Leu Leu Val Thr
 275 280 285

Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu Glu Asp Val Ser Gln Ala
 290 295 300

Gln Ala Gly Thr Tyr Thr Cys His Ile His Leu Gln Glu Gln Gln Leu
 305 310 315 320

Asn Ala Thr Val Thr Leu Ala Ile Ile Thr Val Thr Pro Lys Ser Phe
 325 330 335

Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu Cys Glu Val Thr Pro Val
 340 345 350

Ser Gly Gln Glu Arg Phe Val Trp Ser Ser Leu Asp Thr Pro Ser Gln
 355 360 365

Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu
 370 375 380

Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly
 385 390 395 400

Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser
 405 410 415

Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly His Leu Ile Glu Gly Arg
 420 425 430

Met Asp Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 435 440 445

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
450 455 460

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
465 470 475 480

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
485 490 495

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
500 505 510

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
515 520 525

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
530 535 540

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
545 550 555 560

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
565 570 575

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
580 585 590

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
595 600 605

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
610 615 620

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
625 630 635 640

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
645 650 655

Lys Ser Leu Ser Leu Ser Pro Gly Lys

660

665

<210> 588
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 <212> PRT
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<220>
 <223> hLAG3 extracellular domain P18627

<400> 588

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys
 1 5 10 15

Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
 20 25 30

Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
 35 40 45

Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
 50 55 60

Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
 65 70 75 80

Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
 85 90 95

Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
 100 105 110

Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
 115 120 125

Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
 130 135 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
 145 150 155 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
 165 170 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
180 185 190

Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser
195 200 205

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
210 215 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
225 230 235 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
245 250 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
325 330 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
340 345 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
355 360 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
370 375 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
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385		390		395		400
Glu	Leu	Ser	Ser	Pro	Gly	Ala
				405		
					Ser	Gly
				410		
					Arg	Ala
					Pro	Gly
						415
						Ala

Leu	Pro	Ala	Gly	His	Leu
			420		

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<220>
 <223> hLAG3 epitope

<400> 589

Leu	Arg	Arg	Ala	Gly	Val	Thr	Trp	Gln	His	Gln	Pro	Asp	Ser	Gly	Pro
1				5					10					15	

Pro	Ala	Ala	Ala	Pro	Gly	His	Pro	Leu	Ala	Pro	Gly	Pro	His	Pro	Ala
			20					25					30		

Ala	Pro	Ser	Ser	Trp	Gly	Pro	Arg	Pro	Arg	Arg	Tyr
		35					40				