

# SEQUENCE LISTING

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

<120> RADIOLABELED ANTI-PD-L1 ANTIBODIES FOR IMMUNO-PET IMAGING

<130> 10305W001

<140> TBD

<141> 2017-12-01

<160> 344

<170> PatentIn version 3.5

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Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
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Ala Asn Ile Asn Gln Asp Gly Thr Glu Lys Tyr Tyr Val Asp Ser Val  
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
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35 40 45

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

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

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

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 35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
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Thr Phe Gly Gly Gly Thr Lys Val Ala Ile Lys  
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35 40 45

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

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

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

Asp Arg Phe 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 Leu Tyr Phe Cys Met Gln Ala  
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Thr His Phe Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
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Met Glu Leu Thr Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg Asp Glu Asp Trp Asn Tyr Gly Ser Trp Phe Asp Thr Trp Gly  
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Gln Gly Thr Leu Val Thr Val Ser Ser  
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<400> 68

Gly Tyr Thr Phe Thr Gly Tyr Tyr  
1 5

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24

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<400> 70

Leu Asn Pro Asn Thr Gly Thr Thr

1 5

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<211> 42

<212> DNA

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<400> 71

gcgagagatg aggactggaa ttatgggagc tggttcgaca cc

42

<210> 72

<211> 14

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<400> 72

Ala Arg Asp Glu Asp Trp Asn Tyr Gly Ser Trp Phe Asp Thr

1 5 10

<210> 73

<211> 336

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 73

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cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgattc 180

tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac gctgaaaatc 240

agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acattttccg 300

atcaccttcg gccaaaggac acgactggag attaga

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<400> 74

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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Pro Ser Leu Val His Ser  
20 25 30

Asp Gly Asn 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 Phe 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

Thr His Phe Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Arg  
100 105 110

<210> 75  
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<400> 75

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33

<210> 76  
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<212> PRT  
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<400> 76

Pro Ser Leu Val His Ser Asp Gly Asn Thr Tyr  
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<400> 77  
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9

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<400> 78

Lys Ile Ser  
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<400> 80

Met Gln Ala Thr His Phe Pro Ile Thr  
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ccagggaggg gcctggaatg ggtctctggt attcattggc atggtaaacg cacaggttat 180  
gcagactctg tgaagggccg attcaccata tccagagaca acgccaagaa atccctgtat 240  
ctgcaaatga acagtctgaa aggcgaggac acggccttgt atcattgtgt gaggggggga 300  
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<400> 82

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

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

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

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

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

Leu Gln Met Asn Ser Leu Lys Gly Glu Asp Thr Ala Leu Tyr His Cys  
85 90 95

Val Arg Gly Gly Met Ser Thr Gly Asp Trp Phe Asp Pro Trp Gly Gln  
100 105 110

Gly Thr Leu Val Ile Val Ser Ser  
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<400> 83  
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<400> 84

Gly Phe Thr Phe Asp Asp Tyr Gly  
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<210> 85  
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<400> 86

Ile His Trp His Gly Lys Arg Thr  
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<210> 87  
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<400> 87

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39

<210> 88  
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<400> 88

Val Arg Gly Gly Met Ser Thr Gly Asp Trp Phe Asp Pro  
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<400> 89

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atcacttgcc gggcaagtca gaggcattaac agttatttaa attggtatca gcagaaacca

120

gggaaagccc ctaaactcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca

180

aggttcagtg gcagtggatc tgggacagaa ttcactctca ccatcagcaa tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300  
caagggacac gactggagat taaa 324

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<400> 90

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn 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 Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asn 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> 91  
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<400> 91

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<210> 92  
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<400> 92

Gln Ser Ile Asn Ser Tyr  
1 5

<210> 93  
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<400> 93  
gttgcattcc

9

<210> 94  
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<400> 94

Val Ala Ser  
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<400> 96

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

<210> 97  
<211> 360  
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<400> 97

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ccagggaagg ggctggagtg ggtctctggt attcattgga gtggtagaag cacaggttat 180  
gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240  
ctgcaaatga acagtctgag agccgaggac acggccttgt attactgtgc gagggggggga 300  
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<400> 98

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

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

Gly Met Thr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 99  
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<400> 99  
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24

<210> 100  
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Gly Phe Thr Phe Asp Asp Tyr Gly  
 1 5

<210> 101  
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24

<210> 102  
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<400> 102

Ile His Trp Ser Gly Arg Ser Thr  
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<210> 103  
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39

<210> 104  
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<400> 104

Ala Arg Gly Gly Met Ser Thr Gly Asp Trp Phe Asp Pro  
1 5 10

<210> 105  
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<400> 105

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

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<400> 106

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 Val 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> 107  
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<210> 108  
<211> 6  
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<400> 108

Gln Ser Ile Ser Ser Tyr  
1 5

<210> 109  
<211> 9  
<212> DNA  
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<400> 109  
gttgcattcc

9

<210> 110  
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<400> 110

Val Ala Ser  
1

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caacagagtt acagtacccc tccgatcacc 30

<210> 112  
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Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr  
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<400> 113  
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ccagggaagg gactggagtg ggtctcagtt atttatagtg gtggtagtag atactacgca 180  
gattccgtga agggccgatt caccatctcc agactcactt ccaagaacac actgtatctt 240  
caaatgagca gcctgagacc tgaggacacg gccgtgtatt attgtgtagg agggattagg 300  
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1 5 10 15

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

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

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

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

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

Arg Gly Ile Arg Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
100 105 110

Val Ser Ser  
115

<210> 115  
<211> 24  
<212> DNA  
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<400> 115  
gggttcaccg tcggtagtaa ctac

24

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<400> 116

Gly Phe Thr Val Gly Ser Asn Tyr  
1 5

<210> 117

<211> 21  
<212> DNA  
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<400> 117  
atttatagtg gtggtagtac a

21

<210> 118  
<211> 7  
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<400> 118

Ile Tyr Ser Gly Gly Ser Thr  
1 5

<210> 119  
<211> 27  
<212> DNA  
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<400> 119  
gcgagaggga ttaggggtct ggacgtc

27

<210> 120  
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<400> 120

Ala Arg Gly Ile Arg Gly Leu Asp Val  
1 5

<210> 121  
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<212> DNA  
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<220>

<223> synthetic

<400> 121

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gggagagccc ctaggctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaccag agttacagta cccctccgat caccttcggc      300
caagggacac gactggagat taaa                                             324
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<220>

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1           5           10           15
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asn Ile Tyr
          20           25           30
```

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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Arg Leu Leu Ile
          35           40           45
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Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
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Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Ser Tyr Ser Thr Pro Pro
          85           90           95
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Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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<210> 124  
<211> 6  
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<400> 124

Gln Thr Ile Asn Ile Tyr  
1 5

<210> 125  
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<212> DNA  
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<400> 125  
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<210> 126  
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<220>  
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<400> 126

Ala Ala Ser  
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<210> 127  
<211> 30

<212> DNA  
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30

<210> 128  
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<220>  
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<400> 128

His Gln Ser Tyr Ser Thr Pro Pro Ile Thr  
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<212> DNA  
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<400> 129  
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ccagggaagg gactggagtg ggtctcagtt atttctagcg gtggtaatac acactacgca 180  
gactccgtga agggccgatt cattatgtcc agacaaactt ccaaaaacac gctgtatctt 240  
cagatgaata gcctggaaac tgaggacacg gccgtatatt attgtgagag ggggatcaga 300  
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<220>  
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<400> 130

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 1 5 10 15

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

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

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

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

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

Arg Gly Ile Arg Gly Leu Asp Val Trp Gly Gln Gly Thr Met Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 131  
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<400> 131  
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24

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<400> 132

Gly Ile Thr Val Gly Thr Asn Tyr  
1 5

<210> 133  
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21

<210> 134  
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<400> 134

Ile Ser Ser Gly Gly Asn Thr  
1 5

<210> 135  
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<400> 135  
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27

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<400> 136

Ala Arg Gly Ile Arg Gly Leu Asp Val  
1 5

<210> 137  
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 gggagagccc ctaagctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttcacttca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300  
 caagggacac gactggagat taaa 324

<210> 138  
 <211> 108  
 <212> PRT  
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<220>  
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<400> 138

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 Met Ser Ser Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Lys 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 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> 139  
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<220>  
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<400> 139  
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18

<210> 140  
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<212> PRT  
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<220>  
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<400> 140

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

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

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

Met Glu Leu Ser Ser Leu Lys Ser Gly Asp Thr Ala Val Tyr Phe Cys  
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Met Val Thr Val Ser Ser  
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Gly Gly Ile Phe Ser Ser Ser Thr  
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cctggccagg ctcccagact cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcaa caggctggag 240  
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Asn Phe Asn  
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 Asn Arg Leu Glu  
Page 50

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |
| Pro | Glu | Asp | Phe | Gly | Val | Phe |
|     |     |     |     | 85  |     |     |
|     |     |     |     |     | Tyr | Cys |
|     |     |     |     |     | 90  |     |
|     |     |     |     |     |     | Gln |
|     |     |     |     |     |     | Gln |
|     |     |     |     |     |     | Tyr |
|     |     |     |     |     |     | Glu |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Ala |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | 95  |

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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Gly Ala Ser

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Gln Gln Tyr Glu Ser Ala Pro Trp Thr

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5

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ccagggaagg gcctggagtg ggtctcaggt attagttgga gtaataataa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgcaaaaaa ctccctgtat 240

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Asp Glu Tyr  
 20 25 30

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

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

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

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

Ala Lys Ser Gly Ile Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Thr  
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Val Ser Ser  
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Gly Phe Pro Phe Asp Glu Tyr Ala  
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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 Leu Leu Ile Tyr Ala Ala  
35 40 45

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

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

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Cys Thr Pro Pro Ile Thr Phe  
85 90 95

Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

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

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

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

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

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

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

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30

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

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

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

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

Cys Ala Arg Ser Thr Ser Leu Thr Phe Tyr Tyr Phe Asp Tyr Trp Gly  
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Gln Gly Thr Leu Val Thr Val Ser Ser  
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Ala Arg Ser Thr Ser Leu Thr Phe Tyr Tyr Phe Asp Tyr  
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300  
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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  
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gactccgtga agggccgatt caccatctcc agacacactt ccaagaacac gctgtatctt 240

caaatgaaca gcctgacagc agaggacacg gccgtatatt actgtgcgcg aggattgggg 300

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

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

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

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

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

Arg Gly Leu Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
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Val Ser Ser  
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Ile Tyr Ser Gly Gly Asn Thr  
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 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Ser Asn Tyr  
 20 25 30

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

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

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

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

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

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<400> 211  
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18

<210> 212  
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<220>  
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<400> 212

Gln Val Ile Ser Asn Tyr  
1 5

<210> 213  
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<400> 213  
gctgcatcc

9

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<400> 214

Ala Ala Ser  
1

<210> 215  
 <211> 27  
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<400> 215  
 caaaagtata acagtgtccc tcggacg

27

<210> 216  
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<220>  
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<400> 216

Gln Lys Tyr Asn Ser Ala Pro Arg Thr  
 1 5

<210> 217  
 <211> 360  
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<400> 217  
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 tactgtgcag cctctggatt cacctttagt aaatattgga tgaactgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtggccaac ataaaggag atggaagtga gaaatactat 180  
 gtggactctg tgaagggccg gttcaccatc tccagagaca acgccaagaa ctcactatat 240  
 ctacaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagagattat 300  
 tggggatcag gctactactt tgacttctgg ggccaggga ccctgggtcac cgtctcctca 360

<210> 218  
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 <213> Artificial Sequence

<220>

<223> synthetic

<400> 218

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 219

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

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<400> 219

ggattcacct ttagtaaata ttgg

24

<210> 220

<211> 8

<212> PRT

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<220>

<223> synthetic

<400> 220

Gly Phe Thr Phe Ser Lys Tyr Trp  
1 5

<210> 221

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 221

ataaaggagg atggaagtga gaaa

24

<210> 222

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 222

Ile Lys Gly Asp Gly Ser Glu Lys  
1 5

<210> 223

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 223

gcgagagatt attggggatc aggctactac tttgacttc

39

<210> 224

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 224

Ala Arg Asp Tyr Trp Gly Ser Gly Tyr Tyr Phe Asp Phe  
 1 5 10

<210> 225  
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<220>  
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<400> 225  
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 atcacttgcc gggcaagtca gaacattaac aactatttaa attggtatca gcagaaacca 120  
 gggaaagccc ctaaactcct gatctatgct gcatccagtt tccaaaatgc ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacaata ccccgctcac tttcggcggg 300  
 gggaccaagg tggagatcaa a 321

<210> 226  
 <211> 107  
 <212> PRT  
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<220>  
 <223> synthetic

<400> 226

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 Asn Ile Asn 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 Ala Ala Ser Ser Phe Gln Asn Ala 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 Asn Thr Pro Leu  
85 90 95

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

<210> 227  
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<400> 227  
cagaacatta acaactat

18

<210> 228  
<211> 6  
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<220>  
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<400> 228

Gln Asn Ile Asn Asn Tyr  
1 5

<210> 229  
<211> 9  
<212> DNA  
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<400> 229  
gctgcatcc

9

<210> 230  
<211> 3  
<212> PRT  
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<220>  
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<400> 230

Ala Ala Ser  
1

<210> 231

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 231

caacagagtt acaatacccc gtcact

27

<210> 232

<211> 9

<212> PRT

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<220>

<223> synthetic

<400> 232

Gln Gln Ser Tyr Asn Thr Pro Leu Thr  
1 5

<210> 233

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 233

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagt ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240

ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatgat 300

attgtagtag taccagctcc tatgggatat tactactact acttcggtat ggacgtctgg 360

ggccaaggga ccacgggtcac cgtctcctca 390

<210> 234  
<211> 130  
<212> PRT  
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<220>  
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<400> 234

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

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

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

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

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

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

Ala Arg Asp Asp Ile Val Val Val Pro Ala Pro Met Gly Tyr Tyr Tyr  
100 105 110

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

Ser Ser  
130

<210> 235  
<211> 24  
<212> DNA  
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<220>  
<223> synthetic

<400> 235  
ggattcacct ttagtagcta ttgg 24

<210> 236  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 236  
Gly Phe Thr Phe Ser Ser Tyr Trp  
1 5

<210> 237  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 237  
ataaagcaag atggaagtga gaaa 24

<210> 238  
<211> 8  
<212> PRT  
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<220>  
<223> synthetic

<400> 238  
Ile Lys Gln Asp Gly Ser Glu Lys  
1 5

<210> 239  
<211> 69  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 239  
gcgagagatg atattgtagt agtaccagct cctatgggat attactacta ctacttcggt 60

atggacgtc

69

<210> 240  
<211> 23  
<212> PRT  
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<220>  
<223> synthetic

<400> 240

Ala Arg Asp Asp Ile Val Val Val Pro Ala Pro Met Gly Tyr Tyr Tyr  
1 5 10 15

Tyr Tyr Phe Gly Met Asp Val  
20

<210> 241  
<211> 321  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 241  
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atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120  
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240  
gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag 300  
gggaccaagc tggagatcaa a 321

<210> 242  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 242

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

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

<210> 243  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 243  
 cagggcatta gaaatgat

18

<210> 244  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 244

Gln Gly Ile Arg Asn Asp  
 1                      5

<210> 245  
 <211> 9

<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 245  
gctgcatcc

9

<210> 246  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 246

Ala Ala Ser  
1

<210> 247  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 247  
ctacagcata atagttaccc gtacact

27

<210> 248  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 248

Leu Gln His Asn Ser Tyr Pro Tyr Thr  
1 5

<210> 249  
<211> 369  
<212> DNA  
<213> Artificial Sequence

<220>

<223> synthetic

<400> 249

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gaagtgcagc tgggtggagtc tgggggaggc ttggttcagc ctggcaggtc cctgagactc      60
tcctgtgcag cctctggatt cacctttgat gattttgcc a tgcaactgggt ccgacaagct      120
ccagggaagg gcctggagtg ggtctcaggt attagttgga ctggtggtaa catggactat      180
gcgaactctg tgaagggccg attcaccatc tccagagagg acgccaagaa ttccctgtat      240
ctgcaaatga acagtctgag agctgcggac acggccttgt attactgtgt aaaagatata      300
agggggatag tggctacggg gggggctttt gatattctggg gccgagggac aatggtcacc      360
gtctcttca                                                                    369
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<210> 250

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 250

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1              5              10              15
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Phe
                20              25              30
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```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35              40              45
```

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Ser Gly Ile Ser Trp Thr Gly Gly Asn Met Asp Tyr Ala Asn Ser Val
50              55              60
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```
Lys Gly Arg Phe Thr Ile Ser Arg Glu Asp Ala Lys Asn Ser Leu Tyr
65              70              75              80
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Leu Gln Met Asn Ser Leu Arg Ala Ala Asp Thr Ala Leu Tyr Tyr Cys
85              90              95
```

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Val Lys Asp Ile Arg Gly Ile Val Ala Thr Gly Gly Ala Phe Asp Ile
100             105             110
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Trp Gly Arg Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 251  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 251  
ggattcacct ttgatgattt tgcc

24

<210> 252  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 252

Gly Phe Thr Phe Asp Asp Phe Ala  
1 5

<210> 253  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 253  
attagttgga ctggtggtaa catg

24

<210> 254  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 254

Ile Ser Trp Thr Gly Gly Asn Met

1

5

<210> 255  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 255  
 gtaaaagata taagggggat agtggctacg gggggggcctt ttgatatc 48

<210> 256  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 256

Val Lys Asp Ile Arg Gly Ile Val Ala Thr Gly Gly Ala Phe Asp Ile  
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<210> 257  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 257  
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 atctcttgcc gggcaagtca gaccattagc acttatttaa attggtttca gcagaaacca 120  
 gggaaagccc ctaagctcct gatctatgtt gtgtccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttatta ctgtcaacag agttacagta cccattcac tttcggccct 300  
 gggaccaaag tggatatcaa a 321

<210> 258  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 258

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

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

Tyr Val Val 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 Phe  
85 90 95

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

<210> 259

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 259

cagaccatta gcacttat

18

<210> 260

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 260

Gln Thr Ile Ser Thr Tyr  
1 5

<210> 261  
<211> 9  
<212> DNA  
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<220>  
<223> synthetic

<400> 261  
gttgtgtcc

9

<210> 262  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 262

Val Val Ser  
1

<210> 263  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 263  
caacagagtt acagtacccc attcact

27

<210> 264  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 264

Gln Gln Ser Tyr Ser Thr Pro Phe Thr  
1 5

<210> 265  
<211> 345  
<212> DNA  
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<400> 265  
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tcctgtgcag cctctggatt caccgtcggg accaactaca tgaactgggt ccgccaggct 120  
ccagggaagg gactggagtg gatctcagtt atttatagcg gtggtagcac attctacgca 180  
gactccgtga agggccgatt caccatctcc agacagactt cccagaacac gctgtatctt 240  
caaatgaaca gcctgagacc tgaggacacg gccgtatatt actgtgagag aggtatacgt 300  
ggttttgata tctggggcca agggacaatg gtcaccgtct cttca 345

<210> 266  
<211> 115  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 266

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 Val Gly Thr Asn  
20 25 30

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

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

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

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85

90

95

Arg Gly Ile Arg Gly Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 267  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 267  
 ggattcaccg tcggtaccaa ctac

24

<210> 268  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 268

Gly Phe Thr Val Gly Thr Asn Tyr  
 1 5

<210> 269  
 <211> 21  
 <212> DNA  
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<400> 269  
 atttatagcg gtggtagcac a

21

<210> 270  
 <211> 7  
 <212> PRT  
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<220>

<223> synthetic

<400> 270

Ile Tyr Ser Gly Gly Ser Thr  
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<210> 271

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 271

gcgagaggta tacgtgggtt tgatatc

27

<210> 272

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 272

Ala Arg Gly Ile Arg Gly Phe Asp Ile  
1 5

<210> 273

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 273

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

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> 274  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 274

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> 275  
<211> 18  
<212> DNA  
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<220>  
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<400> 275  
cagagcatta gcagctat

18

<210> 276  
<211> 6  
<212> PRT  
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<220>

<223> synthetic

<400> 276

Gln Ser Ile Ser Ser Tyr  
1 5

<210> 277

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 277

gctgcatcc

9

<210> 278

<211> 3

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 278

Ala Ala Ser  
1

<210> 279

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 279

caacagagtt acagtacccc tccgatcacc

30

<210> 280

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 280

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

<210> 281

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 281

gaggtgcagc tgggtggagtc tggaggaggc ttggtccagc cggggggggtc cctgagactc 60  
tcctgtgcag cctctggggtt taccatcagt accaactaca tgaactgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtcgcagtt atttatagca gtggttccac atactatatac 180  
gactccgtga agggccgatt caccatctcc agactcactt ccaagaacac ggtgtatctt 240  
caaatgagca gcctgaattc tgaagacacg gccgtgtatt actgtgcgag ggggatcagg 300  
ggttttgata tttggggcca agggacaatg gtcaccgtct cttca 345

<210> 282

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 282

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 Ile Ser Thr Asn  
20 25 30

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

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

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

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

Arg Gly Ile Arg Gly Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr  
100 105 110

Val Ser Ser  
115

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<400> 284

Gly Phe Thr Ile Ser Thr Asn Tyr  
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<400> 286

Ile Tyr Ser Ser Gly Ser Thr  
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<210> 287  
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27

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<400> 288

Ala Arg Gly Ile Arg Gly Phe Asp Ile  
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ccagggaagg gcctggagtg ggtctcaggt attagttgga aaagtggtag cataggttat 180  
gcggactctg tgaggggccg attcaccatc tccagagaca acgccaagaa ttccctctat 240

ctgcaaatga acagtctgag agttgaggac acggccttgt attactgtgt aaaagatata 300  
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 actgtctcct ca 372

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<400> 290

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

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

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

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

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

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

Val Lys Asp Ile Arg Gly Asn Trp Asn Tyr Gly Gly Asn Trp Phe Asp  
 100 105 110

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

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Gly Phe Thr Ile Asp Asp Ser Ala  
 1 5

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24

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<400> 294

Ile Ser Trp Lys Ser Gly Ser Ile  
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Val Lys Asp Ile Arg Gly Asn Trp Asn Tyr Gly Gly Asn Trp Phe Asp  
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ccagggaagg gtctggagtg ggtctcagtt attttcagta gtggtaggac attctacgga 180  
gactacgtga aggggcgatt aaccatcttc agacaaacct ccgagaacac ggtgtatctt 240  
caaatgaata gcctgagaag tgaggacacg gccatatatt actgtgagag agggattggc 300  
ggtttggaca tctggggccg agggacaatg gtcaccgtct cttca 345

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<400> 298  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly



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<400> 301  
attttcagta gtggtaggac a

21

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<400> 302

Ile Phe Ser Ser Gly Arg Thr  
1 5

<210> 303  
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<400> 303  
gcgagaggga ttggcggttt ggacatc

27

<210> 304  
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<400> 304

Ala Arg Gly Ile Gly Gly Leu Asp Ile  
1 5

<210> 305

<211> 369  
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<400> 305  
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ccagggaagg gcctggagtg ggtctcaggt attagttgga ctggtggtac tatagactat 180  
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240  
ctgcaaatga gcagtctgag aactgaggac acggccatat attactgtac aagagatatc 300  
cgggggaact ggaagtacgg aggctggttc gaccctggg gccagggaac cctggtcacc 360  
gtctcctca 369

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<400> 306

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

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

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

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

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

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

Thr Arg Asp Ile Arg Gly Asn Trp Lys Tyr Gly Gly Trp Phe Asp Pro  
100 105 110

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

<210> 307  
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<400> 307  
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24

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<211> 8  
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Gly Phe Thr Phe Asp Asp Tyr Ala  
1 5

<210> 309  
<211> 24  
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<400> 309  
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24

<210> 310  
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Ile Ser Trp Thr Gly Gly Thr Ile  
1 5

<210> 311

<211> 48

<212> DNA

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acaagagata tccgggggaa ctggaagtac ggaggctggt tcgacccc

48

<210> 312

<211> 16

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Thr Arg Asp Ile Arg Gly Asn Trp Lys Tyr Gly Gly Trp Phe Asp Pro  
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<400> 313

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cctgggtcaag gacttgactg gatgggatgg atcagcccta acagtggttt cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa cacattttat 240

atggagctga gtggactgag atctgacgac acggccgtat attactgtgc gcgagagggt 300

tctactcacc acaattcttt cgacccttgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 314  
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<220>  
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<400> 314

Gln Val Gln Leu Val Gln Ser Gly Thr 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 Ala Tyr  
 20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 315  
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<400> 315

ggatacacct tcaccgccta ctat

24

<210> 316

<211> 8  
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<220>  
<223> synthetic

<400> 316

Gly Tyr Thr Phe Thr Ala Tyr Tyr  
1 5

<210> 317  
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<212> DNA  
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<400> 317  
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<210> 318  
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<400> 318

Ile Ser Pro Asn Ser Gly Phe Thr  
1 5

<210> 319  
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39

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<400> 320

Ala Arg Glu Gly Ser Thr His His Asn Ser Phe Asp Pro  
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<211> 342

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ccagggaagg ggctggagtg ggtctcagcg atttatagcg gtggtaccgc taactacgca 180  
gactccgtga agggccgatt caccatttcc agagacactt ccaggaacac gctgtatctt 240  
caaatgaaca gcctgagaac tgaggacacg gccgtttatt attgtgagag aggggggggt 300  
atggacgtct ggggcccaagg gaccacggtc accgtctcct ca 342

<210> 322

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 322

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 Val Gly Thr Asn  
20 25 30

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

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

55

60

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

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

Arg Gly Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
100 105 110

Ser Ser

<210> 323  
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<400> 323  
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<220>  
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<400> 324

Gly Phe Thr Val Gly Thr Asn Phe  
1 5

<210> 325  
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<212> DNA  
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<220>  
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<400> 325  
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21

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<400> 326

Ile Tyr Ser Gly Gly Thr Ala  
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<210> 327  
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<400> 328

Ala Arg Gly Gly Gly Met Asp Val  
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<210> 329  
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<212> DNA  
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tcctgcaagg cttctggagg caccttcaac acctatgttc tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagag atcatcccta tcttaggtgc agcaaactac 180  
gcacagaact tccagggcag agtcactttt accacggacg aatccacgaa tacagcctac 240  
atggacctga gcagcctaag atctgaggac acggccgtgt attactgtgc gagagatcgg 300  
acctccgggg ggttcgaccc ctggggccag ggaaccctgg tcactgtctc ctca 354

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<400> 330

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asn Thr Tyr  
20 25 30

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

Gly Glu Ile Ile Pro Ile Leu Gly Ala Ala Asn Tyr Ala Gln Asn Phe  
50 55 60

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

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

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

Leu Val Thr Val Ser Ser  
115

<210> 331  
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ggaggcacct tcaacaccta tggt

24

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<400> 332

Gly Gly Thr Phe Asn Thr Tyr Val

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5

<210> 333

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<210> 334

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<400> 334

Ile Ile Pro Ile Leu Gly Ala Ala

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<210> 335

<211> 33

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<210> 336  
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<400> 336  
Ala Arg Asp Arg Thr Ser Gly Gly Phe Asp Pro  
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<210> 337  
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<212> DNA  
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cctggacaag gacttgagtg ggtgggctgg atcagccctt acaatgggta cacagactat 180  
gcacagaaac tccagggcag agtcaccttg accacagaca catccacgac cacagcctac 240  
atggagctga ggaacctgag atctgacgac acggccatgt attactgttc gagagggagg 300  
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr His Tyr  
20 25 30

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

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

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

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

Ser Arg Gly Arg Gly Pro Tyr Trp Ser Phe Asp Leu Trp Gly Arg Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
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<400> 339  
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24

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<400> 340

Gly Tyr Ile Phe Thr His Tyr Gly  
1 5

<210> 341

<211> 24  
<212> DNA  
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<220>  
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<400> 341  
atcagccctt acaatggtta caca

24

<210> 342  
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<212> PRT  
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<400> 342

Ile Ser Pro Tyr Asn Gly Tyr Thr  
1 5

<210> 343  
<211> 36  
<212> DNA  
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<400> 343  
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36

<210> 344  
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<220>  
<223> synthetic

<400> 344

Ser Arg Gly Arg Gly Pro Tyr Trp Ser Phe Asp Leu  
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