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<110> ANAPTYSBIO, INC.

<120> ANTIBODIES DIRECTED AGAINST PROGRAMMED DEATH-1 (PD-1)

<130> 716746

<150> US 61/818,755
<151> 2013-05-02

<160> 64

<170> PatentIn version 3.5

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

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

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

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

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

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

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

Ser Val Ile Ser Ser Gly Gly Asp Tyr Ala Tyr Tyr Pro Asp Ser Val
    50                  55                  60
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Gln 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 His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
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1 5 10 15

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

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

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

Gln 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

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

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

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

Gln 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala
        115                 120
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

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

Gln 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
115 120

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

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

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

Gln 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
115 120

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

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

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

Gln 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 Glu Tyr Tyr Gly Ser Ser His Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala
        115                 120
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<400> 11

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

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

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

Gln 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 Glu His Tyr Gly Ser Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
115 120

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Gly Phe Thr Phe Ser Ser Tyr Thr Met Ser
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<400> 13

Val Ile Ser Ser Gly Gly Asn Ser Thr Tyr
1 5 10

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Glu His Tyr Gly Ser Ser His Phe Ala Tyr
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Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala Ala
115 120

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

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

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

35 40 45

Ser Val Ile Ser Ser Gly Gly Asn Ser Thr Tyr Tyr Pro 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 Glu His Tyr Gly Ser Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
115 120

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

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

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

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

Gln 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala

115 120

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<400> 18

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

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

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

Ser Val Ile Ser Ser Gly Gly Asn Tyr Ala Tyr Tyr Pro 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 Glu His Tyr Gly Thr Ser His Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
115 120

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Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

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Thr Ile Ser Gly Gly Gly Ser Tyr Thr Tyr
1 5 10

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

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

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

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

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

Ala Ser Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser Ala
        115

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<400>  23

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

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

Ser Thr Ile Ser Gly Gly Gly Ser Tyr Thr Tyr Tyr Gln 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 Ser Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
            100                 105                 110

Thr Val Ser Ser Ala
        115

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

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

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

Lys Gly Arg Phe Ile 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 Ser Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Ala
115

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

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

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

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

100 105 110

Thr Val Ser Ser Ala
115

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Arg Ala Ser Glu Ser Val Asp Asn Phe Gly Ile Ser Phe Met Ser
1 5 10 15

<210> 27
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<400> 27

Ala Ala Ser Asn Pro Gly Ser
1 5

<210> 28
<211> 112
<212> PRT
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<400> 28

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

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

Gly Ile Ser Phe Met Ser Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Ser Leu Asn Ile His

65 70 75 80

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

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

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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 Glu Ser Val Asp Asn Phe
20 25 30

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

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

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

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

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

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Ala Ala Ser Asn Gln Gly Ser
1 5

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

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

Gly Ile Ser Phe Met Ser Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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<400> 33

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

Gly Ile Ser Phe Met Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

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

Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110
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<400> 34

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

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

Gly Ile Thr Phe Met Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Lys
                85                  90                  95
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Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu

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Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala
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<400> 36

Trp Ala Ser Thr Arg His Thr
1 5

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<400> 37

Gln His Tyr Ser Ser Tyr Pro Trp Thr
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<400> 38

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
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Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

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

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

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

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

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

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<400> 39

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ser Ser Tyr Pro Trp

85 90 95

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

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<400> 40

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

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

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

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

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

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

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

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<400> 41

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

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

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

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

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

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

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

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tcgccagact 120

ccggggaaga ggctggagtg ggtcgcagtc attagtagtg gtggtgatta
cgcctactat 180

ccagacagtg tgcagggccg attcaccatc tccagagaca atgccaagaa
caccctgtac 240

ctgcaaatga acagtctgaa gtctgaggac acagccatgt attactgttc
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ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtgattc cgcctactat 180

ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagcac 300

tacggtacta gtcactttgc ttactggggc caaggaaccc tggtcaccgt ctcctcagca 360

tc 362

<210> 45
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 45
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agttatacca tgtcttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtaattc cgcctactat 180

ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagcac 300

tacggtacta gtcactttgc ttactggggc caaggaaccc tggtcaccgt ctcctcagca 360

tc 362

<210> 46
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 46
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tcctgtgcag cctctggatt cactttcagt agttatacca tgtcttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtaatta cgcctactat 180

ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagcac 300

tacggtacta gtcactttgc ttactggggc caaggaaccc tggtcaccgt ctcctcagca 360

tc 362

<210> 47
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 47
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agttatacca tgtcttgggt ccgccaggct 120

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ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagcac 300

tacggtacta gtcactttgc ttactggggc caaggaaccc tggtcaccgt ctcctcagca 360

tc 362

<210> 48
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 48
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ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtaattc cgcctactat 180

ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagtac 300

tacggttcta gtcactttgc ttactggggc caaggaaccc tggtcaccgt ctcctcagca 360

tc 362

<210> 49
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 49
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cctgaaagtc 60

tcctgtgcag cctctggatt cactttcagt agctatacca tgtcttgggt
tcgccagact 120

ccggagaaga ggctggagtg ggtcgcagtc attagtagtg gtggtaattc
cacctactat 180

ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa
caccctgtac 240

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtac
aagagagcac 300

tacggtagta gtcactttgc ttactggggc caagggactc tggtcactgt
ctctgcagcc 360

<210> 50
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 50
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agctatacca tgtcttgggt
ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtaattc
cacctactat 180

ccagacagtg tgaagggccg gttcaccatc tccagagaca attccaagaa
cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc
gaaagagcac 300

tacggtagta gtcactttgc ttactggggc caaggaaccc tggtcaccgt
ctcctcagca 360

<210> 51
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 51
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agctataccc tgtcttgggt
ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc attagtagtg gtggtaatta

cgcctactat 180

ccagacagtg tgcagggccg gttcaccatc tccagagaca attccaagaa
cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc
gaaagagcac 300

tacggtacta gtcactttgc ttactggggc caaggaaccc tggtcaccgt
ctcctcagca 360

<210> 52
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 52
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cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt agctatgaca tgtcttgggt
tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtggtg gtggtagtta
cacctactat 180

caagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa
caccctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt attactgtgc
ctccccttac 300

tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc a
351

<210> 53
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 53
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agctatgaca tgtcttgggt
ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaacc attagtggtg gtggtagtta
cacctactat 180

caagacagtg tgaaggggcg gttcaccatc tccagagaca attccaagaa
cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc

gtcccttac 300

tatgctatgg actactgggg gcaagggacc acggtcaccg tctcctcagc a
351

<210> 54
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 54
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agctatgaca tgtcttgggt
ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaacc attagtggtg gtggtagtta
cacctactat 180

caagacagtg tgaaggggcg gttcatcatc tccagagaca attccaagaa
cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc
gtcccttac 300

tatgctatgg actactgggg gcaagggacc acggtcaccg tctcctcagc a
351

<210> 55
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 55
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cctgagactc 60

tcctgtgcag cctctggatt cactttcagt agctatgaca tgtcttgggt
ccgccgggct 120

ccagggaagg ggctggagtg ggtctcaacc attagtggtg gtggtagtta
cacctactat 180

caagacagtg tgaaggggcg gttcaccatc tccagagaca attccaagaa
cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc
gtcccttac 300

tatgctatgg actactgggg gcaagggacc acggtcaccg tctcctcagc a
351

<210> 56
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 56
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gagggccacc 60

atctcctgca gagccagcga aagtgttgat aattttggca ttagttttat
gagctggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa
cccaggatcc 180

ggggtccctg ccaggtttag tggcagtgta tctgggacag acttcagcct
caacatccat 240

cctatggagg aggatgatgc tgcaatgtat ttctgtcagc aaagtaagga
ggttccgtac 300

acgttcggag gggggaccaa gctggaaata aaacgg
336

<210> 57
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 57
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aagagccacc 60

ctctcctgca gagccagcga aagtgttgat aattttggca ttagttttat
gagctggtac 120

caacagaaac ctggccaggc tcccaggctc ctcatctatg ctgcatccaa
cccaggatcc 180

ggcatcccag ccaggttcag tggcagtggg tctgggacag acttcactct
caccatcagc 240

agcctagagc ctgaagattt tgcagtttat tactgtcagc aaagtaagga
ggttccgtac 300

acgtttggcc aggggaccaa gctggagatc aaacgg
336

<210> 58
<211> 336
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 58
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gagggccacc 60

atctcctgca gagccagcga aagtgttgat aaatatggca ttagttttat
gagctggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa
ccaaggatcc 180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct
caacatccat 240

cctatggagg aggatgatac tgcaatgtat ttctgtcagc aaagtaagga
ggttccgtac 300

acgttcggag gggggaccaa gctggaaata aaacgg
336

<210> 59
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 59
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gagggccacc 60

atcaactgca gagccagcga aagtgttgat aaatatggca ttagttttat
gagctggtac 120

cagcagaaac caggacagcc tcctaagctg ctcatttacg ctgcatccaa
ccaaggatcc 180

ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct
caccatcagc 240

agcctgcagg ctgaagatgt ggcagtttat tactgtcagc aaagtaagga
ggttccgtac 300

acgtttggcc aggggaccaa gctggagatc aaacgg
336

<210> 60
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 60
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gagggccacc 60

atcaactgca gagccagcga aagtgttgat aaatatggca ttacttttat gagctggtac 120

cagcagaaac caggacagcc tcctaagctg ctcatttacg ctgcatccaa ccaaggatcc 180

ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc 240

agcctgcagg ctgaagatgt ggcagtttat tactgtcagc aaagtaagga ggttccgtac 300

acgtttggcc aggggaccaa gctggagatc aaacgg 336

<210> 61
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 61
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atcacctgca aggccagtca ggatgtgggt actgctgtag cctggtatca acagaaacca 120

gggcaatctc ctaaactact gatttactgg gcatccaccc ggcacactgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcagtct 240

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ggcaccaaac tggaaatcaa acgg 324

<210> 62
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 62
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atcacttgca aggccagtca ggatgtgggt actgctgtag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctattgg gcatccaccc ggcacactgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag
cctgcagcct 240

gaagattttg caacttatta ctgtcagcat tatagcagct atccgtggac
gtttggccag 300

gggaccaagc tggagatcaa acgg
324

<210> 63
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 63
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cagagtcacc 60

atcacttgca aggccagtca ggatgtgggt actgctgtag cctggtatca
gcaaaaacca 120

gggaaagccc ctaagctcct gatctattgg gcatccaccc tgcacactgg
ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag
cctgcagcct 240

gaagattttg caacttatta ctgtcagcat tatagcagct atccgtggac
gtttggccag 300

gggaccaagc tggagatcaa acgg
324

<210> 64
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 64
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cagagtcacc 60

atcacttgca aggccagtca ggatgtgggt actgctgtag cctggtatca
gcaaaaacca 120

gggaaagccc ctaagctcct gatctattgg gcatccaccc ggcacactgg
ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag
cctgcagcct 240

gaagattttg caacttatta ctgtcagcat tataacagct atccgtggac
gtttggccag 300

716746_ST25
gggaccaagc tggagatcaa acgg
324