SEQUENCE LISTING

<110> ALPINE IMMUNE SCIENCES, INC.

<120> APRIL AND BAFF INHIBITORY IMMUNOMODULATORY PROTEINS WITH AND WITHOUT A T CELL INHIBITORY PROTEIN AND METHODS OF USE THEREOF

<130> 761612002340

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> 63/022,373
<151> 2020-05-08

<150> 63/034,361
<151> 2020-06-03

<150> 63/080,643
<151> 2020-09-18

<160> 824

<170> PatentIn version 3.5

<210> 1
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CTLA-4 ECD

<400> 1

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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<223> CTLA-4 ECD

<400> 2

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln

115 120 125

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<223> L12P/A26T/L63P/L98Q/Y105L ECD

<400> 3

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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<220>
<223> L63P/L98R/N110K ECD

<400> 4

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1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
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<400> 5

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
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Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
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<400> 6

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 7
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<220>
<223> L63P/L98Q/Y105L ECD

<400> 7

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> L98Q/Y105L ECD

<400> 8

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 9
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P ECD

<400> 9

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 10
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L98R/N110K ECD

<400> 10

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 11
<211> 126
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<223> L12P/A26T/L63P/L98Q/M99L/Y105L ECD

<400> 11

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

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

<220>
<223> E33M/Q82H/L98Q/M99L/Y105L ECD

<400> 12

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile His Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> L63P/S72G/L98Q/M99L/Y105L ECD

<400> 13

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


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


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  14
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  S14N/R16C/I18T/M56K/T61A/L63P/A86T/M99L ECD

<400>  14

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Asn Ser Cys
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
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```
Val Cys Ala Ala Thr Tyr Met Lys Gly Asn Glu Leu Ala Phe Pro Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Thr Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
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<210> 15
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> S27P/M56K/L63P/S72G/S73R/T89A/M99L/Y105L/I117M ECD

<400> 15

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

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

Gln Ile Tyr Val Met Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 16
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<212> PRT
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<220>
<223> M56K/L63P/N75D/V96I/M99L/Y105L/L106I ECD

<400> 16

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Ile
85 90 95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 17
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> L63P/S72G/Y105L ECD

<400> 17

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 18
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q/M99L/Y105L/I117M ECD

<400> 18

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Met Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 19
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/L98Q/M99L/Y105L/L106I/I117L ECD

<400> 19

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 20
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/S72G/L98Q/Y105L/L106I/I117L ECD

<400> 20

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

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

115 120 125

<210> 21
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q/V116A ECD

<400> 21

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Ala Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 22
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L98Q/M99L/Y105L ECD

<400> 22

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  23
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  T37S/M56V/L98Q/Y105L ECD

<400>  23

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Ser Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
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Val Cys Ala Ala Thr Tyr Met Val Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

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

<220>
<223> A26T/Y54F/M56K/M99L/Y105L ECD

<400> 24

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Phe Met Lys Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 25
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/I18T/A26T/M55T/T69S/S72G/M99L/Y105L ECD

<400> 25

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 26
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> V22I/L63P/L98Q/Y105L/I117M ECD

<400> 26

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Ile Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Met Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 27
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 27

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Thr Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  28
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  28

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

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

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 29
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/E97Q/M99L/Y105F ECD

<400> 29

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Gln Leu Leu Tyr Pro Pro Pro Tyr Phe Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 30
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/S72G/L98Q/M99L/Y105L ECD

<400> 30

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 31
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> R16C/G29W/E33V/M55T/L63P/L98Q/Y105L ECD

<400> 31

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Cys
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


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


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  32
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L12P/A26T/L63P/L98Q/Y105L/L106I ECD

<400>  32

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 33
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M56L/L63P/L98Q/Y105L/L106I/I117L ECD

<400> 33

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 34
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> S15P/I18V/M56T/L98Q/M99L/Y105L ECD

<400> 34

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Pro Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 35
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> I18T/G29W/L63P/L98Q/Y105L ECD

<400> 35

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 36
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/Q82H/L98Q/M99L/Y105L ECD

<400> 36

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile His Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 37
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L98Q/M99L/Y105L/L106I/I117T ECD

<400> 37

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Thr Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 38
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L98Q/M99L/Y105L/L106I/Y115N ECD

<400> 38

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Asn Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 39
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/L63P/T71I/M99L/Y105L ECD

<400> 39

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 40
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/T53S/M56K/L63P/L98Q/Y105L ECD

<400> 40

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


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


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  41
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I18T/A26T/L63P/Q82R/L98Q/Y105L ECD

<400>  41

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 42
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/M55T/E59D/L63P/M99L ECD

<400> 42

Lys Ala Met His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Asp Leu Thr Phe Pro Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 43
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/L63P/S72G/L98Q/Y105L/I108V ECD

<400> 43

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Val Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 44
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> I18T/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 44

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 45
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> T61A/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 45

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  46
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  V38I/L63P/S72G/L98Q/M99L/Y105L ECD

<400>  46

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Ile Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 47
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/I93L/L98Q/M99L/Y105L ECD

<400> 47

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Leu Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

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

<220>
<223> L12I/M55T/M56V/I67T/M99L/L106R/I108F ECD

<400> 48

Lys Ala Met His Val Ala Gln Pro Ala Val Val Ile Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Val Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 49
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18N/A26T/L63H/T89A/L98Q/M99L/Y105L ECD

<400> 49

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe His Asp
    50                  55                  60


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


Ile Gln Gly Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


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

<220>
<223>  I18T/E48R/L63P/T69S/L98Q/Y105L/N110Y ECD

<400>  50

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Arg
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Tyr Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 51
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18N/L63P/S72T/M87T/L98Q/Y105L/N110S ECD

<400> 51

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Thr Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> G29W/M56T/L63P/L98Q/Y105L/L106I/I117L ECD

<400> 52

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 53
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/M87T/L98Q/M99L/Y105L ECD

<400> 53

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Thr Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> G29W/N58S/L63P/D64N/L98Q/M99L/Y105L ECD

<400> 54

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  55
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I18T/L63P/S72G/M87K/L98Q/M99L/Y105L ECD

<400>  55

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 56
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M56V ECD

<400> 56

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Val Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 57
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/K95R ECD

<400> 57

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Arg Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 58
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q ECD

<400> 58

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 59
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L98Q/M99L/Y105L ECD

<400> 59

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 60
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/M87K/M99L/L106R ECD

<400> 60

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Arg Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 61
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/M99L/Y105L/I108F ECD

<400> 61

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Phe Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 62
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> V10A/L63P/L98Q/Y105L ECD

<400> 62

Lys Ala Met His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 63
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M56T/L91R/L98Q/Y105L ECD

<400> 63

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Arg Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  64
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  A26T/L63P/M87V/N110K/I117E ECD

<400>  64

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Lys Gly Thr
100 105 110

Gln Ile Tyr Val Glu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 65
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/L98Q/M99L/Y105L ECD

<400> 65

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 66
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/V46E/L63P/D65G/L98Q ECD

<400> 66

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Glu Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 67
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/L98Q/Y105L ECD

<400> 67

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 68
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/E59G/L63P/L98Q/Y105L ECD

<400> 68

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Gly Leu Thr Phe Pro Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 69
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/L63P/S72G/L98Q/Y105L ECD

<400> 69

Lys Ala Met His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 70
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A6T/A26T/M55T/M99L/Y105L ECD

<400> 70

Lys Ala Met His Val Thr Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 71
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> A26T/L63P/D65G/L98Q/M99L/Y105L ECD

<400> 71

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 72
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> V10A/L63P/D64V/S72G/L98Q/M99L/Y105L ECD

<400> 72

Lys Ala Met His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Val
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 73
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/G29W/D43N/N58S/L63P/L98Q/M99L/Y105L ECD

<400> 73

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asn Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 74
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18V/A26T/L63P/D64E/L98Q/Y105L/L106R/N110K ECD

<400> 74

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Glu
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

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

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 75
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A19V/G29W/R35K/L63P/L98Q/M99L/Y105L ECD

<400> 75

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Val Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Lys Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 76
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T/L63P/S72G/T89M/L98Q/M99L/Y105L ECD

<400> 76

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Met Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 77
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> P28L/E33V/L63P/S72G/L98R/M99L/Y105L ECD

<400> 77

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Arg Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 78
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> E24Q/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 78

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 79
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/G29R/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 79

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 80
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> L63P/L98Q/M99L/Y105L ECD

<400> 80

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 81
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Q41L/Y54F/M56K/M99L/I108F ECD

<400> 81

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Leu Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Phe Met Lys Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Phe Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


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

<220>
<223>  S72G/L98Q/M99L/Y105L/I117T ECD

<400>  82

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Thr Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> M56R/L63P/L98Q/M99L/Y105L ECD

<400> 83

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

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

<220>
<223> E33M/L63P/S72G/L98Q/Y105L ECD

<400> 84

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> L63P/L98Q/M99L/Y105L/L106I ECD

<400> 85

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

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

<220>
<223> A26T/M55R/L98Q/M99L/Y105L ECD

<400> 86

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

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

<220>
<223> L63P/S72G/M87A/L98Q/Y105L ECD

<400> 87

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

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

<220>
<223> A26D/S72G/L98Q/M99L/Y105L ECD

<400> 88

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 89
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> V22A/L63P/L98Q/M99L/Y105L/P119H ECD

<400> 89

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Ala Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp His Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 90
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/M55T/L63P/L98Q/M99L/Y105L ECD

<400> 90

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Thr Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 91
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> E33V/A42S/M55T/L98Q/M99L/Y105L ECD

<400> 91

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Val Val Arg Val Thr Val Leu Arg Gln Ser Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 92
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/Q82R/L98Q/Y105L ECD

<400> 92

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 93
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> E33M/L63P/S72G/L98Q/Y105L/I117L ECD

<400> 93

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 94
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/I67N/S72G/L98Q/M99L/Y105L ECD

<400> 94

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  95
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L12F/A26T/L63P/L98Q/Y105L/L106R ECD

<400>  95

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Arg Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 96
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> S20N/A26T/L63P/L98Q/M99L/Y105L ECD

<400> 96

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 97
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T61I/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 97

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Ile Phe Pro Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 98
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/T69I/L98Q/M99L/Y105L ECD

<400> 98

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 99
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/L63P/S72G/L98Q/M99L/Y105L/L106N ECD

<400> 99

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Asn Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  100
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L63P/T69A/L98Q/M99L/Y105L/L106R/V116A ECD

<400>  100

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Ala Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Arg Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Ala Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 101
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/L98Q/Y105L ECD

<400> 101

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 102
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/D65G/S72G/L98Q/Y105L ECD

<400> 102

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 103
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> T53S/M56V/L98Q/Y105L ECD

<400> 103

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 104
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/L98Q/Y105L ECD

<400> 104

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

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

<220>
<223> I18A/L63P/S72G/L98Q/Y105L ECD

<400> 105

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> G29W/T53S/M56K/L63P/L98Q/Y105L ECD

<400> 106

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 107
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> I18V/G29W/L63P/S72G/L98Q/Y105L ECD

<400> 107

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 108
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/L106I ECD

<400> 108

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

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

<220>
<223> G29W/L63P/I67V/S72G/L98Q/Y105L ECD

<400> 109

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Val Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> G29W/M55V/E59G/L63P/L98Q/Y105L ECD

<400> 110

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Val Met Gly Asn Gly Leu Thr Phe Pro Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

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

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/I117L ECD

<400> 111

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 112
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/L98Q/Y105L/L106I/I117L ECD

<400> 112

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 113
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12F/R16H/G29W/M56T/L98Q/Y105L ECD

<400> 113

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

```
Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

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

<220>
<223> L12P/G29W/L63P/S72G/L98Q/Y105L ECD

<400> 114

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95
```

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> L12P/G29W/L63P/S72G/L98Q/Y105L/L106I ECD

<400> 115

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 116
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/L106I/I117L ECD

<400> 116

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 117
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/L98Q/Y105L/L106I ECD

<400> 117

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 118
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/T53S/L63P/L98Q/Y105L/L106I/I117L ECD

<400> 118

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 119
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/M87V/L98Q/Y105L ECD

<400> 119

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 120
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/S72G/Q76R/L98Q/Y105L/L106I/Q113H ECD

<400> 120

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

His Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 121
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/L98Q/Y105L/L106V ECD

<400> 121

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Val Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 122
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/L98Q/M99L/Y105L ECD

<400> 122

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 123
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58D/I67V/L98Q/M99L/Y105L ECD

<400> 123

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asp Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 124
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I67V/S72G/Q82H/T89A/L98Q/M99L/Y105L ECD

<400> 124

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile His Gly Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 125
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> S72G/R85G/L98Q/M99L/Y105L/L106I ECD

<400> 125

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Gly Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

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

<220>
<223> A26T/T47A/M56K/L63P/S72G/Q82R/L98Q/M99L/Y105L ECD

<400> 126

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Thr Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Ala Glu
        35                  40                  45

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

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

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  127
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  A26T/M55T/L63P/S72G/L98Q/M99L/Y105L ECD

<400>  127

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 128
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/I18V/A42T/M55T/N58D/L98R/Y105L/L106I/P121S ECD

<400> 128

Lys Ala Met His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Thr Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Thr Met Gly Asp Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Arg Met Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Asp

115 120 125

<210> 129
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/A26T/L63P/S72G/L98Q/Y105L ECD

<400> 129

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 130
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12F/K30R/S72G/Q82R/L98Q/M99L/Y105L ECD

<400> 130

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


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


Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  131
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L12P/L63P/S72G/L98Q/M99L/Y105L/L106N/I117L ECD

<400>  131

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Asn Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 132
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/M87K/I93V/L98Q/M99L/Y105L ECD

<400> 132

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Lys Asp Thr Gly Leu Tyr Val Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 133
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> P28L/E33V/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 133

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 134
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/L63P/Q82H/L98Q/M99I/Y105L ECD

<400> 134

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile His Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Ile Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 135
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18F/L63P/L98Q/M99L/Y105L/P121S ECD

<400> 135

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Phe Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Asp
        115                 120                 125


<210>  136
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L63P/L98Q/M99L/Y105L/I108V ECD

<400>  136

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Val Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 137
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/A42V/Q45H/I67N/M87K/E97Q/M99L ECD

<400> 137

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Val Asp Ser His Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Gln Leu Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 138
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> M56V/E59G/L63P/S72G/M87K/I93V/L98Q/M99L/Y105L/I117E ECD

<400> 138

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Val Gly Asn Gly Leu Thr Phe Pro Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Lys Asp Thr Gly Leu Tyr Val Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Glu Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 139
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/M87K/T89S/L98Q/M99L/Y105L/I108V/I117L ECD

<400> 139

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


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


Ile Gln Gly Leu Arg Ala Lys Asp Ser Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Val Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Leu Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  140
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L12P/M56V/L63P/V96I/L98Q/M99L/Y105L/Y115H ECD

<400>  140

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1               5                   10                  15


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


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Ile
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile His Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 141
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/T61N/L63P/L98Q/Y105L ECD

<400> 141

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 142
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/A26S/M55T/M56V/L63P/S72G/L98Q/M99L/Y105L/I117K ECD

<400> 142

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Lys Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 143
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> I18T/T61R/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 143

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 144
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/L63P/S72G/L98Q/M99L/Y105L ECD

<400> 144

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr

```
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  145
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  E33M/L63P/S72G/L98Q/Y105L/I108F ECD

<400>  145

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

Asp Ser Ile Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr
```

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Phe Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 146
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/R16H/A26T/T61S/L63P/M87V/L98Q/M99L/Y105L/L106I/I117L ECD

<400> 146

Lys Ala Met His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser His
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

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

115 120 125

<210> 147
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/N58S/L63P/M87V/L98Q/Y105L/P121S ECD

<400> 147

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Asp
115 120 125

<210> 148
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/P121S ECD

<400> 148

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


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


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Asp
        115                 120                 125


<210>  149
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  G29W/T53S/M56K/N58S/L63P/M87V/L98Q/Y105L ECD

<400>  149

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 150
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/N58S/L63P/M87V/L98Q/Y105L/I108V ECD

<400> 150

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Val Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 151
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/L63P/S72G/L98Q/Y105L ECD

<400> 151

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 152
<211> 126
<212> PRT

<213> Artificial Sequence

<220>
<223> V10A/G29W/T53S/M56K/L63P/L98Q/Y105L/P121S ECD

<400> 152

Lys Ala Met His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Asp
115 120 125

<210> 153
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> CTLA-4 ECD

<400> 153

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr

20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln
115 120 125

<210> 154
<211> 126
<212> PRT
<213> artificial sequence

<220>
<223> Belatacept ECD with C121C

<400> 154

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr

65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 155
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> CTLA-4 ECD

<400> 155

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln

115 120 125

<210> 156
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA-4 ECD

<400> 156

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp
115 120 125

<210> 157
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T89A/L98Q/M99L/Y105L/L106I/Y115N/E120D/C122P/D124P/S125I/D126P ECD

<400> 157

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Ile Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Asn Val Ile Asp Pro Asp Pro Pro Pro Pro Ile Pro
115 120 125

<210> 158
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> N58S/L63P/T71A/S72G/L98Q/M99L/Y105L/D124I/S125P/D126T ECD

<400> 158

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Ile Pro Thr
        115   120   125

<210> 159
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> R16G/E33M/N58S/E59G/L63P/L98Q/Y105L/E120D/C122P/D124P/S125I/D126P
       ECD

<400> 159

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

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Gly Leu Thr Phe Pro Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val

85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Asp Pro Pro Pro Pro Ile Pro
115 120 125

<210> 160
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/P121S/D126T ECD

<400> 160

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Ser Cys Pro Asp Ser Thr
115 120 125

<210> 161

<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12H/E33M/L98Q/Y105L ECD

<400> 161

Lys Ala Met His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg
1 5 10 15

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

Met Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 162
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/L98Q/Y105L ECD

<400> 162

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

```
Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  163
<211>  126
<212>  PRT
<213>  Artificial sequence

<220>
<223>  I18T/A26T/M55T/M56K/L63P/L98Q/M99L/Y105L ECD

<400>  163

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Thr Lys Gly Asn Glu Leu Thr Phe Pro Asp
    50                  55                  60
```

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 164
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> I18T/A26T/M56K/L63P/L98Q/Y105L ECD

<400> 164

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 165
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/L63P/L98Q ECD

<400> 165

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 166
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/L63P/Y105L ECD

<400> 166

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 167
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/L98Q ECD

<400> 167

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu

```
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 168
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/Y105L ECD

<400> 168

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
```

```
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 169
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/L98Q/Y105L ECD

<400> 169

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 170

<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/M87V/L98Q/Y105L ECD

<400> 170

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 171
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/L63P/M87V/L98Q/Y105L ECD

<400> 171

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

```
Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  172
<211>  126
<212>  PRT
<213>  Artificial sequence

<220>
<223>  T53S/N58S/L63P/M87V/L98Q/Y105L ECD

<400>  172

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Ser Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50                  55                  60
```

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 173
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> M56K/N58S/L63P/M87V/L98Q/Y105L ECD

<400> 173

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

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

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

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 174
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/L98Q/Y105L ECD

<400> 174

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 175
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/M99L/Y105L ECD

<400> 175

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Leu Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 176
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/L98Q/M99L ECD

<400> 176

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu

```
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 177
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/M99L ECD

<400> 177

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Val Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
```

```
                85                  90                  95

Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 178
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/M56T/L98Q ECD

<400> 178

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 179

<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/M56T/Y105L ECD

<400> 179

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 180
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/L98Q/Y105L ECD

<400> 180

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1 5 10 15

```
Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 181
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/M56T/L98Q/Y105L ECD

<400> 181

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60
```

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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  182
<211>  126
<212>  PRT
<213>  Artificial sequence

<220>
<223>  G29W/M56T/L98Q/Y105L ECD

<400>  182

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110
```

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 183
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/G29W/L98Q/Y105L ECD

<400> 183

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115   120   125

<210> 184
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/L98Q/Y105L ECD

<400> 184

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 185
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> R16H/L98Q/Y105L ECD

<400> 185

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser His
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu

```
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  186
<211>  126
<212>  PRT
<213>  Artificial sequence

<220>
<223>  G29W/L98Q/Y105L ECD

<400>  186

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
```

85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 187
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> M56T/L98Q/Y105L ECD

<400> 187

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 188

<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/M56T/S72G/L98Q/Y105L ECD

<400> 188

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 189
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/M56T/S72G/L98Q/Y105L ECD

<400> 189

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

```
Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

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

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125
```

<210> 190
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> I18T, T61R, L63P, S72G, L98Q, M99L, P102L, Y105L ECD

<400> 190

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

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

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

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

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


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Leu Tyr Pro Leu Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  191
<211>  102
<212>  PRT
<213>  artificial sequence

<220>
<223>  unmodified CTLA-4 IgV (39-140 of P16410.3)

<400>  191

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


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


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


Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 192
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T/L63P/L98Q/Y105L IgV

<400> 192

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 193
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98R IgV domain (of L63P/L98R/N110K - IgV doesn't contain N110 residue)

<400> 193

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

```
Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

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

Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 194
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T IgV domain

<400> 194

```
His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80
```

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 195
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T/L63P IgV domain

<400> 195

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 196
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q/Y105L IgV domain

<400> 196

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 197
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L98Q/Y105L IgV domain

<400> 197

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60
```

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 198
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P IgV domain

<400> 198

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 199
<211> 102

<212> PRT
<213> Artificial Sequence

<220>
<223> L98R IgV domain (of L98R/N110K - IgV doesn't contain N110 residue)

<400> 199

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 200
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T/L63P/L98Q/M99L/Y105L IgV domain

<400> 200

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 201
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> E33M/Q82H/L98Q/M99L/Y105L IgV domain

<400> 201

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50   55   60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile His Gly
65   70   75   80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 202
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 202

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 203
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S14N/R16C/I18T/M56K/T61A/L63P/A86T/M99L IgV domain

<400> 203

His Val Ala Gln Pro Ala Val Val Leu Ala Asn Ser Cys Gly Thr Ala

1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Thr Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Leu
85 90 95

Tyr Pro Pro Pro Tyr Tyr
100

<210> 204
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S27P/M56K/L63P/S72G/S73R/T89A/M99L/Y105L IgV domain

<400> 204

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

Cys Thr Gly Thr Gly Arg Gly Asn Gln Val Asn Leu Thr Ile Gln Gly

65 70 75 80

Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val Glu Leu Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 205
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M56K/L63P/N75D/V96I/M99L/Y105L IgV domain

<400> 205

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 206
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/Y105L IgV domain

<400> 206

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

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

Tyr Pro Pro Pro Tyr Leu
            100

<210> 207
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q/M99L/Y105L IgV domain

<400> 207

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 208
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/S72G/L98Q/Y105L IgV domain

<400> 208

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 209
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/L98Q IgV domain

<400> 209

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Tyr
            100

<210> 210
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L98Q/M99L/Y105L IgV domain

<400> 210

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg

```
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 211
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> T37S/M56V/L98Q/Y105L IgV domain

<400> 211

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Ser Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 212
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/Y54F/M56K/M99L/Y105L IgV domain

<400> 212

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Phe Met Lys Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 213
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/I18T/A26T/M55T/T69S/S72G/M99L/Y105L IgV domain

<400> 213

```
His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Thr Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


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


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


Tyr Pro Pro Pro Tyr Leu
            100


<210>  214
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  V22I/L63P/L98Q/Y105L IgV domain

<400>  214

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Ile Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
            20                  25                  30


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60
```

```
Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  215
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  A26T/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400>  215

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  216
<211>  102
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> E33M/A42T/L98Q/Y105L IgV domain

<400> 216

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Thr Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 217
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/E97Q/M99L/Y105F IgV domain

<400> 217

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala

```
        35                  40                  45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Gln Leu Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Phe
            100
```

<210> 218
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/S72G/L98Q/M99L/Y105L IgV domain

<400> 218

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
```

100

<210> 219
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> R16C/G29W/E33V/M55T/L63P/L98Q/Y105L IgV domain

<400> 219

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Cys Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Val Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 220
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M56L/L63P/L98Q/Y105L IgV domain

<400> 220

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

```
Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Leu Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 221
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S15P/I18V/M56T/L98Q/M99L/Y105L IgV domain

<400> 221

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Pro Arg Gly Val Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80
```

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 222
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/G29W/L63P/L98Q/Y105L IgV domain

<400> 222

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 223
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/Q82H/L98Q/M99L/Y105L IgV domain

<400> 223

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile His Gly
65                  70                  75                  80


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 224
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L98Q/M99L/Y105L IgV domain

<400> 224

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
```

50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 225
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M55T/L63P/T71I/M99L/Y105L IgV domain

<400> 225

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 226

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/T53S/M56K/L63P/L98Q/Y105L IgV domain

<400> 226

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 227
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/A26T/L63P/Q82R/L98Q/Y105L IgV domain

<400> 227

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Arg Gly
65   70   75   80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 228
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/M55T/E59D/L63P/M99L IgV domain

<400> 228

His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

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

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

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 229
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/L63P/S72G/L98Q/Y105L IgV domain

<400> 229

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 230
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 230

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala

1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 231
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> T61A/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 231

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Ala Phe Pro Asp Asp Ser Ile
50 55 60

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly

65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 232
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> V38I/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 232

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Ile Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 233
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/I93L/L98Q/M99L/Y105L IgV domain

<400> 233

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

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

Tyr Pro Pro Pro Tyr Leu
            100

<210> 234
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12I/M55T/M56V/I67T/M99L IgV domain

<400> 234

His Val Ala Gln Pro Ala Val Val Ile Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

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

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

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

Tyr Pro Pro Pro Tyr Tyr
            100

<210> 235
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18N/A26T/L63H/T89A/L98Q/M99L/Y105L IgV domain

<400> 235

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Asn Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe His Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 236
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/E48R/L63P/T69S/L98Q/Y105L IgV domain

<400> 236

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Arg Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 237
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18N/L63P/S72T/M87T/L98Q/Y105L IgV domain

<400> 237

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Asn Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg

```
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Thr Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100


<210>  238
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  G29W/M56T/L63P/L98Q/Y105L IgV domain

<400>  238

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 239
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/M87T/L98Q/M99L/Y105L IgV domain

<400> 239

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Thr Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 240
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/D64N/L98Q/M99L/Y105L IgV domain

<400> 240

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asn Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 241
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/L63P/S72G/M87K/L98Q/M99L/Y105L IgV domain

<400> 241

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60
```

```
Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  242
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  M56V IgV domain

<400>  242

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


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


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


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


Tyr Pro Pro Pro Tyr Tyr
            100


<210>  243
<211>  102
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> L63P/K95R IgV domain

<400> 243

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 244
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/M87K/M99L IgV domain

<400> 244

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala

```
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 245
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/M99L/Y105L IgV domain

<400> 245

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

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

Tyr Pro Pro Pro Tyr Leu
```

100

<210> 246
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> V10A/L63P/L98Q/Y105L IgV domain

<400> 246

His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 247
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M56T/L91R/L98Q/Y105L IgV domain

<400> 247

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

```
Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Arg Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 248
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/M87V IgV domain

<400> 248

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80
```

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

Tyr Pro Pro Pro Tyr Tyr
100

<210> 249
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/L98Q/M99L/Y105L IgV domain

<400> 249

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 250
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/V46E/L63P/D65G/L98Q IgV domain

<400> 250

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Glu Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Gly Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 251
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/L98Q/Y105L IgV domain

<400> 251

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
```

```
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 252
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/E59G/L63P/L98Q/Y105L IgV domain

<400> 252

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 253

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/L63P/S72G/L98Q/Y105L IgV domain

<400> 253

His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 254
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A6T/A26T/M55T/M99L/Y105L IgV domain

<400> 254

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

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 255
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/L63P/D65G/L98Q/M99L/Y105L IgV domain

<400> 255

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Gly Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 256
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> V10A/L63P/D64V/S72G/L98Q/M99L/Y105L IgV domain

<400> 256

His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 257
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/G29W/D43N/N58S/L63P/L98Q/M99L/Y105L IgV domain

<400> 257

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala

1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asn Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 258
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18V/A26T/L63P/D64E/L98Q/Y105L IgV domain

<400> 258

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Val Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Glu Asp Ser Ile
50 55 60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly

65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 259
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A19V/G29W/R35K/L63P/L98Q/M99L/Y105L IgV domain

<400> 259

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Val
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Lys
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 260
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/A26T/L63P/S72G/T89M/L98Q/M99L/Y105L IgV domain

<400> 260

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Met Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 261
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> P28L/E33V/L63P/S72G/L98R/M99L/Y105L IgV domain

<400> 261

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

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

Tyr Pro Pro Pro Tyr Leu
            100

<210> 262
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> E24Q/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 262

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 263
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/G29R/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 263

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Arg Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 264
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Q41L/Y54F/M56K/M99L IgV domain

<400> 264

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg

```
            20                  25                  30

Val Thr Val Leu Arg Leu Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Phe Met Lys Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

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

Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 265
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S72G/L98Q/M99L/Y105L IgV domain

<400> 265

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 266
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M56R/L63P/L98Q/M99L/Y105L IgV domain

<400> 266

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 267
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> E33M/L63P/S72G/L98Q/Y105L IgV domain

<400> 267

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  268
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  A26T/M55R/L98Q/M99L/Y105L IgV domain

<400>  268

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Arg Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60
```

```
Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  269
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L63P/S72G/M87A/L98Q/Y105L IgV domain

<400>  269

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Ala Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  270
<211>  102
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> A26D/S72G/L98Q/M99L/Y105L IgV domain

<400> 270

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 271
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> V22A/L63P/L98Q/M99L/Y105L IgV domain

<400> 271

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala

```
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 272
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/M55T/L63P/L98Q/M99L/Y105L IgV domain

<400> 272

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
```

100

<210> 273
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> E33V/A42S/M55T/L98Q/M99L/Y105L IgV domain

<400> 273

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ser Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 274
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/Q82R/L98Q/Y105L IgV domain

<400> 274

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

```
Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Arg Gly
65                  70                  75                  80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 275
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/I67N/S72G/L98Q/M99L/Y105L IgV domain

<400> 275

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Asn
    50                  55                  60

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80
```

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 276
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12F/A26T/L63P/L98Q/Y105L IgV domain

<400> 276

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 277
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S20N/A26T/L63P/L98Q/M99L/Y105L IgV domain

<400> 277

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 278
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/M87K/T89S/L98Q/M99L/Y105L IgV domain

<400> 278

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
```

```
    50                  55                  60

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

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

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 279
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T61I/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 279

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Ile Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 280

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/T69I/L98Q/M99L/Y105L IgV domain

<400> 280

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 281
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 281

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 282
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/T69A/L98Q/M99L/Y105L IgV domain

<400> 282

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 283
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/L98Q/Y105L IgV domain

<400> 283

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 284
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> T53S/M56V/L98Q/Y105L IgV domain

<400> 284

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala

1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 285
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L63P/S72G/L98Q/Y105L IgV domain

<400> 285

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly

65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 286
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18A/L63P/S72G/L98Q/Y105L IgV domain

<400> 286

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ala Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 287
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/L63P/L98Q/Y105L IgV domain

<400> 287

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 288
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18V/G29W/L63P/S72G/L98Q/Y105L IgV domain

<400> 288

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Val Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 289
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L IgV domain

<400> 289

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 290
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/L63P/I67V/S72G/L98Q/Y105L IgV domain

<400> 290

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 291
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/M55V/E59G/L63P/L98Q/Y105L IgV domain

<400> 291

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg

```
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 292
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12F/R16H/G29W/M56T/L98Q/Y105L IgV domain

<400> 292

```
His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 293
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/G29W/L63P/S72G/L98Q/Y105L IgV domain

<400> 293

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 294
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/T53S/L63P/L98Q/Y105L IgV domain

<400> 294

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 295
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58S/L63P/S72G/M87V/L98Q/Y105L IgV domain

<400> 295

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60
```

```
Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  296
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  G29W/S72G/Q76R/L98Q/Y105L IgV domain

<400>  296

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


Cys Thr Gly Thr Gly Ser Gly Asn Arg Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  297
<211>  102
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> A26T/L63P/L98Q/M99L/Y105L IgV domain

<400> 297

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 298
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/N58D/I67V/L98Q/M99L/Y105L IgV domain

<400> 298

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala

```
        35                  40                  45

Ala Thr Tyr Met Met Gly Asp Glu Leu Thr Phe Leu Asp Asp Ser Val
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 299
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I67V/S72G/Q82H/T89A/L98Q/M99L/Y105L IgV domain

<400> 299

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile His Gly
65                  70                  75                  80

Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
```

100

<210> 300
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> S72G/R85G/L98Q/M99L/Y105L IgV domain

<400> 300

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Gly Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 301
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/T47A/M56K/L63P/S72G/Q82R/L98Q/M99L/Y105L IgV domain

<400> 301

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Ala Glu Val Cys Ala
        35   40   45

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

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Arg Gly
65   70   75   80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 302
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/M55T/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 302

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Thr Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 303
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12H/I18V/A42T/M55T/N58D/L98R/Y105L IgV domain

<400> 303

His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg Gly Val Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Thr Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Thr Met Gly Asp Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 304
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/A26T/L63P/S72G/L98Q/Y105L IgV domain

<400> 304

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 305
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12F/K30R/S72G/Q82R/L98Q/M99L/Y105L IgV domain

<400> 305

```
His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
```

50 55 60

Cys Thr Gly Thr Gly Ser Gly Asn Gln Val Asn Leu Thr Ile Arg Gly
65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 306
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/M87K/I93V/L98Q/M99L/Y105L IgV domain

<400> 306

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 307

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> P28L/E33V/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 307

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 308
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/L63P/Q82H/L98Q/M99I/Y105L IgV domain

<400> 308

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile His Gly
65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Ile
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 309
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18F/L63P/L98Q/M99L/Y105L IgV domain

<400> 309

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Phe Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 310
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> A26T/A42V/Q45H/I67N/M87K/E97Q/M99L IgV domain

<400> 310

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Val Asp Ser His Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Asn
50 55 60

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

Leu Arg Ala Lys Asp Thr Gly Leu Tyr Ile Cys Lys Val Gln Leu Leu
85 90 95

Tyr Pro Pro Pro Tyr Tyr
100

<210> 311
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> M56V/E59G/L63P/S72G/M87K/I93V/L98Q/M99L/Y105L IgV domain

<400> 311

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala

```
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

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

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

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 312
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/M56V/L63P/V96I/L98Q/M99L/Y105L IgV domain

<400> 312

```
His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
```

65 70 75 80

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 313
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/T61N/L63P/L98Q/Y105L IgV domain

<400> 313

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 314
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/A26S/M55T/M56V/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 314

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


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


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 315
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I18T/T61R/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 315

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45
```

```
Ala Thr Tyr Met Met Gly Asn Glu Leu Arg Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 316
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/L63P/S72G/L98Q/M99L/Y105L IgV domain

<400> 316

```
His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 317
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> L12P/R16H/A26T/T61S/L63P/M87V/L98Q/M99L/Y105L IgV domain

<400> 317

His Val Ala Gln Pro Ala Val Val Pro Ala Ser Ser His Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Ser Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 318
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/M56K/N58S/L63P/M87V/L98Q/Y105L IgV domain

<400> 318

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg

```
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 319
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> G29W/T53S/L63P/S72G/L98Q/Y105L IgV domain

<400> 319

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 320
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> V10A/G29W/T53S/M56K/L63P/L98Q/Y105L IgV domain

<400> 320

His Val Ala Gln Pro Ala Ala Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 321
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA-4 IgV

<400> 321

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


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


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


Tyr Pro Pro Pro Tyr Tyr
            100


<210>  322
<211>  102
<212>  PRT
<213>  Artificial sequence

<220>
<223>  T89A/L98Q/M99L/Y105L/L106I/Y115N/E120D/C122P/D124P/S125I/D126P
       IgV domain

<400>  322

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60
```

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

Leu Arg Ala Met Asp Ala Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 323
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> N58S/L63P/T71A/S72G/L98Q/M99L/Y105L/D124I/S125P/D126T IgV domain

<400> 323

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 324
<211> 102

<212> PRT
<213> Artificial sequence

<220>
<223> R16G/E33M/N58S/E59G/L63P/L98Q/Y105L/E120D/C122P/D124P/S125I/D126P IgV

<400> 324

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

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 325
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/L63P/S72G/L98Q/Y105L/P121S/D126T IgV domain

<400> 325

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

```
Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 326
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12H/E33M/L98Q/Y105L IgV domain

<400> 326

```
His Val Ala Gln Pro Ala Val Val His Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95
```

Tyr Pro Pro Pro Tyr Leu
100

<210> 327
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/L98Q/Y105L IgV domain

<400> 327

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 328
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> I18T/A26T/M55T/M56K/L63P/L98Q/ M99L/Y105L IgV domain

<400> 328

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala

1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 329
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> I18T/A26T/M56K/L63P/L98Q/Y105L IgV domain

<400> 329

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly

65 70 75 80

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 330
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/L63P/L98Q IgV domain

<400> 330

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Tyr
100

<210> 331
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/L63P/Y105L IgV domain

<400> 331

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

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

Tyr Pro Pro Pro Tyr Leu
            100

<210> 332
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/L98Q IgV domain

<400> 332

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Tyr
            100

<210> 333
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/M87V/Y105L IgV domain

<400> 333

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50   55   60

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

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

Tyr Pro Pro Pro Tyr Leu
            100

<210> 334
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/L63P/L98Q/Y105L IgV domain

<400> 334

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 335
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/M56K/N58S/M87V/L98Q/Y105L IgV domain

<400> 335

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
```

```
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Ser Tyr Met Lys Gly Ser Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100


<210>  336
<211>  102
<212>  PRT
<213>  Artificial sequence

<220>
<223>  T53S/M56K/L63P/M87V/L98Q/Y105L IgV domain

<400>  336

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

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

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
```

85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 337
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> T53S/N58S/L63P/M87V/L98Q/Y105L IgV domain

<400> 337

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Ser Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 338
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> M56K/N58S/L63P/M87V/L98Q/Y105L IgV domain

<400> 338

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Lys Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Leu
            100
```

<210> 339
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/L98Q/Y105L IgV domain

<400> 339

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60
```

```
Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
65                  70                  75                  80


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95


Tyr Pro Pro Pro Tyr Leu
            100


<210>  340
<211>  102
<212>  PRT
<213>  Artificial sequence

<220>
<223>  E33V/M99L/Y105L IgV domain

<400>  340

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


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


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


Tyr Pro Pro Pro Tyr Leu
            100


<210>  341
<211>  102
<212>  PRT
```

<213> Artificial sequence

<220>
<223> E33V/L98Q/M99L IgV domain

<400> 341

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45


Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60


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


Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
                85                  90                  95


Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 342
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> E33V/M99L IgV domain

<400> 342

```
His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1               5                   10                  15


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


Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
```

```
        35                  40                  45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

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

Tyr Pro Pro Pro Tyr Tyr
            100
```

<210> 343
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/M56T/L98Q IgV domain

<400> 343

```
His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1               5                   10                  15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20                  25                  30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35                  40                  45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50                  55                  60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85                  90                  95

Tyr Pro Pro Pro Tyr Tyr
```

100

<210> 344
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/M56T/Y105L IgV domain

<400> 344

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

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

Tyr Pro Pro Pro Tyr Leu
100

<210> 345
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/G29W/L98Q/Y105L IgV domain

<400> 345

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 346
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/R16H/M56T/L98Q/Y105L IgV domain

<400> 346

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1   5   10   15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 347
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/M56T/L98Q/Y105L IgV domain

<400> 347

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 348
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/G29W/L98Q/Y105L IgV domain

<400> 348

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 349
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> L12F/L98Q/Y105L IgV domain

<400> 349

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile

50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 350
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> R16H/L98Q/Y105L IgV domain

<400> 350

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

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 351

<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/L98Q/Y105L IgV domain

<400> 351

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 352
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> M56T/L98Q/Y105L IgV domain

<400> 352

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
            100

<210> 353
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223>   L12F/R16H/G29W/M56T/S72G/L98Q/Y105L IgV domain

<400> 353

His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His Gly Ile Ala
1   5   10   15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
            20   25   30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
        35   40   45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
    50   55   60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
                85   90   95

Tyr Pro Pro Pro Tyr Leu
100

<210> 354
<211> 102
<212> PRT
<213> Artificial sequence

<220>
<223> G29W/M56T/S72G/L98Q/Y105L IgV domain

<400> 354

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
1 5 10 15

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
20 25 30

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
50 55 60

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
85 90 95

Tyr Pro Pro Pro Tyr Leu
100

<210> 355
<211> 102
<212> PRT
<213> artificial sequence

<220>
<223> I18T, T61R, L63P, S72G, L98Q, M99L, P102L, Y105L IgV domain

<400> 355

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Thr Ala

1 5 10 15

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

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
35 40 45

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

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

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Leu
85 90 95

Tyr Pro Leu Pro Tyr Leu
100

<210> 356
<211> 53
<212> PRT
<213> artificial sequence

<220>
<223> BCMA WT ECD

<400> 356

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 357

<211> 53
<212> PRT
<213> artificial sequence

<220>
<223> BCMA H19Y ECD

<400> 357

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 358
<211> 53
<212> PRT
<213> artificial sequence

<220>
<223> BCMA H19Y, S30G ECD

<400> 358

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 359
<211> 53
<212> PRT

<213> artificial sequence

<220>
<223> BCMA H19Y, V45A ECD

<400> 359

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Ala Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 360
<211> 53
<212> PRT
<213> artificial sequence

<220>
<223> BCMA F14Y, H19Y ECD

<400> 360

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Tyr Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 361
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, V45D ECD

<400> 361

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Asp Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 362
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, A43E ECD

<400> 362

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Glu Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 363
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T36A ECD

<400> 363

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Ala Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 364
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, I22V ECD

<400> 364

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 365
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11D, H19Y ECD

<400> 365

Leu Gln Met Ala Gly Gln Cys Ser Gln Asp Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 366
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T36M ECD

<400> 366

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Met Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 367
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11S, H19Y ECD

<400> 367

Leu Gln Met Ala Gly Gln Cys Ser Gln Ser Glu Tyr Phe Asp Ser Leu

1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 368
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, L35P, T46A ECD

<400> 368

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Pro Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Ala Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 369
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, N47D ECD

<400> 369

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asp Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 370
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9D, H19Y ECD

<400> 370

Leu Gln Met Ala Gly Gln Cys Asp Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 371
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, S30G, V45D ECD

<400> 371

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Gly Asn Thr Pro

```
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Asp Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
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<210> 372
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, R39Q ECD

<400> 372

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Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

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

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
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<210> 373
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, L35P ECD

<400> 373

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

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

Pro Pro Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 374
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9D, H19Y, R27H ECD

<400> 374

Leu Gln Met Ala Gly Gln Cys Asp Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu His Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 375
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA Q10P, H19Y, Q25H ECD

<400> 375

Leu Gln Met Ala Gly Gln Cys Ser Pro Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Ile Pro Cys His Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val

```
        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  376
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA H19Y, R39L, N47D ECD

<400>  376

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


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


Pro Leu Thr Cys Gln Leu Tyr Cys Asn Ala Ser Val Thr Asp Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  377
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA N11D, H19Y, N47D ECD

<400>  377

Leu Gln Met Ala Gly Gln Cys Ser Gln Asp Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


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


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asp Ser Val
        35                  40                  45
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Lys Gly Thr Asn Ala
    50

<210> 378
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T32S ECD

<400> 378

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 379
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11S, H19Y, S29P ECD

<400> 379

Leu Gln Met Ala Gly Gln Cys Ser Gln Ser Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala

50

<210> 380
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, R39Q, N47D ECD

<400> 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asp Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 381
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S16A, H19Y, R39Q ECD

<400> 381

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ala Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 382
<211> 53
<212> PRT
<213> artificial sequence

<220>
<223> BCMA S9N, H19Y, N31K, T46I ECD

<400> 382

Leu Gln Met Ala Gly Gln Cys Asn Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Ile Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 383
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, R27L, N31Y, T32S, T36A ECD

<400> 383

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Leu Cys Ser Ser Tyr Ser Pro
20 25 30

Pro Leu Ala Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 384

<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11S, H19Y, T46A ECD

<400> 384

Leu Gln Met Ala Gly Gln Cys Ser Gln Ser Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Ala Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 385
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T32I ECD

<400> 385

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 386
<211> 53
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9G, H19Y, T36S, A43S ECD

<400> 386

Leu Gln Met Ala Gly Gln Cys Gly Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Ser Cys Gln Arg Tyr Cys Asn Ser Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 387
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, S48G ECD

<400> 387

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Gly Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 388
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9N, H19Y, I22V, N31D ECD

<400> 388

Leu Gln Met Ala Gly Gln Cys Asn Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 389
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9N, H19Y, Q25K, N31D ECD

<400> 389

Leu Gln Met Ala Gly Gln Cys Asn Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

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

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 390
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9G, H19Y, T32S ECD

<400> 390

Leu Gln Met Ala Gly Gln Cys Gly Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Ser Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 391
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T36A, N47Y ECD

<400> 391

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Ala Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Tyr Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 392
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, V45A, T46I ECD

<400> 392

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Ala Ile Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 393
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, Q25K, N31D ECD

<400> 393

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Lys Leu Arg Cys Ser Ser Asp Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 394
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, Q25H, R39Q, V45D ECD

<400> 394

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu

1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys His Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Asp Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 395
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T32S, N47D ECD

<400> 395

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Ser Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asp Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 396
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA Q10E, H19Y, A20T, T36S ECD

<400> 396

Leu Gln Met Ala Gly Gln Cys Ser Glu Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Thr Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 397
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T32S, V45I ECD

<400> 397

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Ser Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Ile Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 398
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19A ECD

<400> 398

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Ala Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro

```
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
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<210> 399
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19C ECD

<400> 399

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Cys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
```

<210> 400
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19D ECD

<400> 400

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Asp Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30
```

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 401
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19E ECD

<400> 401

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Glu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 402
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F ECD

<400> 402

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Phe Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val

```
        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  403
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA H19G ECD

<400>  403

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Gly Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  404
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA H19I ECD

<400>  404

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Ile Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45
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Lys Gly Thr Asn Ala
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<210> 405
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19K ECD

<400> 405

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Lys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 406
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L ECD

<400> 406

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala

50

<210> 407
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19M ECD

<400> 407

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Met Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 408
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19N ECD

<400> 408

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Asn Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 409
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19P ECD

<400> 409

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Pro Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 410
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Q ECD

<400> 410

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Gln Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 411

<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19R ECD

<400> 411

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Arg Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 412
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19S ECD

<400> 412

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Ser Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 413
<211> 53
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19T ECD

<400> 413

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Thr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 414
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19V ECD

<400> 414

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Val Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 415
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19W ECD

<400> 415

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Trp Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 416
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25E, N31L, L35Y, T36S ECD

<400> 416

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Phe Ala Cys Ile Pro Cys Glu Leu Arg Cys Ser Ser Leu Thr Pro
            20   25   30

Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 417
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25F, N31S, T36S ECD

<400> 417

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Phe Ala Cys Ile Pro Cys Phe Leu Arg Cys Ser Ser Ser Thr Pro
20 25 30

Pro Leu Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 418
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19I, Q25F, N31S, T36V ECD

<400> 418

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Ile Ala Cys Ile Pro Cys Phe Leu Arg Cys Ser Ser Ser Thr Pro
20 25 30

Pro Leu Val Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 419
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25V, N31M, T36S ECD

<400> 419

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Phe Ala Cys Ile Pro Cys Val Leu Arg Cys Ser Ser Met Thr Pro
20 25 30

Pro Leu Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 420
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, Q25Y, N31L, L35Y, T36S ECD

<400> 420

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Tyr Leu Arg Cys Ser Ser Leu Thr Pro
20 25 30

Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 421
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25I, N31M, L35A, T36S ECD

<400> 421

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu

1 5 10 15

Leu Phe Ala Cys Ile Pro Cys Ile Leu Arg Cys Ser Ser Met Thr Pro
20 25 30

Pro Ala Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 422
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19I, Q25L, N31L, L35Y, T36S ECD

<400> 422

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Ile Ala Cys Ile Pro Cys Leu Leu Arg Cys Ser Ser Leu Thr Pro
20 25 30

Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 423
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25L, N31G, L35P, T36A ECD

<400> 423

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Phe Ala Cys Ile Pro Cys Leu Leu Arg Cys Ser Ser Gly Thr Pro
            20   25   30

Pro Pro Ala Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 424
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, I22L, N31G ECD

<400> 424

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Leu Pro Cys Gln Leu Arg Cys Ser Ser Gly Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 425
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, I22V, Q25M, N31P, T36M ECD

<400> 425

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Phe Ala Cys Val Pro Cys Met Leu Arg Cys Ser Ser Pro Thr Pro

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            20                  25                  30

Pro Leu Met Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
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<210> 426
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, N31L, L35Y, T36S ECD

<400> 426

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Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Leu Thr Pro
            20                  25                  30

Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala
    50
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<210> 427
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L, S30G, N31H, L35A ECD

<400> 427

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Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Gly His Thr Pro
            20                  25                  30
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Pro Ala Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 428
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L, Q25S, N31V, L35S, T36V ECD

<400> 428

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Leu Ala Cys Ile Pro Cys Ser Leu Arg Cys Ser Ser Val Thr Pro
            20   25   30

Pro Ser Val Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 429
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L, Q25S, S30Y, N31G, L35M, T36V ECD

<400> 429

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Leu Ala Cys Ile Pro Cys Ser Leu Arg Cys Ser Tyr Gly Thr Pro
            20   25   30

Pro Met Val Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val

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        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  430
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA H19F, Q25F, N31L, L35Y, T36S ECD

<400>  430

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Phe Ala Cys Ile Pro Cys Phe Leu Arg Cys Ser Ser Leu Thr Pro
            20                  25                  30


Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala
    50


<210>  431
<211>  53
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA H19F, Q25F, N31S, T36G ECD

<400>  431

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Phe Ala Cys Ile Pro Cys Phe Leu Arg Cys Ser Ser Ser Thr Pro
            20                  25                  30


Pro Leu Gly Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45
```

Lys Gly Thr Asn Ala
    50

<210> 432
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, I22V, Q25S, N31V, L35S, T36V ECD

<400> 432

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Phe Ala Cys Val Pro Cys Ser Leu Arg Cys Ser Ser Val Thr Pro
            20   25   30

Pro Ser Val Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala
    50

<210> 433
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25G, N31S, L35V, T36N ECD

<400> 433

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Phe Ala Cys Ile Pro Cys Gly Leu Arg Cys Ser Ser Ser Thr Pro
            20   25   30

Pro Val Asn Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala

50

<210> 434
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L, Q25H, N31D, L35S ECD

<400> 434

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Leu Ala Cys Ile Pro Cys His Leu Arg Cys Ser Ser Asp Thr Pro
20 25 30

Pro Ser Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 435
<211> 53
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25F, N31S, L35Y, T36S ECD

<400> 435

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Phe Ala Cys Ile Pro Cys Phe Leu Arg Cys Ser Ser Ser Thr Pro
20 25 30

Pro Tyr Ser Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala
50

<210> 436
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA WT ECD

<400> 436
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gcacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 437
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y ECD

<400> 437
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 438
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, S30G ECD

<400> 438
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actcattgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaggcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 439
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, V45A ECD

<400> 439
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc agctgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ctaccaacag tgtcaaaggg actaatgcg 159

<210> 440
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA F14Y, H19Y ECD

<400> 440
ctgcaaatgg ccgggcagtg tagccagaac gaatactatg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 441
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, V45D ECD

<400> 441
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatccg ataccaacag tgtcaaaggg actaatgcg 159

<210> 442
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, A43E ECD

<400> 442
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgaatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 443
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T36A ECD

<400> 443
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcgcgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 444
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, I22V ECD

<400> 444
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

gttccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 445
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11D, H19Y ECD

<400> 445
ctgcaaatgg ccgggcagtg cagccaggac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 446

<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, T36M ECD

<400> 446
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccatgcc aactgcgctg ttcaagcaac acccccccgc tcatgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 447
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA N11S, H19Y ECD

<400> 447
ctgcaaatgg ccgggcagtg cagccagagc gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 448
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, L35P, T46A ECD

<400> 448
ctgcaaatgg ccgggcagtg cagtcagaac gaatactttg actccttgtt gtacgcatgt 60

attccatgcc aactacgctg ttcaagcaac acccccccgc ccacgtgtca gcggtactgc 120

aacgcatctg ttgccaacag tgtcaaaggg actaatgcg 159

<210> 449
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, N47D ECD

<400> 449
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccgacag tgtcaaaggg actaatgcg 159

<210> 450
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9D, H19Y ECD

<400> 450
ctgcaaatgg ccgggcagtg cgaccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 451
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, S30G, V45D ECD

<400> 451
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcgtgt 60

attccttgcc aactgcgctg ttcaggcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ataccaacag tgtcaaaggg actaatgcg 159

<210> 452
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, R39Q ECD

<400> 452
ctgcaaatgg ccgggcagtg cagtcagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcagtactgc 120

aacgcatctg ttaccaatag tgtcaaaggg actaatgcg 159

<210> 453
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19Y, L35P ECD

<400> 453
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gtacgcatgt 60

attccatgcc aactacgctg ttcaagcaac acccccccgc ccacgtgtca gcggtactgc 120

aacgcatctg ttaccaatag tgtcaaaggg actaatgcg 159

<210> 454
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA S9D, H19Y, R27H ECD

<400> 454
ctgcaaatgg ccgggcagtg cgaccagaac gaatactttg actccttgtt gtacgcatgt 60

attccttgcc aactgcactg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 455
<211> 159
<212> DNA
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<210> 509
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attccttgca gtctgcgctg ttcatatggg acccccccga tggtgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 510
<211> 159
<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25F, N31L, L35Y, T36S ECD

<400> 510
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attccttgct ttctgcgctg ttcaagcttg acccccccgt atagttgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 511
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25F, N31S, T36G ECD

<400> 511
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attccttgct ttctgcgctg ttcaagctct acccccccgc tgggttgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 512
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, I22V, Q25S, N31V, L35S, T36V ECD

<400> 512
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gttccttgct ctctgcgctg ttcaagcgtt acccccccga gtgtgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 513
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BMCA H19F, Q25G, N31S, L35V, T36N ECD

<400> 513

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aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 514
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19L, Q25H, N31D, L35S ECD

<400> 514
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attccttgcc atctgcgctg ttcaagcgat acccccccgt ctacgtgtca gcagtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 515
<211> 159
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA H19F, Q25F, N31S, L35Y, T36S ECD

<400> 515
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attccttgct ttctgcgctg ttcaagctct acccccccgt atagttgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcg 159

<210> 516
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI WT ECD

<400> 516

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg

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            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
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<210> 517
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P ECD

<400> 517

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Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Pro Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
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<210> 518

<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85E, K98T ECD

<400> 518

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Glu Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Thr Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 519
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87L, K98T ECD

<400> 519

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Leu Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Thr Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 520
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R60G, Q75E, L82P ECD

<400> 520

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Gly
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Glu Gly
        35   40   45

Lys Phe Tyr Asp His Pro Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 521
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R60G, C86Y ECD

<400> 521

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Gly
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Lys Phe Tyr Asp His Leu Leu Arg Asp Tyr Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 522
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 522

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu

65 70 75 80

Arg Ser

<210> 523
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI C86Y ECD

<400> 523

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Tyr Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 524
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI W40R, L82P, F103Y ECD

<400> 524

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Arg Asp Pro Leu Leu
1 5 10 15

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Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Pro Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Tyr Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
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<210> 525
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI W40R, Q59R, T61P, K98T ECD

<400> 525

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Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Arg Asp Pro Leu Leu
1               5                   10                  15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Arg Arg
            20                  25                  30

Pro Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Thr Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
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<210> 526
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P, I87L ECD

<400> 526

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Pro Leu Arg Asp Cys Leu Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 527
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI G76S, P97S ECD

<400> 527

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Ser

```
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Ser Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
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<210> 528
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI WT ECD

<400> 528

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Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35                  40
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<210> 529
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85V ECD

<400> 529

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Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Val Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30
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Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 530
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI E74V ECD

<400> 530

Ser Leu Ser Cys Arg Lys Val Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 531
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84L ECD

<400> 531

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Leu Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 532
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84L, F103Y ECD

<400> 532

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1   5   10   15

Leu Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Tyr Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 533
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F, Q99E ECD

<400> 533

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Phe Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Glu
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 534
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F ECD

<400> 534

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Phe Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln

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            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35                  40


<210>  535
<211>  43
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI R84G ECD

<400>  535

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15


Gly Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30


Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35                  40


<210>  536
<211>  82
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI L83S, F103S ECD

<400>  536

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45


Lys Phe Tyr Asp His Leu Ser Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60
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Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Ser Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 537
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82H ECD

<400> 537

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His His Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 538
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 538

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu

1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 539
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84Q ECD

<400> 539

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 540
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D ECD

<400> 540

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 541
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, F78Y, Y102D ECD

<400> 541

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 542
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75E, R84Q ECD

<400> 542

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 543
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75R, R84G, I92V ECD

<400> 543

Ser Leu Ser Cys Arg Lys Glu Arg Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Gly Asp Cys Ile Ser Cys Ala Ser Val Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 544
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D, Y102D ECD

<400> 544

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Asp Asp Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 545
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q ECD

<400> 545

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser

35 40

<210> 546
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, S88N, A101D ECD

<400> 546

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Asn Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 547
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E ECD

<400> 547

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 548
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, F103V ECD

<400> 548

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Val Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 549
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, Q95R, A101D ECD

<400> 549

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Arg His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 550
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87M, A101D ECD

<400> 550

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Met Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 551
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI WT ECD

<400> 551
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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 552
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P ECD

<400> 552
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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ctttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 553
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85E, K98T ECD

<400> 553

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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga atgtataagc 180

tgtgcgtcta tttgtggaca acaccctaca caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 554
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87L, K98T ECD

<400> 554
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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctgtttaagc 180

tgtgcgtcta tttgtggaca acaccctaca caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 555
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R60G, Q75E, L82P ECD

<400> 555
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agctgcaaga ccatctgtaa tcatcaatcc caagggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagga aggcaaattt tacgaccatc ctttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 556
<211> 246
<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R60G, C86Y ECD

<400> 556
gtggcaatgc gctcatgccc agaggaacaa tattgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caagggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctacataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 557
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 557
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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgatt atttctgtga aaataagctt 240

cgatct 246

<210> 558
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI C86Y ECD

<400> 558
gtggcaatgc gctcatgccc agaggaacaa tattgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctatataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 559
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI W40R, L82P, F103Y ECD

<400> 559
gtggcaatgc gctcatgccc agaggaacaa tatcgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ctttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggtca acaccctaaa caatgtgctt attactgtga aaataagctt 240

cgatct 246

<210> 560
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI W40R, Q59R, T61P, K98T ECD

<400> 560
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agctgcaaga ccatctgtaa tcatcaatcc cgaaggccat gcgcagcatt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ttttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaca caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 561
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P, I87L ECD

<400> 561
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agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc ctttgcgaga ctgtttaagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 562
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI G76S, P97S ECD

<400> 562
gtggcaatgc gctcatgccc agaggaacaa tattgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aagcaaattt tacgaccatc ttttgcgaga ctgtataagc 180

tgtgcgtcta tttgtggtca acactctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 563
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI WT ECD

<400> 563
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 564
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85V ECD

<400> 564

agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttgcg agtctgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 565
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI E74V ECD

<400> 565
agtctctctt gcaggaaagt gcaaggcaaa ttttacgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 566
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84L ECD

<400> 566
agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttgct agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 567
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84L, F103Y ECD

<400> 567
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttattactg tgaaaataag 120

cttcgatct 129

<210> 568
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F, Q99E ECD

<400> 568
agtctctctt gcaggaaaga gcaaggcaaa tttttcgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaagaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 569
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F ECD

<400> 569
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 570
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84G ECD

<400> 570
agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttggg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 571
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L83S, F103S ECD

<400> 571
gtggcaatgc gctcatgccc agaggaacaa tattgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc tttcgcgaga ctgtataagc 180

tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt attcctgtga aaataagctt 240

cgatct 246

<210> 572
<211> 246
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82H ECD

<400> 572
gtggcaatgc gctcatgccc agaggaacaa tattgggatc cgcttcttgg gacgtgtatg 60

agctgcaaga ccatctgtaa tcatcaatcc caaaggacat gcgcagcttt ctgcaggagt 120

ctctcttgca ggaaagagca aggcaaattt tacgaccatc atttgcgaga ctgtataagc 180

tgtgcgtcta tctgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 240

cgatct 246

<210> 573
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 573
agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg attatttctg tgaaaataag 120

cttcgatct 129

<210> 574
<211> 129
<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84Q ECD

<400> 574
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 575
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D ECD

<400> 575
agtctctctt gcaggaaaga gcaaggcgaa ttttacgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg attatttctg tgaaaataag 120

cttcgatct 129

<210> 576
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, F78Y, Y102D ECD

<400> 576
agtctctctt gcaggaaaga gcaaggcgaa tattacgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg ctgatttctg tgaaaataag 120

cttcgatct 129

<210> 577
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75E, R84Q ECD

<400> 577

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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 578
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75R, R84G, I92V ECD

<400> 578
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agctgtgcgt ctgtttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 579
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D, Y102D ECD

<400> 579
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg atgatttctg tgaaaataag 120

cttcgatct 129

<210> 580
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q ECD

<400> 580
agtctctctt gcaggaaaga gcaaggcaaa ttttatgacc atcttttgca agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 581
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, S88N, A101D ECD

<400> 581
agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttgca agactgtata 60

aactgtgcgt ctatatgtgg acaacaccct aaacaatgtg attatttctg tgaaaataag 120

cttcgatct 129

<210> 582
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E ECD

<400> 582
agtctctctt gcaggaaaga gcaaggcgaa ttttacgacc atcttttgcg agactgtata 60

agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatttctg tgaaaataag 120

cttcgatct 129

<210> 583
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, F103V ECD

<400> 583
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agctgtgcgt ctatttgtgg acaacaccct aaacaatgtg cttatgtctg tgaaaataag 120

cttcgatct 129

<210> 584
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, Q95R, A101D ECD

<400> 584
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agctgtgcgt ctatttgtgg acgacaccct aaacaatgtg attatttctg tgaaaataag 120

cttcgatct 129

<210> 585
<211> 129
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87M, A101D ECD

<400> 585
agtctctctt gcaggaaaga gcaaggcaaa ttttacgacc atcttttgcg agactgtatg 60

agctgtgcgt caatttgtgg acaacaccct aaacaatgtg attatttctg tgaaaataag 120

cttcgatct 129

<210> 586
<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> IgG1 Fc

<400> 586

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 587
<211> 224
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CD86 ECD (24-247)

<400> 587

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro

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1               5                   10                  15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
            20                  25                  30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
        35                  40                  45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
                85                  90                  95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn
            100                 105                 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
        115                 120                 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
    130                 135                 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145                 150                 155                 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
                165                 170                 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
            180                 185                 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
        195                 200                 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
    210                 215                 220
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<210> 588
<211> 8
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> FLAG-tag

<400> 588

Asp Tyr Lys Asp Asp Asp Asp Lys
1   5

<210> 589
<211> 231
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc C220S/L234A/L235E/G237A/K447del

<400> 589

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

```
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly
225                 230
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<210> 590
<211> 7
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Linker

<400> 590

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Gly Ser Gly Gly Gly Gly Ser
1               5
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<210> 591
<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc C220S/L234A/L235E/G237A/E356D/M358L

<400> 591

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
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210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 592
<211> 5
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Linker

<400> 592

Gly Ser Gly Gly Ser
1 5

<210> 593
<211> 5
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 593

Gly Gly Gly Gly Ser
1 5

<210> 594
<211> 10
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 594

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 595
<211> 15
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 595

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 596
<211> 7
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 596

Gly Gly Gly Gly Ser Ser Ala
1   5

<210> 597
<211> 231
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc (E356D and M358L)

<400> 597

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly
225 230

<210> 598
<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc (C5S (C220S), R77C, (R292C), N82G (N297G), V87C (V302C))

<400> 598

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

```
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
65                  70                  75                  80

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
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<210> 599
<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc with C220S/L234A/L235E/G237A

<400> 599

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175
```

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 600
<211> 20
<212> PRT
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<220>
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<400> 600

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 601
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 186 GSG4S Fc- (G4S)4 BCMA 406

<400> 601

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu

```
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255
```

```
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
            420                 425                 430

Lys Gly Thr Asn Ala
        435
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<210> 602
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 602

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65   70   75   80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115   120   125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130   135   140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145   150   155   160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165   170   175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180   185   190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

```
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415
```

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
420 425 430

Lys Gly Thr Asn Ala
435

<210> 603
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 186GSG4S Fc- (G4S)4 BCMA 381

<400> 603

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

```
Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
```

```
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ala Leu
385                 390                 395                 400

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
            420                 425                 430

Lys Gly Thr Asn Ala
        435


<210>  604
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 186GSG4S  Fc- (G4S)4  BCMA 411

<400>  604

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
```

```
               85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
               165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
               245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300
```

```
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380


Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400


Leu Arg Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
            420                 425                 430


Lys Gly Thr Asn Ala
        435


<210>  605
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 186GSG4S  Fc- (G4S)4 BCMA 405

<400>  605

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30
```

```
Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
```

245 250 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
260 265 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
275 280 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
290 295 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305 310 315 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
325 330 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
340 345 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385 390 395 400

Leu Lys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
405 410 415

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
420 425 430

Lys Gly Thr Asn Ala
435

<210> 606
<211> 437
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)4 BCMA 381

<400> 606

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140


Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160


Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175


Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190
```

```
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ala Leu
385                 390                 395                 400

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
```

405 410 415

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
420 425 430

Lys Gly Thr Asn Ala
435

<210> 607
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)4 BCMA 411

<400> 607

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys

```
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350
```

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385 390 395 400

Leu Arg Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
405 410 415

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
420 425 430

Lys Gly Thr Asn Ala
435

<210> 608
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)4 BCMA 405

<400> 608

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

```
Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
```

```
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400

Leu Lys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
            420                 425                 430

Lys Gly Thr Asn Ala
        435


<210>  609
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA 381 GSG4S Fc- (G4S)4 CTLA4 186

<400>  609

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ala Leu
1               5                   10                  15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
```

```
            20                  25                  30

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240
```

```
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400

Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro Tyr Leu
                405                 410                 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420                 425                 430

Cys Pro Asp Ser Asp
        435
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<210> 610

<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 186 GSG4S Fc (G4S)4 TACI 541

<400> 610

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
165 170 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

```
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
385                 390                 395                 400
```

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
405 410 415

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
420 425

<210> 611
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)4 TACI 541

<400> 611

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

```
Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
```

```
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
385                 390                 395                 400

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425

<210>  612
<211>  427
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 186 GSG4S Fc (G4S)4 (TACI 542

<400>  612

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
```

```
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320
```

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
325 330 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
340 345 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
385 390 395 400

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
405 410 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
420 425

<210> 613
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)4 (TACI 542

<400> 613

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

```
Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
```

```
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425


<210>  614
<211>  427
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 542 GSG4S Fc (G4S)4 (CTLA4 186

<400>  614

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
```

```
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Ser Gly Gly Gly
        35                  40                  45

Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
    50                  55                  60

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
65                  70                  75                  80

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                85                  90                  95

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            100                 105                 110

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        115                 120                 125

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    130                 135                 140

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
145                 150                 155                 160

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                165                 170                 175

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            180                 185                 190

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        195                 200                 205

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    210                 215                 220

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
225                 230                 235                 240
```

```
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                245                 250                 255

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            260                 265                 270

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
    290                 295                 300

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
305                 310                 315                 320

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
                325                 330                 335

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
            340                 345                 350

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
        355                 360                 365

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
    370                 375                 380

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
385                 390                 395                 400

Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
                405                 410                 415

Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
            420                 425
```

<210> 615
<211> 460
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 516 (G4S)2 Fc (G4S)2 CTLA 4 668

<400> 615

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Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                  10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45


Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60


Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80


Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
                85                  90                  95


Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
            100                 105                 110


Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        115                 120                 125


Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    130                 135                 140


His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
145                 150                 155                 160


Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                165                 170                 175


Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            180                 185                 190


Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
```

```
        195                 200                 205

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    210                 215                 220

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
225                 230                 235                 240

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                245                 250                 255

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            260                 265                 270

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        275                 280                 285

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    290                 295                 300

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
305                 310                 315                 320

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
                325                 330                 335

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
            340                 345                 350

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
        355                 360                 365

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
    370                 375                 380

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
385                 390                 395                 400

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
                405                 410                 415
```

```
Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met
            420                 425                 430


Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
        435                 440                 445


Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln
    450                 455                 460


<210>  616
<211>  421
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 528  (G4S)2 Fc (G4S)2 CTLA 4 WT ECD 1

<400>  616

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15


Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30


Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Gly Gly Gly Ser
        35                  40                  45


Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    50                  55                  60


Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
65                  70                  75                  80


Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                85                  90                  95


Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            100                 105                 110


Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        115                 120                 125
```

```
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    130                 135                 140

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
145                 150                 155                 160

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                165                 170                 175

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            180                 185                 190

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        195                 200                 205

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    210                 215                 220

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
225                 230                 235                 240

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                245                 250                 255

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            260                 265                 270

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        275                 280                 285

Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala Val
    290                 295                 300

Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala
305                 310                 315                 320

Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala
                325                 330                 335

Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn
```

340 345 350

Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly
355 360 365

Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly
370 375 380

Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu
385 390 395 400

Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys
405 410 415

Pro Asp Ser Asp Gln
420

<210> 617
<211> 421
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (G4S)2 Fc (G4S)2 CTLA 4 668

<400> 617

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
50 55 60

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
65 70 75 80

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

```
                85                  90                  95

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            100                 105                 110

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        115                 120                 125

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    130                 135                 140

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
145                 150                 155                 160

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                165                 170                 175

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            180                 185                 190

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        195                 200                 205

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    210                 215                 220

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
225                 230                 235                 240

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                245                 250                 255

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            260                 265                 270

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        275                 280                 285

Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala Val
    290                 295                 300
```

```
Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala
305                 310                 315                 320


Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala
                325                 330                 335


Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn
            340                 345                 350


Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly
        355                 360                 365


Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly
    370                 375                 380


Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu
385                 390                 395                 400


Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser
                405                 410                 415


Pro Asp Ser Asp Gln
            420


<210>  618
<211>  253
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 516  (EAAAK)6 CTLA 4 WT ECD 1

<400>  618

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45
```

```
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
                85                  90                  95

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
            100                 105                 110

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
        115                 120                 125

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
    130                 135                 140

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
145                 150                 155                 160

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
                165                 170                 175

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
            180                 185                 190

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
        195                 200                 205

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
    210                 215                 220

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Asp
225                 230                 235                 240

Tyr Lys Asp Asp Asp Asp Lys His His His His His His
                245                 250
```

<210> 619

<211> 253
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 516 (EAAAK)6 CTLA 4 668

<400> 619

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
85 90 95

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
100 105 110

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
115 120 125

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
130 135 140

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
145 150 155 160

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
165 170 175

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr

```
            180                 185                 190

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
        195                 200                 205

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
    210                 215                 220

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln Asp
225                 230                 235                 240

Tyr Lys Asp Asp Asp Asp Lys His His His His His His
                245                 250
```

<210> 620
<211> 214
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (EAAAK)6 CTLA 4 WT ECD 1

<400> 620

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Glu Ala Ala Ala Lys
        35                  40                  45

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
    50                  55                  60

Ala Ala Ala Lys Glu Ala Ala Ala Lys Lys Ala Met His Val Ala Gln
65                  70                  75                  80

Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys
                85                  90                  95

Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu
```

```
            100                 105                 110

Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met
        115                 120                 125

Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr
    130                 135                 140

Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met
145                 150                 155                 160

Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro
                165                 170                 175

Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro
            180                 185                 190

Glu Pro Cys Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
        195                 200                 205

His His His His His His
    210
```

<210> 621
<211> 214
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (EAAAK)6 CTLA 4 668

<400> 621

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Glu Ala Ala Ala Lys
        35                  40                  45

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
```

```
    50                  55                  60

Ala Ala Ala Lys Glu Ala Ala Ala Lys Lys Ala Met His Val Ala Gln
65                  70                  75                  80

Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys
                85                  90                  95

Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu
            100                 105                 110

Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met
        115                 120                 125

Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr
    130                 135                 140

Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met
145                 150                 155                 160

Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro
                165                 170                 175

Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro
            180                 185                 190

Glu Pro Ser Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
        195                 200                 205

His His His His His His
    210


<210>  622
<211>  238
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 516  (G4S)3 CTLA 4 668

<400>  622

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
```

```
1               5                   10                  15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                85                  90                  95

Ser Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser
            100                 105                 110

Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala
        115                 120                 125

Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr
    130                 135                 140

Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu
145                 150                 155                 160

Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu
                165                 170                 175

Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys
            180                 185                 190

Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly
        195                 200                 205

Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln
    210                 215                 220
```

Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
225 230 235

<210> 623
<211> 199
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (G4S)3 CTLA 4 668

<400> 623

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala
50 55 60

Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val
65 70 75 80

Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val
85 90 95

Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr
100 105 110

Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly
115 120 125

Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala
130 135 140

Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro
145 150 155 160

```
Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp
                165                 170                 175


Pro Glu Pro Ser Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp
            180                 185                 190


Lys His His His His His His
        195


<210>  624
<211>  460
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 WT ECD 1 (G4S)2 Fc (G4S)2 TACI 516

<400>  624

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Gly
        115                 120                 125
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
    130                 135                 140

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145                 150                 155                 160

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
```

340 345 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys
370 375 380

Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys
385 390 395 400

Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys
405 410 415

Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu
420 425 430

Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys
435 440 445

Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
450 455 460

<210> 625
<211> 460
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA 4 668 (G4S)2 Fc (G4S)2 TACI 516

<400> 625

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp

```
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
    130                 135                 140

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145                 150                 155                 160

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270
```

```
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            340                 345                 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys
    370                 375                 380

Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys
385                 390                 395                 400

Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys
                405                 410                 415

Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu
            420                 425                 430

Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys
        435                 440                 445

Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455                 460
```

<210> 626
<211> 421
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 (G4S)2 Fc (G4S)2 TACI 528

<400> 626

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
    130                 135                 140


Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145                 150                 155                 160


Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175


Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190


Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
```

```
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            340                 345                 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg Lys
    370                 375                 380

Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys
385                 390                 395                 400

Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu
                405                 410                 415
```

Asn Lys Leu Arg Ser
420

<210> 627
<211> 421
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA 4 668 (G4S)2 Fc (G4S)2 TACI 528

<400> 627

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
130 135 140

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145 150 155 160

```
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            340                 345                 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg Lys
```

370 375 380

Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys
385 390 395 400

Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu
405 410 415

Asn Lys Leu Arg Ser
420

<210> 628
<211> 294
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc (G4S)2 BCMA (356)

<400> 628

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

```
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225                 230                 235                 240

Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
                245                 250                 255

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            260                 265                 270

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        275                 280                 285

Val Lys Gly Thr Asn Ala
    290
```

<210> 629
<211> 294
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc (G4S)2 BCMA (357)

<400> 629

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
```

```
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225                 230                 235                 240

Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
                245                 250                 255

Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            260                 265                 270

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        275                 280                 285

Val Lys Gly Thr Asn Ala
    290
```

<210> 630
<211> 323
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc (G4S)2 TACI (516)

<400> 630

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80
```

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225                 230                 235                 240

Ser Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu
                245                 250                 255

Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln
            260                 265                 270

Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln
        275                 280                 285

Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser
```

```
    290                 295                 300

Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys
305                 310                 315                 320

Leu Arg Ser
```

<210> 631
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)2 BCMA 356

<400> 631

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
```

```
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350
```

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355   360   365

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
    370   375   380

Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg
385   390   395   400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
                405   410   415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
            420   425

<210> 632
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 92 GSG4S Fc (G4S)2 BCMA 356

<400> 632

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50   55   60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65   70   75   80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

```
Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
```

```
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
    370                 375                 380

Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg
385                 390                 395                 400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
                405                 410                 415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
            420                 425


<210>  633
<211>  427
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 165 GSG4S Fc (G4S)2 BCMA 356

<400>  633

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp
```

```
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270
```

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275   280   285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290   295   300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305   310   315   320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325   330   335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340   345   350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355   360   365

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
    370   375   380

Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg
385   390   395   400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
                405   410   415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
            420   425

<210> 634
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD 1 GSG4S Fc (G4S)2 BCMA 357

<400> 634

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

```
Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
```

225 230 235 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
245 250 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
260 265 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
275 280 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
290 295 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305 310 315 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
325 330 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
340 345 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
370 375 380

Glu Tyr Phe Asp Ser Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg
385 390 395 400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
405 410 415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
420 425

<210> 635
<211> 427
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 92 GSG4S Fc (G4S)2 BCMA 357

<400> 635

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
165 170 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
180 185 190

```
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
    370                 375                 380

Glu Tyr Phe Asp Ser Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg
385                 390                 395                 400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
```

405 410 415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
420 425

<210> 636
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 165 GSG4S Fc (G4S)2 BCMA 357

<400> 636

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu

```
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365
```

Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn
370 375 380

Glu Tyr Phe Asp Ser Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg
385 390 395 400

Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala
405 410 415

Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
420 425

<210> 637
<211> 456
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA 4 92 GSG4S Fc (G4S)2 TACI 516

<400> 637

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

```
Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
```

```
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys Pro Glu Glu Gln
    370                 375                 380

Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
385                 390                 395                 400

Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                405                 410                 415

Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
            420                 425                 430

Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
        435                 440                 445

Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455


<210>  638
<211>  456
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA 4 165 GSG4S Fc (G4S)2 TACI 516

<400>  638

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
```

```
        35                  40                  45

Val Cys Ala Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255
```

```
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys Pro Glu Glu Gln
    370                 375                 380

Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
385                 390                 395                 400

Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                405                 410                 415

Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
            420                 425                 430

Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
        435                 440                 445

Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455
```

<210> 639

<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 92 GSG4S Fc K (G4S)4 BCMA 357

<400> 639

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
165 170 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

```
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400
```

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
405 410 415

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
420 425 430

Lys Gly Thr Asn Ala
435

<210> 640
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 92 GSG4S Fc K (G4S)4 TACI 528

<400> 640

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

```
Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
```

```
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425


<210>  641
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 113 GSG4S Fc K (G4S)4 BCMA 357

<400>  641

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
```

```
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300
```

```
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380


Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
385                 390                 395                 400


Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
                405                 410                 415


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
            420                 425                 430


Lys Gly Thr Asn Ala
        435


<210>  642
<211>  427
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 113 GSG4S Fc H (G4S)4 TACI 528

<400>  642

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30
```

```
Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
```

```
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425
```

<210> 643
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 113 GSG4S Fc (G4S)4 TACI 535 (68-110)

<400> 643

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205
```

```
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400

Gly Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
```

420 425

<210> 644
<211> 466
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 113 GSG4S Fc (G4S)4 TACI 535 (29-110)

<400> 644

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

```
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380
```

```
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
385                 390                 395                 400


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
                405                 410                 415


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
            420                 425                 430


Lys Phe Tyr Asp His Leu Leu Gly Asp Cys Ile Ser Cys Ala Ser Ile
        435                 440                 445


Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
    450                 455                 460


Arg Ser
465


<210>  645
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA 411 GSG4S Fc (G4S)4 CTLA4 186

<400>  645

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Arg Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60


Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80
```

```
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
```

```
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400

Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro Tyr Leu
                405                 410                 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420                 425                 430

Cys Pro Asp Ser Asp
        435


<210>  646
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA 405 GSG4S Fc (G4S)4 CTLA4 186

<400>  646

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Lys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
```

```
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240
```

```
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400

Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro Tyr Leu
                405                 410                 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420                 425                 430

Cys Pro Asp Ser Asp
        435
```

<210> 647

<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 406 GSG4S Fc (G4S)4 CTLA4 186

<400> 647

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                  10                  15


Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60


Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80


Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95


Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110


His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125


Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140


Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160


Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175


Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
```

```
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400
```

Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro Tyr Leu
405 410 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
420 425 430

Cys Pro Asp Ser Asp
435

<210> 648
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 541 GSG4S Fc (G4S)4 CTLA4 186

<400> 648

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser Gly Ser Gly Gly Gly
35 40 45

Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
50 55 60

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
65 70 75 80

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
85 90 95

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
100 105 110

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
115 120 125

```
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    130                 135                 140

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
145                 150                 155                 160

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                165                 170                 175

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            180                 185                 190

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        195                 200                 205

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    210                 215                 220

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
225                 230                 235                 240

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                245                 250                 255

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            260                 265                 270

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
    290                 295                 300

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
305                 310                 315                 320

Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg
                325                 330                 335

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
```

340 345 350

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
355 360 365

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
370 375 380

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met
385 390 395 400

Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
405 410 415

Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
420 425

<210> 649
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 381 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400> 649

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ala Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
50 55 60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65 70 75 80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

```
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300
```

```
Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320


Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335


Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350


Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365


Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380


Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400


Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr
                405                 410                 415


Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420                 425                 430


Cys Pro Asp Ser Asp
        435


<210>  650
<211>  437
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  BCMA 411 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400>  650

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Arg Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30
```

```
Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
```

```
               245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400

Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr
                405                 410                 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420                 425                 430

Cys Pro Asp Ser Asp
        435
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<210> 651
<211> 437
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 405 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400> 651

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Lys Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
50 55 60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65 70 75 80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
85 90 95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
100 105 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
115 120 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
130 135 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145 150 155 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
165 170 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
180 185 190

```
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370                 375                 380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385                 390                 395                 400

Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr
```

405 410 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
420 425 430

Cys Pro Asp Ser Asp
435

<210> 652
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 406 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400> 652

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
50 55 60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65 70 75 80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
85 90 95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
100 105 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
115 120 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

```
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350
```

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355   360   365

Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
    370   375   380

Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr
385   390   395   400

Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr
                405   410   415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
            420   425   430

Cys Pro Asp Ser Asp
        435

<210> 653
<211> 427
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 541 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400> 653

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser Gly Ser Gly Gly Gly
        35   40   45

Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
    50   55   60

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
65   70   75   80

```
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                85                  90                  95

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            100                 105                 110

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        115                 120                 125

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    130                 135                 140

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
145                 150                 155                 160

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                165                 170                 175

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            180                 185                 190

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        195                 200                 205

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    210                 215                 220

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
225                 230                 235                 240

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                245                 250                 255

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            260                 265                 270

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
```

```
    290                 295                 300

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
305                 310                 315                 320

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
                325                 330                 335

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
            340                 345                 350

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
        355                 360                 365

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
    370                 375                 380

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met
385                 390                 395                 400

Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
                405                 410                 415

Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
            420                 425


<210>  654
<211>  427
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 542 GSG4S Fc (G4S)4 CTLA4 WT ECD 1

<400>  654

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Ser Gly Gly Gly
```

```
        35                  40                  45

Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
    50                  55                  60

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
65                  70                  75                  80

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                85                  90                  95

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            100                 105                 110

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        115                 120                 125

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    130                 135                 140

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
145                 150                 155                 160

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                165                 170                 175

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            180                 185                 190

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        195                 200                 205

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    210                 215                 220

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
225                 230                 235                 240

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                245                 250                 255
```

```
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            260                 265                 270

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
    290                 295                 300

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
305                 310                 315                 320

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg
                325                 330                 335

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
            340                 345                 350

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
        355                 360                 365

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
    370                 375                 380

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met
385                 390                 395                 400

Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
                405                 410                 415

Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
            420                 425
```

<210> 655
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 357 (G4S)3 CTLA4 92 GSG4S Fc

<400> 655

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    50                  55                  60

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln
65                  70                  75                  80

Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys
                85                  90                  95

Glu Tyr Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu
            100                 105                 110

Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met
        115                 120                 125

Met Gly Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile Cys Thr Gly Thr
    130                 135                 140

Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Arg Gly Leu Arg Ala Met
145                 150                 155                 160

Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro
                165                 170                 175

Tyr Leu Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro
            180                 185                 190

Glu Pro Cys Pro Asp Ser Asp Gly Ser Gly Gly Gly Gly Ser Glu Pro
        195                 200                 205

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
```

```
    210                 215                 220

Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
225                 230                 235                 240

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                245                 250                 255

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            260                 265                 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        275                 280                 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    290                 295                 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
305                 310                 315                 320

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                325                 330                 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            340                 345                 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        355                 360                 365

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    370                 375                 380

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
385                 390                 395                 400

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                405                 410                 415

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            420                 425                 430
```

Ser Leu Ser Pro Gly
        435

<210> 656
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA 357 GSG4S Fc (G4S)3 CTLA4 92

<400> 656

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1   5   10   15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20   25   30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35   40   45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50   55   60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65   70   75   80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85   90   95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100   105   110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115   120   125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130   135   140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145   150   155   160

```
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala Gln Pro Ala
305                 310                 315                 320

Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr
                325                 330                 335

Ala Ser Pro Trp Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln
            340                 345                 350

Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly
        355                 360                 365

Ser Glu Leu Thr Phe Pro Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser
```

370 375 380

Gly Asn Gln Val Asn Leu Thr Ile Arg Gly Leu Arg Ala Met Asp Thr
385 390 395 400

Gly Leu Tyr Ile Cys Lys Val Glu Gln Met Tyr Pro Pro Pro Tyr Leu
405 410 415

Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro
420 425 430

Cys Pro Asp Ser Asp
435

<210> 657
<211> 437
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 92 (G4S)4 BCMA 357 GSG4S Fc

<400> 657

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr

```
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp
145                 150                 155                 160

Ser Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn
                165                 170                 175

Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn
            180                 185                 190

Ser Val Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro
        195                 200                 205

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
    210                 215                 220

Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
225                 230                 235                 240

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                245                 250                 255

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            260                 265                 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        275                 280                 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    290                 295                 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
305                 310                 315                 320
```

```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                325                 330                 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            340                 345                 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        355                 360                 365

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    370                 375                 380

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
385                 390                 395                 400

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                405                 410                 415

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            420                 425                 430

Ser Leu Ser Pro Gly
        435


<210>  658
<211>  432
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 92 GSG4S Fc (G4S)3 BCMA 357

<400>  658

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

```
Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
```

```
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Gln Met Ala Gly
    370                 375                 380

Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu Tyr Ala Cys Ile
385                 390                 395                 400

Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln
                405                 410                 415

Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
            420                 425                 430


<210>  659
<211>  442
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 92 GSG4S Fc (G4S)5 BCMA 357

<400>  659

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
```

```
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220
```

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240


Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255


Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270


Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285


Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300


Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380


Gly Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu
385                 390                 395                 400


Tyr Phe Asp Ser Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys
                405                 410                 415


Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser
            420                 425                 430


Val Thr Asn Ser Val Lys Gly Thr Asn Ala
```

435 440

<210> 660
<211> 291
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> BCMA (357) GSG4S Fc H

<400> 660

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
50 55 60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65 70 75 80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
85 90 95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
100 105 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
115 120 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
130 135 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145 150 155 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

```
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly
    290


<210>  661
<211>  294
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  Fc (G4S)4 TACI (541)

<400>  661

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
```

```
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225                 230                 235                 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg
                245                 250                 255
```

Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu Arg Asp Cys Ile Ser
            260   265   270

Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Asp Phe Cys
        275   280   285

Glu Asn Lys Leu Arg Ser
    290

<210> 662
<211> 364
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 (92) GSG4S Fc K

<400> 662

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50   55   60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65   70   75   80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115   120   125

```
Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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            340                 345                 350


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360


<210>  663
<211>  364
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  CTLA4 (113)  GSG4S FcK

<400>  663

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140


Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
```

```
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360
```

<210> 664
<211> 510
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 (92) GSG4S Fc K (G4S)4 (92)

<400> 664

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
165 170 175

```
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
```

385 390 395 400

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
405 410 415

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
420 425 430

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
435 440 445

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
450 455 460

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
465 470 475 480

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
485 490 495

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
500 505 510

<210> 665
<211> 30
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 665

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
20 25 30

<210> 666
<211> 293
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> FULL LENGTH TACI

<400> 666

```
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1               5                  10                  15


Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
            20                  25                  30


Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
        35                  40                  45


Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
    50                  55                  60


Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65                  70                  75                  80


His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
                85                  90                  95


Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
            100                 105                 110


Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
        115                 120                 125


Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
    130                 135                 140


Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145                 150                 155                 160


Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
                165                 170                 175


Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
            180                 185                 190


Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
```

```
        195                 200                 205

Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
    210                 215                 220

Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225                 230                 235                 240

Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
                245                 250                 255

Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
            260                 265                 270

His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
        275                 280                 285

Gly Gly Pro Gly Ala
    290


<210>  667
<211>  184
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  FULL LENGTH BCMA

<400>  667

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1               5                   10                  15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            20                  25                  30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        35                  40                  45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
    50                  55                  60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
```

65 70 75 80

Asn Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
130 135 140

Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145 150 155 160

Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
165 170 175

Ile Glu Lys Ser Ile Ser Ala Arg
180

<210> 668
<211> 126
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 WT ECD C122S

<400> 668

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp

50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp
115 120 125

<210> 669
<211> 230
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Fc K S139C, D141E, L143M, T151W

<400> 669

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

```
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro
225                 230


<210>  670
<211>  230
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  Fc H Y134C, D141E, L143M, T151S, L153A

<400>  670

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
```

```
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro
225                 230
```

<210> 671
<211> 25
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> LINKER

<400> 671

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 672
<211> 126
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 A31Y/L106E

<400> 672

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp

115 120 125

<210> 673
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P ECD

<400> 673

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Pro Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 674
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85E, K98T ECD

<400> 674

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Glu Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Thr Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 675
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87L, K98T ECD

<400> 675

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Leu Ser Cys Ala Ser Ile Cys Gly Gln His Pro Thr Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 676
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 676

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 677
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI C86Y ECD

<400> 677

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Tyr Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 678
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82P, I87L ECD

<400> 678

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Pro Leu
1 5 10 15

Arg Asp Cys Leu Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 679
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI G76S, P97S ECD

<400> 679

Ser Leu Ser Cys Arg Lys Glu Gln Ser Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Ser Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 680
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L83S, F103S ECD

<400> 680

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Ser
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Ser Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 681
<211> 43
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI L82H ECD

<400> 681

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His His Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 682
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI D85V ECD

<400> 682

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg

20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Val Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 683
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI E74V ECD

<400> 683

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Val Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 684

<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84L ECD

<400> 684

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Leu Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 685
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84L, F103Y ECD

<400> 685

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Glu Phe Tyr Asp His Leu Leu Leu Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Tyr Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 686
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F, Q99E ECD

<400> 686

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Lys Phe Phe Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Glu Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 687
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Y79F ECD

<400> 687

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Phe Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 688
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84G ECD

<400> 688

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Gly Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu

65 70 75 80

Arg Ser

<210> 689
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI A101D ECD

<400> 689

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 690
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, R84Q ECD

<400> 690

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

```
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Glu Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
```

<210> 691
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D ECD

<400> 691

```
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Glu Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser
```

<210> 692
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, F78Y, Y102D ECD

<400> 692

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Glu Tyr Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Ala Asp Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 693
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75E, R84Q ECD

<400> 693

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Glu Gly

35 40 45

Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 694
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI Q75R, R84G, I92V ECD

<400> 694

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Arg Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Gly Asp Cys Ile Ser Cys Ala Ser Val
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 695
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, A101D, Y102D ECD

<400> 695

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Glu Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Asp Asp Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 696
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q ECD

<400> 696

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 697
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, S88N, A101D ECD

<400> 697

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Asn Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 698
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E ECD

<400> 698

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu

1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Glu Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 699
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI R84Q, F103V ECD

<400> 699

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Val Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser

<210> 700
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI K77E, Q95R, A101D ECD

<400> 700

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Glu Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Arg His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 701
<211> 82
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI I87M, A101D ECD

<400> 701

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1   5   10   15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20   25   30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35   40   45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Met Ser Cys Ala Ser Ile
    50   55   60

Cys Gly Gln His Pro Lys Gln Cys Asp Tyr Phe Cys Glu Asn Lys Leu
65   70   75   80

Arg Ser

<210> 702
<211> 660
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> CTLA4 113 GSG4S Fc K/ BCMA 357 GSG4S Fc H

<400> 702

Lys Ala Met His Val Ala Gln Pro Ala Val Val Phe Ala Ser Ser His
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65   70   75   80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100   105   110

```
Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            260                 265                 270

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
```

```
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Leu Gln Met Ala
        355                 360                 365

Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu Tyr Ala Cys
    370                 375                 380

Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys
385                 390                 395                 400

Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn
                405                 410                 415

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Glu Pro
            420                 425                 430

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        435                 440                 445

Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    450                 455                 460

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
465                 470                 475                 480

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                485                 490                 495

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            500                 505                 510

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        515                 520                 525

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    530                 535                 540
```

```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
545                 550                 555                 560


Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
                565                 570                 575


Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile
            580                 585                 590


Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        595                 600                 605


Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys
    610                 615                 620


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
625                 630                 635                 640


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                645                 650                 655


Ser Leu Ser Pro
            660


<210>  703
<211>  247
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  TACI 516  (EAAAK)6 CTLA 4 WT ECD 1

<400>  703

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45
```

```
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
                85                  90                  95

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
            100                 105                 110

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
        115                 120                 125

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
    130                 135                 140

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
145                 150                 155                 160

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
                165                 170                 175

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
            180                 185                 190

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
        195                 200                 205

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
    210                 215                 220

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Asp
225                 230                 235                 240

Tyr Lys Asp Asp Asp Asp Lys
                245
```

<210> 704

<211> 247
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 516 (EAAAK)6 CTLA 4 668

<400> 704

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
85 90 95

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
100 105 110

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
115 120 125

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
130 135 140

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
145 150 155 160

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
165 170 175

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr

```
            180                 185                 190

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
        195                 200                 205

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
    210                 215                 220

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Asp
225                 230                 235                 240

Tyr Lys Asp Asp Asp Asp Lys
                245
```

<210> 705
<211> 208
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (EAAAK)6 CTLA 4 WT ECD 1

<400> 705

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Glu Ala Ala Ala Lys
        35                  40                  45

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
    50                  55                  60

Ala Ala Ala Lys Glu Ala Ala Ala Lys Lys Ala Met His Val Ala Gln
65                  70                  75                  80

Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys
                85                  90                  95

Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu
```

```
            100                 105                 110

Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met
        115                 120                 125

Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr
    130                 135                 140

Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met
145                 150                 155                 160

Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro
                165                 170                 175

Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro
            180                 185                 190

Glu Pro Cys Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
        195                 200                 205
```

<210> 706
<211> 208
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (EAAAK)6 CTLA 4 668

<400> 706

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Glu Ala Ala Ala Lys
        35                  40                  45

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
    50                  55                  60

Ala Ala Ala Lys Glu Ala Ala Ala Lys Lys Ala Met His Val Ala Gln
```

65 70 75 80

Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys
85 90 95

Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu
100 105 110

Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met
115 120 125

Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr
130 135 140

Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met
145 150 155 160

Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro
165 170 175

Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro
180 185 190

Glu Pro Ser Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
195 200 205

<210> 707
<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 516 (G4S)3 CTLA 4 668

<400> 707

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly

```
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                85                  90                  95

Ser Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser
            100                 105                 110

Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala
        115                 120                 125

Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr
    130                 135                 140

Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu
145                 150                 155                 160

Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu
                165                 170                 175

Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys
            180                 185                 190

Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly
        195                 200                 205

Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Ser Pro Asp Ser Asp Gln
    210                 215                 220

Asp Tyr Lys Asp Asp Asp Asp Lys
225                 230
```

<210> 708
<211> 193
<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>
<223> TACI 528 (G4S)3 CTLA 4 668

<400> 708

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                  10                  15


Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30


Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Gly Gly Gly Gly Ser
        35                  40                  45


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met His Val Ala
    50                  55                  60


Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val
65                  70                  75                  80


Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val
                85                  90                  95


Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr
            100                 105                 110


Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly
        115                 120                 125


Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala
    130                 135                 140


Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro
145                 150                 155                 160


Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp
                165                 170                 175


Pro Glu Pro Ser Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp Asp Asp
            180                 185                 190
```

Lys

<210> 709
<211> 166
<212> PRT
<213> artificial sequence

<220>
<223> TACI ECD (1-166)

<400> 709

```
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1               5                  10                  15


Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
            20                  25                  30


Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
        35                  40                  45


Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
    50                  55                  60


Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65                  70                  75                  80


His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
                85                  90                  95


Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
            100                 105                 110


Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
        115                 120                 125


Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
    130                 135                 140


Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145                 150                 155                 160
```

Ala Leu Val Tyr Ser Thr
                165

<210> 710
<211> 54
<212> PRT
<213> artificial sequence

<220>
<223> BCMA ECD (1-54)

<400> 710

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1   5   10   15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            20   25   30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        35   40   45

Val Lys Gly Thr Asn Ala
    50

<210> 711
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> 1xEAAAK

<400> 711

Glu Ala Ala Ala Lys
1   5

<210> 712
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> 2xEAAAK

<400> 712

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10

<210> 713
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> 3xEAAAK

<400> 713

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

<210> 714
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> 4xEAAAK

<400> 714

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys
20

<210> 715
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> 5xEAAAK

<400> 715

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Glu Ala Ala Ala Lys
20 25

<210> 716
<211> 232
<212> PRT
<213> artificial sequence

<220>
<223> knob Fc

<400> 716

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175
```

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180   185   190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195   200   205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210   215   220

Ser Leu Ser Leu Ser Pro Gly Lys
225   230

<210> 717
<211> 232
<212> PRT
<213> artificial sequence

<220>
<223> hole Fc

<400> 717

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 718
<211> 81
<212> PRT
<213> artificial sequence

<220>
<223> atacicept (TACI portion, 30-110)

<400> 718

Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly
1 5 10 15

Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr
20 25 30

Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys
35 40 45

Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys
    50   55   60

Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg
65   70   75   80

Ser

<210> 719
<211> 106
<212> PRT
<213> artificial sequence

<220>
<223> telitacicept (TACI portion, 13-118)

<400> 719

Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
1   5   10   15

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
            20   25   30

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
        35   40   45

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
    50   55   60

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
65   70   75   80

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
                85   90   95

Arg Ser Pro Val Asn Leu Pro Pro Glu Leu
            100   105

<210> 720
<211> 313
<212> PRT

<213> artificial sequence

<220>
<223> atacicept

<400> 720

```
Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly
1               5                  10                  15


Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr
            20                  25                  30


Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys
        35                  40                  45


Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys
    50                  55                  60


Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg
65                  70                  75                  80


Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                85                  90                  95


Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            100                 105                 110


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        115                 120                 125


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    130                 135                 140


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
145                 150                 155                 160


Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                165                 170                 175


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            180                 185                 190
```

```
Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        195                 200                 205


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    210                 215                 220


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
225                 230                 235                 240


Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                245                 250                 255


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            260                 265                 270


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        275                 280                 285


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    290                 295                 300


Lys Ser Leu Ser Leu Ser Pro Gly Lys
305                 310


<210>  721
<211>  13
<212>  PRT
<213>  artificial sequence

<220>
<223>  linker

<400>  721

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala
1               5                   10


<210>  722
<211>  231
<212>  PRT
<213>  artificial sequence

<220>
<223>  Fc with C220S/E233P/L234V/L235A/G236del/S267K
```

<400> 722

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20                  25                  30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35                  40                  45

Asp Val Lys His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    50                  55                  60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65                  70                  75                  80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85                  90                  95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            100                 105                 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    130                 135                 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        195                 200                 205
```

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210   215   220

Leu Ser Leu Ser Pro Gly Lys
225   230

<210> 723
<211> 231
<212> PRT
<213> artificial sequence

<220>
<223> Fc (C5S (C220S), R77C, (R292C), N82G (N297G), V87C (V302C),
       L232del (K447del))

<400> 723

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
65   70   75   80

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115   120   125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130   135   140

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly
225                 230


<210>  724
<211>  231
<212>  PRT
<213>  artificial sequence

<220>
<223>  Fc with C220S/L234A/L235E/G237A/K447del

<400>  724

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80
```

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly
225                 230
```

<210> 725
<211> 230
<212> PRT
<213> artificial sequence

<220>
<223> Fc with C220S/E233P/L234V/L235A/G236del/S267K/K447del

<400> 725

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15
```

```
Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20                  25                  30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35                  40                  45

Asp Val Lys His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    50                  55                  60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65                  70                  75                  80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85                  90                  95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            100                 105                 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    130                 135                 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        195                 200                 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
```

Leu Ser Leu Ser Pro Gly
225 230

<210> 726
<211> 235
<212> PRT
<213> artificial sequence

<220>
<223> IgG2 Fc

<400> 726

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
1 5 10 15

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
20 25 30

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
50 55 60

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65 70 75 80

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
85 90 95

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
100 105 110

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
115 120 125

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
130 135 140

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145 150 155 160

```
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                165                 170                 175


Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
            180                 185                 190


Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        195                 200                 205


Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    210                 215                 220


Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230                 235


<210>  727
<211>  229
<212>  PRT
<213>  artificial sequence

<220>
<223>  IgG4 Fc

<400>  727

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1               5                   10                  15


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45


Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65                  70                  75                  80


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100                 105                 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115                 120                 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150                 155                 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165                 170                 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210                 215                 220

Leu Ser Leu Gly Lys
225
```

<210> 728
<211> 229
<212> PRT
<213> artificial sequence

<220>
<223> IgG4 Fc S228P

<400> 728

```
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1               5                   10                  15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30
```

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65                  70                  75                  80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100                 105                 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115                 120                 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150                 155                 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165                 170                 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210                 215                 220

Leu Ser Leu Gly Lys
225
```

<210> 729
<211> 231

<212> PRT
<213> artificial sequence

<220>
<223> Fc K chain

<400> 729

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Lys Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195   200   205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210   215   220

Ser Leu Ser Leu Ser Pro Gly
225   230

<210> 730
<211> 231
<212> PRT
<213> artificial sequence

<220>
<223> Fc D chain

<400> 730

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115   120   125

```
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Asp Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly
225                 230
```

<210> 731
<211> 237
<212> PRT
<213> artificial sequence

<220>
<223> Green Fluorescent protein

<400> 731

```
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1               5                   10                  15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
            20                  25                  30

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
        35                  40                  45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
    50                  55                  60
```

```
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
65                  70                  75                  80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
                85                  90                  95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
            100                 105                 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
        115                 120                 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
    130                 135                 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
145                 150                 155                 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
                165                 170                 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
            180                 185                 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
        195                 200                 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
    210                 215                 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
```

<210> 732
<211> 237
<212> PRT
<213> artificial sequence

<220>
<223> eGFP

<400> 732

```
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1               5                  10                  15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
            20                  25                  30

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
        35                  40                  45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr
    50                  55                  60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
65                  70                  75                  80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
                85                  90                  95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
            100                 105                 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
        115                 120                 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
    130                 135                 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
145                 150                 155                 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
                165                 170                 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
            180                 185                 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
        195                 200                 205
```

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 733
<211> 239
<212> PRT
<213> artificial sequence

<220>
<223> eGFP

<400> 733

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

```
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160


Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175


Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190


Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205


Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220


Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225                 230                 235


<210>  734
<211>  45
<212>  PRT
<213>  artificial sequence

<220>
<223>  Moiety: COMP

<400>  734

Asp Leu Gly Pro Gln Met Leu Arg Glu Leu Gln Glu Thr Asn Ala Ala
1               5                   10                  15


Leu Gln Asp Val Arg Glu Leu Leu Arg Gln Gln Val Arg Glu Ile Thr
            20                  25                  30


Phe Leu Lys Asn Thr Val Met Glu Cys Asp Ala Cys Gly
        35                  40                  45


<210>  735
<211>  33
<212>  PRT
<213>  artificial sequence

<220>
<223>  Moiety: VASP
```

<400> 735

Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu Glu Val Lys Lys Glu
1   5   10   15

Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala Phe Val Gln Glu Leu
            20   25   30

Arg

<210> 736
<211> 40
<212> PRT
<213> artificial sequence

<220>
<223> Moiety: ZZ12.6

<400> 736

Asp Val Gln Ala Ile Ser Ser Thr Ile Gln Asp Leu Gln Asp Gln Val
1   5   10   15

Asp Ser Leu Ala Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp Leu
            20   25   30

Leu Thr Arg Ser Gly Gly Gly Ser
        35   40

<210> 737
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> HSA signal peptide

<400> 737

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1   5   10   15

Tyr Ser

<210> 738
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> Ig kappa light chain

<400> 738

Met Asp Met Arg Ala Pro Ala Gly Ile Phe Gly Phe Leu Leu Val Leu
1 5 10 15

Phe Pro Gly Tyr Arg Ser
20

<210> 739
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> human azurocidin preprotein signal sequence

<400> 739

Met Thr Arg Leu Thr Val Leu Ala Leu Leu Ala Gly Leu Leu Ala Ser
1 5 10 15

Ser Arg Ala

<210> 740
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 740

Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 741
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 741

Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1 5 10 15

Val Gln Cys

<210> 742
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 742

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser

<210> 743
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 743

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 744
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 744

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
1 5 10 15

Val Gln Ser

<210> 745
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 745

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 746
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 746

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1 5 10 15

Val Gln Cys

<210> 747
<211> 26
<212> PRT
<213> artificial sequence

<220>
<223> IgG heavy chain signal peptide

<400> 747

Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
1 5 10 15

Leu Val Ala Ala Pro Arg Trp Val Leu Ser
20 25

<210> 748
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> IgG Kappa light chain signal sequence

<400> 748

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Ser Gly Ala Arg Cys
20

<210> 749
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> IgG Kappa light chain signal sequence

<400> 749

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala
20

<210> 750
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> Gaussia luciferase

<400> 750

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

Ala

<210> 751
<211> 18
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Human albumin

<400> 751

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 752
<211> 18
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Human chymotrypsinogen

<400> 752

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly

<210> 753
<211> 14
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Human interleukin-2

<400> 753

Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val
1   5   10

<210> 754
<211> 15
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Human trypsinogen-2

<400> 754

Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala
1   5   10   15

<210> 755
<211> 227
<212> PRT
<213> artificial sequence

<220>
<223> Fc

<400> 755

Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu Leu Leu Gly
1   5   10   15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 756
<211> 232

<212> PRT
<213> artificial sequence

<220>
<223> Fc

<400> 756

```
Asp Pro Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala
1               5                  10                  15


Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Ala Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
```

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195   200   205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210   215   220

Ser Leu Ser Leu Ser Pro Gly Lys
225   230

<210> 757
<211> 227
<212> PRT
<213> artificial sequence

<220>
<223> Fc variant

<400> 757

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
1   5   10   15

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65   70   75   80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser Ile
            100   105   110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125

```
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 758
<211> 232
<212> PRT
<213> artificial sequence

<220>
<223> Fc variant

<400> 758

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60
```

```
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 759
<211> 427
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 759

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205
```

```
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425
```

<210> 760
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 760

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 761
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 761

Ser Leu Ser Cys Arg Lys Glu Glu Gly Glu Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 762
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 762

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 763
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 763

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 764
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 764

Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 765
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 765

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 766
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 766

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 767
<211> 43
<212> PRT
<213> artificial sequence

<220>

<223> variant TACI

<400> 767

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Tyr Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 768
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 768

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 769
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 769

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Tyr Tyr Asp His Leu Leu
1 5 10 15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 770
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 770

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Asp Tyr Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 771
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 771

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1 5 10 15

Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
20 25 30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
35 40

<210> 772
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 772

Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Asp Asp Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 773
<211> 460
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 773

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr
            20   25   30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35   40   45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50   55   60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65   70   75   80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85   90   95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
            100   105   110

```
Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
    130                 135                 140

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145                 150                 155                 160

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320
```

```
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            340                 345                 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys
    370                 375                 380

Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys
385                 390                 395                 400

Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys
                405                 410                 415

Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu
            420                 425                 430

Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys
        435                 440                 445

Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455                 460


<210>  774
<211>  460
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  774

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30
```

```
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
                85                  90                  95

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
            100                 105                 110

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        115                 120                 125

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    130                 135                 140

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
145                 150                 155                 160

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                165                 170                 175

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            180                 185                 190

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
        195                 200                 205

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    210                 215                 220

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
225                 230                 235                 240

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                245                 250                 255
```

```
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            260                 265                 270

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        275                 280                 285

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    290                 295                 300

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
305                 310                 315                 320

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Ala Met
                325                 330                 335

His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala
            340                 345                 350

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg
        355                 360                 365

Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala
    370                 375                 380

Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile
385                 390                 395                 400

Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly
                405                 410                 415

Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met
            420                 425                 430

Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr
        435                 440                 445

Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln
    450                 455                 460
```

<210> 775
<211> 238
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 775

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ala
130 135 140

Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr
145 150 155 160

Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys
165 170 175

```
Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
            180                 185                 190


Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
        195                 200                 205


Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    210                 215                 220


Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
225                 230                 235


<210>  776
<211>  238
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  776

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                   10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45


Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60


Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80


Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                85                  90                  95


Ser Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser
            100                 105                 110
```

```
Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr
        115                 120                 125


Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr
    130                 135                 140


Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu
145                 150                 155                 160


Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu
                165                 170                 175


Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys
            180                 185                 190


Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly
        195                 200                 205


Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln
    210                 215                 220


Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
225                 230                 235


<210>  777
<211>  238
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  777

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

```
Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Glu
        115                 120                 125

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Val Ala
    130                 135                 140

Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr
145                 150                 155                 160

Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys
                165                 170                 175

Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
            180                 185                 190

Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
        195                 200                 205

Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    210                 215                 220

Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
225                 230                 235
```

<210> 778
<211> 238
<212> PRT
<213> artificial sequence

<220>

<223> variant multi domain immunomodulatory molecule

<400> 778

```
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1               5                  10                  15


Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
            20                  25                  30


Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
        35                  40                  45


Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
    50                  55                  60


Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65                  70                  75                  80


Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
                85                  90                  95


Lys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser
            100                 105                 110


Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr
        115                 120                 125


Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr
    130                 135                 140


Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu
145                 150                 155                 160


Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu
                165                 170                 175


Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys
            180                 185                 190


Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly
        195                 200                 205
```

Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln
210 215 220

Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
225 230 235

<210> 779
<211> 233
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 779

Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80

Arg Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Lys Ala Met His
85 90 95

Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser
100 105 110

Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val
115 120 125

Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala
130 135 140

```
Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys
145                 150                 155                 160


Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu
                165                 170                 175


Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr
            180                 185                 190


Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val
        195                 200                 205


Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Asp Tyr Lys Asp Asp
    210                 215                 220


Asp Asp Lys His His His His His His
225                 230


<210>  780
<211>  460
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  780

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80
```

```
Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gln Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
    130                 135                 140

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro
145                 150                 155                 160

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                165                 170                 175

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            180                 185                 190

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        195                 200                 205

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    210                 215                 220

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
225                 230                 235                 240

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                245                 250                 255

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            260                 265                 270

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        275                 280                 285
```

```
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    290                 295                 300

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
305                 310                 315                 320

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                325                 330                 335

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            340                 345                 350

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys
    370                 375                 380

Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys
385                 390                 395                 400

Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys
                405                 410                 415

Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu
            420                 425                 430

Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys
        435                 440                 445

Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455                 460
```

<210> 781
<211> 456
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 781

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Trp Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Ser Glu Leu Thr Phe Pro Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Arg Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Gln Met Tyr Pro Pro Pro Tyr Leu Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220
```

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys Pro Glu Glu Gln
    370                 375                 380

Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
385                 390                 395                 400

Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                405                 410                 415

Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
            420                 425                 430
```

```
Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
        435                 440                 445


Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455


<210>  782
<211>  456
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  782

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Ser Tyr Met Met Gly Asn Glu Leu Thr Phe Pro Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Gln Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
    130                 135                 140
```

```
Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145                 150                 155                 160

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365
```

```
Ser Gly Gly Gly Gly Ser Val Ala Met Arg Ser Cys Pro Glu Glu Gln
    370                 375                 380

Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
385                 390                 395                 400

Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                405                 410                 415

Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
            420                 425                 430

Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
        435                 440                 445

Phe Cys Glu Asn Lys Leu Arg Ser
    450                 455
```

<210> 783
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 783

```
Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
1               5                   10                  15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20                  25                  30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
        35                  40
```

<210> 784
<211> 43
<212> PRT
<213> artificial sequence

<220>

<223> variant TACI

<400> 784

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Tyr Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 785
<211> 43
<212> PRT
<213> artificial sequence

<220>
<223> variant TACI

<400> 785

Ser Leu Ser Cys Arg Lys Glu Gln Gly Glu Phe Tyr Asp His Leu Leu
1   5   10   15

Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
            20   25   30

Cys Ala Asp Phe Cys Glu Asn Lys Leu Arg Ser
        35   40

<210> 786
<211> 418
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 786

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1   5   10   15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20   25   30

```
Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
    130                 135                 140

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
145                 150                 155                 160

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                165                 170                 175

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
            180                 185                 190

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
        195                 200                 205

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
    210                 215                 220

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
225                 230                 235                 240
```

```
Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
                245                 250                 255

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
            260                 265                 270

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ser Val
        275                 280                 285

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    290                 295                 300

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
305                 310                 315                 320

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                325                 330                 335

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            340                 345                 350

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365

Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg Lys Glu Gln Gly
    370                 375                 380

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
385                 390                 395                 400

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
                405                 410                 415

Arg Ser
```

<210> 787
<211> 424
<212> PRT
<213> artificial sequence

<220>

<223> variant multi domain immunomodulatory molecule

<400> 787

```
Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
    130                 135                 140


Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
145                 150                 155                 160


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                165                 170                 175


Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
            180                 185                 190


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        195                 200                 205
```

```
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    210                 215                 220

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
225                 230                 235                 240

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                245                 250                 255

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
            260                 265                 270

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        275                 280                 285

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    290                 295                 300

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
305                 310                 315                 320

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
                325                 330                 335

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            340                 345                 350

Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser
    370                 375                 380

Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
385                 390                 395                 400

Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
                405                 410                 415
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Phe Cys Glu Asn Lys Leu Arg Ser
420

<210> 788
<211> 427
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 788

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
100 105 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
130 135 140

Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu
145 150 155 160

```
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                165                 170                 175

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            180                 185                 190

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        195                 200                 205

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    210                 215                 220

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
225                 230                 235                 240

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                245                 250                 255

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            260                 265                 270

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        275                 280                 285

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    290                 295                 300

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
305                 310                 315                 320

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                325                 330                 335

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            340                 345                 350

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380
```

```
Ser Leu Ser Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu
385                 390                 395                 400


Gln Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln
                405                 410                 415


Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
            420                 425


<210>  789
<211>  418
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  789

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125
```

```
Gly Gly Gly Gly Ser Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
    130                 135                 140

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
145                 150                 155                 160

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                165                 170                 175

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
            180                 185                 190

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
        195                 200                 205

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
    210                 215                 220

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
225                 230                 235                 240

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
                245                 250                 255

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
            260                 265                 270

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ser Val
        275                 280                 285

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    290                 295                 300

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
305                 310                 315                 320

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                325                 330                 335
```

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
340 345 350

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg Lys Glu Glu Gly
370 375 380

Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser Cys Ala Ser Ile
385 390 395 400

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
405 410 415

Arg Ser

<210> 790
<211> 424
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 790

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1 5 10 15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
35 40 45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
50 55 60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65 70 75 80

```
Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
    130                 135                 140

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
145                 150                 155                 160

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                165                 170                 175

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
            180                 185                 190

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        195                 200                 205

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    210                 215                 220

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
225                 230                 235                 240

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                245                 250                 255

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
            260                 265                 270

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        275                 280                 285

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    290                 295                 300
```

```
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
305                 310                 315                 320


Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
                325                 330                 335


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            340                 345                 350


Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser
    370                 375                 380


Cys Arg Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu Gln Asp Cys
385                 390                 395                 400


Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
                405                 410                 415


Phe Cys Glu Asn Lys Leu Arg Ser
            420


<210>  791
<211>  422
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant multi domain immunomodulatory molecule

<400>  791

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45
```

```
Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
    130                 135                 140

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
145                 150                 155                 160

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                165                 170                 175

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
            180                 185                 190

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        195                 200                 205

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    210                 215                 220

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
225                 230                 235                 240

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                245                 250                 255
```

```
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
            260                 265                 270

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        275                 280                 285

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    290                 295                 300

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
305                 310                 315                 320

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                325                 330                 335

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            340                 345                 350

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg
    370                 375                 380

Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser
385                 390                 395                 400

Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys
                405                 410                 415

Glu Asn Lys Leu Arg Ser
            420
```

<210> 792
<211> 422
<212> PRT
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 792

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Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15

Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30

Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45

Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60

Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80

Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95

Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
    130                 135                 140

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
145                 150                 155                 160

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                165                 170                 175

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
            180                 185                 190

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        195                 200                 205

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    210                 215                 220
```

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
225                 230                 235                 240

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                245                 250                 255

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
            260                 265                 270

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        275                 280                 285

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    290                 295                 300

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
305                 310                 315                 320

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                325                 330                 335

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            340                 345                 350

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
        355                 360                 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Ser Cys Arg
    370                 375                 380

Lys Glu Glu Gly Lys Phe Tyr Asp His Leu Leu Gln Asp Cys Ile Ser
385                 390                 395                 400

Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys
                405                 410                 415

Glu Asn Lys Leu Arg Ser
            420
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<210> 793
<211> 1281
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 793
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ttcgtatgcg aatatgcctc tccatggaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gcagatgtac 300

ccgccacctt acctcctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agcccaaaag ctccgacaag 420

actcacacat gccccccttg tccagcgcct gaagctgagg gtgcgccctc tgtcttcctt 480

ttccccccta agccgaaaga taccctgatg atctcccgca ctcccgaagt cacatgtgtt 540

gttgtcgacg tatctcatga agatcctgag gtgaaattca actggtatgt agacggggtc 600

gaagttcata atgctaagac taagccacga gaagagcaat acaactcaac gtatcgggtg 660

gtgagcgttc tgacggttct gcaccaagat tggcttaatg gaaaagagta taagtgcaag 720

gtgtccaaca aggctcttcc ggcacccatc gaaaagacga tttccaaagc gaaaggccaa 780

cctagggaac cgcaagttta cactttgccc ccgtcaagag acgaacttac caagaatcaa 840

gtttccctga cgtgccttgt gaagggcttc taccctagcg atatagcagt tgagtgggaa 900

tctaacggcc agcccgaaaa taattataag actactccgc ccgtgctgga cagtgatggt 960

tcatttttcc tgtattcaaa actcactgtg gacaaatcta gatggcagca gggtaatgtg 1020

ttctcttgtt cagttatgca cgaggcattg cacaatcact atacgcaaaa aagtttgtct 1080

ctctctccgg gggggggtgg cggatcagga ggtggcggtt caggcggagg aggttctggg 1140

ggtgggggtt ctagtctctc ttgcaggaaa gagcaaggcg aatattacga ccatcttttg 1200

cgagactgta taagctgtgc gtctatttgt ggacaacacc ctaaacaatg tgctgatttc 1260

tgtgaaaata agcttcgatc t 1281

<210> 794
<211> 1281
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 794
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ttcgtatgcg aatatgcctc tccatggaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gcagatgtac 300

ccgccacctt acctcctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agcccaaaag ctccgacaag 420

actcacacat gccccccttg tccagcgcct gaagctgagg gtgcgccctc tgtcttcctt 480

ttccccccta agccgaaaga taccctgatg atctcccgca ctcccgaagt cacatgtgtt 540

gttgtcgacg tatctcatga agatcctgag gtgaaattca actggtatgt agacggggtc 600

gaagttcata atgctaagac taagccacga gaagagcaat acaactcaac gtatcgggtg 660

gtgagcgttc tgacggttct gcaccaagat tggcttaatg gaaaagagta taagtgcaag 720

gtgtccaaca aggctcttcc ggcacccatc gaaaagacga tttccaaagc gaaaggccaa 780

cctagggaac cgcaagttta cactttgccc ccgtcaagag acgaacttac caagaatcaa 840

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tctaacggcc agcccgaaaa taattataag actactccgc ccgtgctgga cagtgatggt 960

tcatttttcc tgtattcaaa actcactgtg gacaaatcta gatggcagca gggtaatgtg 1020

ttctcttgtt cagttatgca cgaggcattg cacaatcact atacgcaaaa aagtttgtct 1080

ctctctccgg gggggggtgg cggatcagga ggtggcggtt caggcggagg aggttctggg 1140

ggtgggggtt ctagtctctc ttgcaggaaa gaggaaggca aattttacga ccatcttttg 1200

caagactgta taagctgtgc gtctatttgt ggacaacacc ctaaacaatg tgcttatttc 1260

tgtgaaaata agcttcgatc t 1281

<210> 795
<211> 1281
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 795
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agcccaaaag ctccgacaag 420

actcacacat gccccccttg tccagcgcct gaagctgagg gtgcgccctc tgtcttcctt 480

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gttgtcgacg tatctcatga agatcctgag gtgaaattca actggtatgt agacggggtc 600

gaagttcata atgctaagac taagccacga gaagagcaat acaactcaac gtatcgggtg 660

gtgagcgttc tgacggttct gcaccaagat tggcttaatg gaaaagagta taagtgcaag 720

gtgtccaaca aggctcttcc ggcacccatc gaaaagacga tttccaaagc gaaaggccaa 780

cctagggaac cgcaagttta cactttgccc ccgtcaagag acgaacttac caagaatcaa 840

gtttccctga cgtgccttgt gaagggcttc taccctagcg atatagcagt tgagtgggaa 900

tctaacggcc agcccgaaaa taattataag actactccgc ccgtgctgga cagtgatggt 960

tcatttttcc tgtattcaaa actcactgtg gacaaatcta gatggcagca gggtaatgtg 1020

ttctcttgtt cagttatgca cgaggcattg cacaatcact atacgcaaaa aagtttgtct 1080

ctctctccgg gggggggtgg cggatcagga ggtggcggtt caggcggagg aggttctggg 1140

ggtgggggtt ctagtctctc ttgcaggaaa gagcaaggcg aatattacga ccatcttttg 1200

cgagactgta taagctgtgc gtctatttgt ggacaacacc ctaaacaatg tgctgatttc 1260

tgtgaaaata agcttcgatc t 1281

<210> 796
<211> 1281
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 796
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agcccaaaag ctccgacaag 420

actcacacat gccccccttg tccagcgcct gaagctgagg gtgcgccctc tgtcttcctt 480

ttccccccta agccgaaaga taccctgatg atctcccgca ctcccgaagt cacatgtgtt 540

gttgtcgacg tatctcatga agatcctgag gtgaaattca actggtatgt agacggggtc 600

gaagttcata atgctaagac taagccacga gaagagcaat acaactcaac gtatcgggtg 660

gtgagcgttc tgacggttct gcaccaagat tggcttaatg gaaaagagta taagtgcaag 720

gtgtccaaca aggctcttcc ggcacccatc gaaaagacga tttccaaagc gaaaggccaa 780

cctagggaac cgcaagttta cactttgccc ccgtcaagag acgaacttac caagaatcaa 840

gtttccctga cgtgccttgt gaagggcttc taccctagcg atatagcagt tgagtgggaa 900

tctaacggcc agcccgaaaa taattataag actactccgc ccgtgctgga cagtgatggt 960

tcatttttcc tgtattcaaa actcactgtg gacaaatcta gatggcagca gggtaatgtg 1020

ttctcttgtt cagttatgca cgaggcattg cacaatcact atacgcaaaa aagtttgtct 1080

ctctctccgg gggggggtgg cggatcagga ggtggcggtt caggcggagg aggttctggg 1140

ggtgggggtt ctagtctctc ttgcaggaaa gagcaaggca aattttacga ccatcttttg 1200

cgagactgta taagctgtgc gtctatttgt ggacaacacc ctaaacaatg tgcttatttc 1260

tgtgaaaata agcttcgatc t 1281

<210> 797
<211> 1254
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 797
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag tggaatgccc tccttgtcct 420

gctcctccag tggctggccc ttccgtgttt ctgttccctc caaagcctaa ggacaccctg 480

atgatcagca gaacccctga agtgacctgc gtggtggtgg atgtgtctca cgaagatccc 540

gaggtgcagt tcaattggta cgtggacggc gtggaagtgc acaacgccaa gaccaagcct 600

agagaggaac agttcaacag caccttcaga gtggtgtccg tgctgaccgt ggtgcatcag 660

gattggctga acggcaaaga gtacaagtgc aaggtgtcca acaagggcct gcctgctcct 720

atcgagaaaa ccatctctaa gaccaagggg cagccccgcg aacctcaggt ttacacactg 780

cctccaagcc gggaagagat gaccaagaac caggtgtccc tgacctgcct cgtgaagggc 840

ttttacccca gcgacattag cgtggaatgg gagagcaatg gccagcctga gaacaactac 900

aagaccacac ctcctatgct ggacagcgac ggctcattct tcctgtacag caagctgaca 960

gtggacaagt ccagatggca gcagggcaac gtgttcagct gcagcgtgat gcacgaggcc 1020

ctgcacaacc actacaccca gaagtccctg agcctgtctc ctggcggggg tggcggatca 1080

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aaagagcaag gcaaatttta cgaccatctt ttgcgagact gtataagctg tgcgtctatt 1200

tgtggacaac accctaaaca atgtgcttat ttctgtgaaa ataagcttcg atct 1254

<210> 798
<211> 1272

<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 798
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agtccaaata tggtccccca 420

tgcccaccat gcccagcacc tgagttcctg gggggaccat cagtcttcct gttccccccа 480

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 540

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 600

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 660

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 720

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 780

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 840

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 900

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 960

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ggtgggggtg gcggatcagg aggtggcggt tcaggcggag gaggttctgg gggtgggggt 1140

tctagtctct cttgcaggaa agagcaaggc aaattttacg accatctttt gcgagactgt 1200

ataagctgtg cgtctatttg tggacaacac cctaaacaat gtgcttattt ctgtgaaaat 1260

aagcttcgat ct 1272

<210> 799
<211> 1281

<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 799
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agcccaaaag ctccgacaag 420

actcacacat gccccccttg tccagcgcct gaagctgagg gtgcgccctc tgtcttcctt 480

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gaagttcata atgctaagac taagccacga gaagagcaat acaactcaac gtatcgggtg 660

gtgagcgttc tgacggttct gcaccaagat tggcttaatg gaaaagagta taagtgcaag 720

gtgtccaaca aggctcttcc ggcacccatc gaaaagacga tttccaaagc gaaaggccaa 780

cctagggaac cgcaagttta cactttgccc ccgtcaagag acgaacttac caagaatcaa 840

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tctaacggcc agcccgaaaa taattataag actactccgc ccgtgctgga cagtgatggt 960

tcatttttcc tgtattcaaa actcactgtg gacaaatcta gatggcagca gggtaatgtg 1020

ttctcttgtt cagttatgca cgaggcattg cacaatcact atacgcaaaa aagtttgtct 1080

ctctctccgg gggggggtgg cggatcagga ggtggcggtt caggcggagg aggttctggg 1140

ggtgggggtt ctagtctctc ttgcaggaaa gaggaaggca aattttacga ccatcttttg 1200

caagactgta taagctgtgc gtctatttgt ggacaacacc ctaaacaatg tgcttatttc 1260

tgtgaaaata agcttcgatc t 1281

<210> 800
<211> 1254

<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 800
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag tggaatgccc tccttgtcct 420

gctcctccag tggctggccc ttccgtgttt ctgttccctc caaagcctaa ggacaccctg 480

atgatcagca gaacccctga agtgacctgc gtggtggtgg atgtgtctca cgaagatccc 540

gaggtgcagt tcaattggta cgtggacggc gtggaagtgc acaacgccaa gaccaagcct 600

agagaggaac agttcaacag caccttcaga gtggtgtccg tgctgaccgt ggtgcatcag 660

gattggctga acggcaaaga gtacaagtgc aaggtgtcca acaagggcct gcctgctcct 720

atcgagaaaa ccatctctaa gaccaagggg cagccccgcg aacctcaggt ttacacactg 780

cctccaagcc gggaagagat gaccaagaac caggtgtccc tgacctgcct cgtgaagggc 840

ttttacccca gcgacattag cgtggaatgg gagagcaatg gccagcctga gaacaactac 900

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aaagaggaag gcaaatttta cgaccatctt ttgcaagact gtataagctg tgcgtctatt 1200

tgtggacaac accctaaaca atgtgcttat ttctgtgaaa ataagcttcg atct 1254

<210> 801
<211> 1272
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 801
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag agtccaaata tggtccccca 420

tgcccaccat gcccagcacc tgagttcctg gggggaccat cagtcttcct gttcccccca 480

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 540

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 600

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 660

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tctagtctct cttgcaggaa agaggaaggc aaattttacg accatctttt gcaagactgt 1200

ataagctgtg cgtctatttg tggacaacac cctaaacaat gtgcttattt ctgtgaaaat 1260

aagcttcgat ct 1272

<210> 802
<211> 1266
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 802
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag acaagactca cacatgcccc 420

ccttgtccag cgcctgaagc tgagggtgcg ccctctgtct tccttttccc ccctaagccg 480

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catgaagatc ctgaggtgaa attcaactgg tatgtagacg gggtcgaagt tcataatgct 600

aagactaagc cacgagaaga gcaatacaac tcaacgtatc gggtggtgag cgttctgacg 660

gttctgcacc aagattggct taatggaaaa gagtataagt gcaaggtgtc caacaaggct 720

cttccggcac ccatcgaaaa gacgatttcc aaagcgaaag gccaacctag ggaaccgcaa 780

gtttacactt tgcccccgtc aagagacgaa cttaccaaga atcaagtttc cctgacgtgc 840

cttgtgaagg gcttctaccc tagcgatata gcagttgagt gggaatctaa cggccagccc 900

gaaaataatt ataagactac tccgcccgtg ctggacagtg atggttcatt tttcctgtat 960

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tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 1260

cgatct 1266

<210> 803
<211> 1266
<212> DNA
<213> artificial sequence

<220>
<223> variant multi domain immunomodulatory molecule

<400> 803
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ttcgtatgcg aatatgcctc tccaggaaaa gcgaccgagg tcagagttac tgtactgaga 120

caagctgatt cacaagtgac tgaggtctgc gctgctactt atatgatggg gaacgagctg 180

actttccttg atgactcaat ctgtaccggc accagcagtg ggaaccaagt aaatcttact 240

attcaaggac tgagggcaat ggacacggga ctttacattt gtaaggtcga gctgatgtac 300

ccgccacctt actacctcgg aatcggtaat ggtacgcaaa tttatgttat agatcctgaa 360

ccgtgccccg attccgacgg atccggtgga ggagggtcag acaagactca cacatgcccc 420

ccttgtccag cgcctgaagc tgagggtgcg ccctctgtct tccttttccc ccctaagccg 480

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aagactaagc cacgagaaga gcaatacaac tcaacgtatc gggtggtgag cgttctgacg 660

gttctgcacc aagattggct taatggaaaa gagtataagt gcaaggtgtc caacaaggct 720

cttccggcac ccatcgaaaa gacgatttcc aaagcgaaag gccaacctag ggaaccgcaa 780

gtttacactt tgcccccgtc aagagacgaa cttaccaaga atcaagtttc cctgacgtgc 840

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gaaaataatt ataagactac tccgcccgtg ctggacagtg atggttcatt tttcctgtat 960

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ggtggcggat caggaggtgg cggttcaggc ggaggaggtt ctgggggtgg gggttctagt 1140

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tgtgcgtcta tttgtggaca acaccctaaa caatgtgctt atttctgtga aaataagctt 1260

cgatct 1266

<210> 804
<211> 227
<212> PRT
<213> artificial sequence

<220>
<223> variant Fc

<400> 804

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Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15


Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30


Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45


Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60


His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110


Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125


Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140


Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala Thr Pro Pro
                165                 170                 175


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
```

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 805
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> linker

<400> 805

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 806
<211> 65
<212> PRT
<213> artificial sequence

<220>
<223> linker

<400> 806

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser
65

<210> 807
<211> 587
<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 807

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Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    50                  55                  60


Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
65                  70                  75                  80


Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
                85                  90                  95


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            100                 105                 110


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        115                 120                 125


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    130                 135                 140


Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
145                 150                 155                 160


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                165                 170                 175
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            180                 185                 190

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        195                 200                 205

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    210                 215                 220

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
225                 230                 235                 240

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                245                 250                 255

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            260                 265                 270

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        275                 280                 285

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                325                 330                 335

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            340                 345                 350

Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
        355                 360                 365

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
    370                 375                 380
```

```
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
385                 390                 395                 400

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                405                 410                 415

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            420                 425                 430

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        435                 440                 445

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    450                 455                 460

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
465                 470                 475                 480

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                485                 490                 495

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            500                 505                 510

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        515                 520                 525

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    530                 535                 540

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
545                 550                 555                 560

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                565                 570                 575

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            580                 585
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<210> 808
<211> 291

<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 808

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1               5                   10                  15


Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60


Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80


Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95


Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110


His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125


Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140


Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160


Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175


Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190
```

```
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205


Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220


Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240


Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255


Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270


Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285


Ser Pro Gly
    290


<210>  809
<211>  359
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant BCMA Fc

<400>  809

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60
```

```
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270
```

```
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp
305                 310                 315                 320

Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn
                325                 330                 335

Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn
            340                 345                 350

Ser Val Lys Gly Thr Asn Ala
        355
```

<210> 810
<211> 587
<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 810

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    50                  55                  60

Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
65                  70                  75                  80
```

```
Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
                85                  90                  95

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            100                 105                 110

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        115                 120                 125

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    130                 135                 140

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
145                 150                 155                 160

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                165                 170                 175

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            180                 185                 190

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        195                 200                 205

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    210                 215                 220

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
225                 230                 235                 240

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                245                 250                 255

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            260                 265                 270

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        275                 280                 285

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                325                 330                 335

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            340                 345                 350

Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
        355                 360                 365

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
    370                 375                 380

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
385                 390                 395                 400

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                405                 410                 415

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            420                 425                 430

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        435                 440                 445

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    450                 455                 460

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
465                 470                 475                 480

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                485                 490                 495

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            500                 505                 510
```

```
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        515                 520                 525


Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    530                 535                 540


Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
545                 550                 555                 560


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                565                 570                 575


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            580                 585
```

<210> 811
<211> 291
<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 811

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
    50                  55                  60


Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65                  70                  75                  80


Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                85                  90                  95
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            100                 105                 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        115                 120                 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    130                 135                 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145                 150                 155                 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                165                 170                 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            180                 185                 190

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly
    290
```

<210> 812
<211> 359

<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 812

Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1 5 10 15

Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
20 25 30

Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
35 40 45

Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser
50 55 60

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
65 70 75 80

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
85 90 95

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
100 105 110

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
115 120 125

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
130 135 140

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
145 150 155 160

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
165 170 175

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
180 185 190

```
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        195                 200                 205

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    210                 215                 220

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
225                 230                 235                 240

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                245                 250                 255

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            260                 265                 270

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        275                 280                 285

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300

Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp
305                 310                 315                 320

Ala Leu Leu Tyr Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn
                325                 330                 335

Thr Pro Pro Leu Thr Cys Gln Gln Tyr Cys Asn Ala Ser Val Thr Asn
            340                 345                 350

Ser Val Lys Gly Thr Asn Ala
        355
```

<210> 813
<211> 359
<212> PRT
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 813

```
Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu
1               5                   10                  15


Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro
            20                  25                  30


Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val
        35                  40                  45


Lys Gly Thr Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    50                  55                  60


Gly Gly Gly Ser Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr
65                  70                  75                  80


Phe Asp Ser Leu Leu Leu Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser
                85                  90                  95


Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val
            100                 105                 110


Thr Asn Ser Val Lys Gly Thr Asn Ala Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
    130                 135                 140


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
145                 150                 155                 160


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                165                 170                 175


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
            180                 185                 190


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        195                 200                 205
```

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    210                 215                 220

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
225                 230                 235                 240

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                245                 250                 255

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
            260                 265                 270

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        275                 280                 285

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    290                 295                 300

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
305                 310                 315                 320

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                325                 330                 335

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            340                 345                 350

Ser Leu Ser Leu Ser Pro Gly
        355
```

<210> 814
<211> 1761
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 814

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ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gcacgcatgt       60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc      120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg tggcgggtca      180
```

ggggggaggtg gaagcgagcc caagtcctca gataagactc atacttgccc cccctgtccc 240

gcccctgagg ccgaaggcgc accgtcagtg tttttgttcc caccaaagcc taaggacaca 300

ctgatgataa gcagaacacc tgaggtaacc tgtgttgttg tggatgtaag ccacgaagat 360

ccggaggtta agtttaactg gtacgtggac ggtgtagaag tccataatgc taagacgaag 420

ccgagggagg aacaatacaa ctccacgtat agagtggtct ccgtcttgac cgtactccat 480

caagactggc tcaacgggaa agagtacaag tgtaaagtct ctaacaaagc tcttcctgca 540

ccgattgaga aaaccatatc taaagccaag ggacaaccga gagaaccaca ggtttacacg 600

ctccccccca gtagagacga acttacaaaa aaccaggtca gtcttacctg cctcgtcaaa 660

ggcttctacc cctctgacat cgctgttgag tgggaatcta acggccaacc tgagaacaat 720

tacaaaacaa ccccgcctgt ccttgactca gacggttcct tttttcttta cagcaagctg 780

accgtcgaca aatcacggtg gcaacaaggc aatgtgtttt cctgttccgt gatgcacgag 840

gcactgcaca accactacac tcaaaaatcc ctttcccttt ccccaggggg aggtggaggg 900

agcggtggag gtggtagcgg gggtggaggc tcaggtggtg ggggttccgg cggtggcgga 960

agtggaggcg gtggctctgg tggtggcgga tctggcggag gaggcagcgg cggaggtggg 1020

tctgggggtg gaggctccgg aggcgggggа agcggtggag gagggtcaga gcccaaaagc 1080

tccgacaaga ctcacacatg ccccccttgt ccagcgcctg aagctgaggg tgcgccctct 1140

gtcttccttt tccccccctaa gccgaaagat accctgatga tctcccgcac tcccgaagtc 1200

acatgtgttg ttgtcgacgt atctcatgaa gatcctgagg tgaaattcaa ctggtatgta 1260

gacggggtcg aagttcataa tgctaagact aagccacgag aagagcaata caactcaacg 1320

tatcgggtgg tgagcgttct gacggttctg caccaagatt ggcttaatgg aaaagagtat 1380

aagtgcaagg tgtccaacaa ggctcttccg gcacccatcg aaaagacgat ttccaaagcg 1440

aaaggccaac ctagggaacc gcaagtttac actttgcccc cgtcaagaga cgaacttacc 1500

aagaatcaag tttccctgac gtgccttgtg aagggcttct accctagcga tatagcagtt 1560

gagtgggaat ctaacggcca gcccgaaaat aattataaga ctactccgcc cgtgctggac 1620

agtgatggtt cattttcct gtattcaaaa ctcactgtgg acaaatctag atggcagcag 1680

ggtaatgtgt tctcttgttc agttatgcac gaggcattgc acaatcacta tacgcaaaaa 1740

agtttgtctc tctctccggg g 1761

<210> 815
<211> 873
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 815
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gcacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg aggagggtca 180

gagcccaaaa gctccgacaa gactcacaca tgccccccct gtccagcgcc tgaagctgag 240

ggtgcgccct ctgtcttcct tttccccccct aagccgaaag ataccctgat gatctcccgc 300

actcccgaag tcacatgtgt tgttgtcgac gtatctcatg aagatcctga ggtgaaattc 360

aactggtatg tagacggggt cgaagttcat aatgctaaga ctaagccacg agaagagcaa 420

tacaactcaa cgtatcgggt ggtgagcgtt ctgacggttc tgcaccaaga ttggcttaat 480

ggaaaagagt ataagtgcaa ggtgtccaac aaggctcttc cggcacccat cgaaaagacg 540

atttccaaag cgaaaggcca acctagggaa ccgcaagttt acactttgcc cccgtcaaga 600

gacgaactta ccaagaatca agtttccctg acgtgccttg tgaagggctt ctaccctagc 660

gatatagcag ttgagtggga atctaacggc cagcccgaaa ataattataa gactactccg 720

cccgtgctgg acagtgatgg ttcatttttc ctgtattcaa aactcactgt ggacaaatct 780

agatggcagc agggtaatgt gttctcttgt tcagttatgc acgaggcatt gcacaatcac 840

tatacgcaaa aaagtttgtc tctctctccg ggg 873

<210> 816
<211> 1077
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 816
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gcacgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg aggagggtca 180

gagcccaaaa gctccgacaa gactcacaca tgccccccct gtccagcgcc tgaagctgag 240

ggtgcgccct ctgtcttcct tttcccccct aagccgaaag ataccctgat gatctcccgc 300

actcccgaag tcacatgtgt tgttgtcgac gtatctcatg aagatcctga ggtgaaattc 360

aactggtatg tagacggggt cgaagttcat aatgctaaga ctaagccacg agaagagcaa 420

tacaactcaa cgtatcgggt ggtgagcgtt ctgacggttc tgcaccaaga ttggcttaat 480

ggaaaagagt ataagtgcaa ggtgtccaac aaggctcttc cggcacccat cgaaaagacg 540

atttccaaag cgaaaggcca acctagggaa ccgcaagttt acactttgcc cccgtcaaga 600

gacgaactta ccaagaatca agtttccctg acgtgccttg tgaagggctt ctaccctagc 660

gatatagcag ttgagtggga atctaacggc cagcccgaaa ataattataa gactactccg 720

cccgtgctgg acagtgatgg ttcatttttc ctgtattcaa aactcactgt ggacaaatct 780

agatggcagc agggtaatgt gttctcttgt tcagttatgc acgaggcatt gcacaatcac 840

tatacgcaaa aaagtttgtc tctctctccg gggggaggtg gtggatcagg cggtggaggt 900

tccggaggag gtggatctct gcaaatggcg ggacagtgta gtcaaaatga gtacttcgac 960

agccttcttc atgcctgtat tccgtgccaa ctgcggtgca gcagtaacac gccaccgctc 1020

acttgccaga ggtattgtaa tgccagtgta actaacagtg taaaagggac taatgct 1077

<210> 817
<211> 1761
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 817
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gctcgcatgt 60

attccttgcc aactgcgctg ttcaagcaac accccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg tggcgggtca 180

gggggaggtg gaagcgagcc caagtcctca gataagactc atacttgccc cccctgtccc 240

gcccctgagg ccgaaggcgc accgtcagtg tttttgttcc caccaaagcc taaggacaca 300

ctgatgataa gcagaacacc tgaggtaacc tgtgttgttg tggatgtaag ccacgaagat 360

ccggaggtta agtttaactg gtacgtggac ggtgtagaag tccataatgc taagacgaag 420

ccgagggagg aacaatacaa ctccacgtat agagtggtct ccgtcttgac cgtactccat 480

caagactggc tcaacgggaa agagtacaag tgtaaagtct ctaacaaagc tcttcctgca 540

ccgattgaga aaaccatatc taaagccaag ggacaaccga gagaaccaca ggtttacacg 600

ctccccccca gtagagacga acttacaaaa aaccaggtca gtcttacctg cctcgtcaaa 660

ggcttctacc cctctgacat cgctgttgag tgggaatcta acggccaacc tgagaacaat 720

tacaaaacaa ccccgcctgt ccttgactca gacggttcct tttttcttta cagcaagctg 780

accgtcgaca aatcacggtg gcaacaaggc aatgtgtttt cctgttccgt gatgcacgag 840

gcactgcaca accactacac tcaaaaatcc ctttcccttt ccccaggggg aggtggaggg 900

agcggtggag gtggtagcgg gggtggaggc tcaggtggtg ggggttccgg cggtggcgga 960

agtggaggcg gtggctctgg tggtggcgga tctggcggag gaggcagcgg cggaggtggg 1020

tctgggggtg gaggctccgg aggcgggggа agcggtggag gagggtcaga gcccaaaagc 1080

tccgacaaga ctcacacatg ccccccttgt ccagcgcctg aagctgaggg tgcgccctct 1140

gtcttccttt tccccccctaa gccgaaagat accctgatga tctcccgcac tcccgaagtc 1200

acatgtgttg ttgtcgacgt atctcatgaa gatcctgagg tgaaattcaa ctggtatgta 1260

gacggggtcg aagttcataa tgctaagact aagccacgag aagagcaata caactcaacg 1320

tatcgggtgg tgagcgttct gacggttctg caccaagatt ggcttaatgg aaaagagtat 1380

aagtgcaagg tgtccaacaa ggctcttccg gcacccatcg aaaagacgat ttccaaagcg 1440

aaaggccaac ctagggaacc gcaagtttac actttgcccc cgtcaagaga cgaacttacc 1500

aagaatcaag tttccctgac gtgccttgtg aagggcttct accctagcga tatagcagtt 1560

gagtgggaat ctaacggcca gcccgaaaat aattataaga ctactccgcc cgtgctggac 1620

agtgatggtt catttttcct gtattcaaaa ctcactgtgg acaaatctag atggcagcag 1680

ggtaatgtgt tctcttgttc agttatgcac gaggcattgc acaatcacta tacgcaaaaa 1740

agtttgtctc tctctccggg g 1761

<210> 818
<211> 873
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 818
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attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg aggagggtca 180

gagcccaaaa gctccgacaa gactcacaca tgcccccctt gtccagcgcc tgaagctgag 240

ggtgcgccct ctgtcttcct tttccccccct aagccgaaag ataccctgat gatctcccgc 300

actcccgaag tcacatgtgt tgttgtcgac gtatctcatg aagatcctga ggtgaaattc 360

aactggtatg tagacggggt cgaagttcat aatgctaaga ctaagccacg agaagagcaa 420

tacaactcaa cgtatcgggt ggtgagcgtt ctgacggttc tgcaccaaga ttggcttaat 480

ggaaaagagt ataagtgcaa ggtgtccaac aaggctcttc cggcacccat cgaaaagacg 540

atttccaaag cgaaaggcca acctagggaa ccgcaagttt acactttgcc cccgtcaaga 600

gacgaactta ccaagaatca agtttccctg acgtgccttg tgaagggctt ctaccctagc 660

gatatagcag ttgagtggga atctaacggc cagcccgaaa ataattataa gactactccg 720

cccgtgctgg acagtgatgg ttcatttttc ctgtattcaa aactcactgt ggacaaatct 780

agatggcagc agggtaatgt gttctcttgt tcagttatgc acgaggcatt gcacaatcac 840

tatacgcaaa aaagtttgtc tctctctccg ggg 873

<210> 819
<211> 1077
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 819
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gctcgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gatccggtgg aggagggtca 180

gagcccaaaa gctccgacaa gactcacaca tgcccccctt gtccagcgcc tgaagctgag 240

ggtgcgccct ctgtcttcct tttccccccct aagccgaaag ataccctgat gatctcccgc 300

actcccgaag tcacatgtgt tgttgtcgac gtatctcatg aagatcctga ggtgaaattc 360

aactggtatg tagacggggt cgaagttcat aatgctaaga ctaagccacg agaagagcaa 420

tacaactcaa cgtatcgggt ggtgagcgtt ctgacggttc tgcaccaaga ttggcttaat 480

ggaaaagagt ataagtgcaa ggtgtccaac aaggctcttc cggcacccat cgaaaagacg 540

atttccaaag cgaaaggcca acctagggaa ccgcaagttt acactttgcc cccgtcaaga 600

gacgaactta ccaagaatca agtttccctg acgtgccttg tgaagggctt ctaccctagc 660

gatatagcag ttgagtggga atctaacggc cagcccgaaa ataattataa gactactccg 720

cccgtgctgg acagtgatgg ttcatttttc ctgtattcaa aactcactgt ggacaaatct 780

agatggcagc agggtaatgt gttctcttgt tcagttatgc acgaggcatt gcacaatcac 840

tatacgcaaa aaagtttgtc tctctctccg gggggaggtg gtggatcagg cggtggaggt 900

tccggaggag gtggatctct gcaaatggcg ggacagtgta gtcaaaatga gtacttcgac 960

gcccttcttt acgcctgtat tccgtgccaa ctgcggtgca gcagtaacac gccaccgctc 1020

acttgccagc agtattgtaa tgccagtgta actaacagtg taaaagggac taatgct 1077

<210> 820
<211> 1077
<212> DNA
<213> artificial sequence

<220>
<223> variant BCMA Fc

<400> 820
ctgcaaatgg ccgggcagtg cagccagaac gaatactttg actccttgtt gctcgcatgt 60

attccttgcc aactgcgctg ttcaagcaac acccccccgc tcacgtgtca gcggtactgc 120

aacgcatctg ttaccaacag tgtcaaaggg actaatgcgg gaggtggtgg atcaggcggt 180

ggaggttccg gaggaggtgg atctctgcaa atggcgggac agtgtagtca aaatgagtac 240

ttcgacagcc ttcttctcgc ctgtattccg tgccaactgc ggtgcagcag taacacgcca 300

ccgctcactt gccagaggta ttgtaatgcc agtgtaacta acagtgtaaa agggactaat 360

gctggatccg gtggaggagg gtcagagccc aaaagctccg acaagactca cacatgcccc 420

ccttgtccag cgcctgaagc tgagggtgcg ccctctgtct tccttttccc ccctaagccg 480

aaagataccc tgatgatctc ccgcactccc gaagtcacat gtgttgttgt cgacgtatct 540

catgaagatc ctgaggtgaa attcaactgg tatgtagacg gggtcgaagt tcataatgct 600

aagactaagc cacgagaaga gcaatacaac tcaacgtatc gggtggtgag cgttctgacg 660

gttctgcacc aagattggct taatggaaaa gagtataagt gcaaggtgtc caacaaggct 720

cttccggcac ccatcgaaaa gacgatttcc aaagcgaaag gccaacctag ggaaccgcaa 780

gtttacactt tgcccccgtc aagagacgaa cttaccaaga atcaagtttc cctgacgtgc 840

cttgtgaagg gcttctaccc tagcgatata gcagttgagt gggaatctaa cggccagccc 900

gaaaataatt ataagactac tccgcccgtg ctggacagtg atggttcatt tttcctgtat 960

tcaaaactca ctgtggacaa atctagatgg cagcagggta atgtgttctc ttgttcagtt 1020

atgcacgagg cattgcacaa tcactatacg caaaaaagtt tgtctctctc tccgggg 1077

<210> 821
<211> 522
<212> PRT
<213> artificial sequence

<220>
<223> variant Fc

<400> 821

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225                 230                 235                 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            260                 265                 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
    290                 295                 300

Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro
305                 310                 315                 320
```

```
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
               325                 330                 335

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            340                 345                 350

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        355                 360                 365

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    370                 375                 380

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
385                 390                 395                 400

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
               405                 410                 415

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
            420                 425                 430

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        435                 440                 445

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    450                 455                 460

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
465                 470                 475                 480

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
               485                 490                 495

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            500                 505                 510

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        515                 520
```

<210> 822
<211> 222
<212> PRT
<213> artificial sequence

<220>
<223> variant Fc

<400> 822

```
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
1               5                  10                  15


Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            20                  25                  30


Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        35                  40                  45


Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                  55                  60


Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
65                  70                  75                  80


Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95


Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110


Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125


Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140


Val Lys Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Ser Asn
145                 150                 155                 160


Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
                165                 170                 175
```

```
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190


Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205


His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    210                 215                 220


<210>  823
<211>  228
<212>  PRT
<213>  artificial sequence

<220>
<223>  variant Fc

<400>  823

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1               5                   10                  15


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45


Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65                  70                  75                  80


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100                 105                 110


Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115                 120                 125
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150                 155                 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165                 170                 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210                 215                 220

Leu Ser Leu Gly
225
```

<210> 824
<211> 226
<212> PRT
<213> artificial sequence

<220>
<223> variant Fc

<400> 824

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
1               5                   10                  15

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly
225
```