SEQUENCE LISTING

<110> DCB-USA LLC
Kaohsiung Medical University

<120> ANTIBODY LOCKER FOR THE INACTIVATION OF PROTEIN DRUG

<130> P2757-1-PCT

<150> PCT/US61/827,763
<151> 2013-05-28

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<170> BiSSAP 1.3

<210> 1
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> infliximab light chain

<400> 1
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 2
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Panitumumab light chain

<400> 2
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Asn
            20                  25                  30
Asn Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95
Ser His Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
Arg Ala Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
        115                 120                 125
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
    130                 135                 140
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
145                 150                 155                 160
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
                165                 170                 175
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
            180                 185                 190
Tyr Glu Lys His Lys Leu Tyr Ala Cys Glu Val Thr His Gln Gly Leu
        195                 200                 205
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
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<210> 3
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Trastuzumab light chain

<400> 3

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Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1               5                   10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr
            20                  25                  30
Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
                85                  90                  95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205
Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 4
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> adalimumab light chain

<400> 4
Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100   105   110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu
            180   185   190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195   200   205
Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 5
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> DENOSUMAB LIGHT CHAIN

<400> 5
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Arg
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100   105   110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

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Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu
            180                 185                 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205
Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 6
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab light chain

<400> 6

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
            20                  25                  30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu
            180                 185                 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205
Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 7
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> tremelimumab light chain

<400> 7

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

```
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
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<210> 8
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> efalizumab light chain

<400> 8

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Ala Ala Gln Pro Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
1               5                   10                  15
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys
            20                  25                  30
Thr Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        35                  40                  45
Pro Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro
    50                  55                  60
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65                  70                  75                  80
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His
                85                  90                  95
Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190
Lys His Lys Leu Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 9
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> ustekinumab light chain

<400> 9
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys Leu Glu
    210   215

<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 hinge

<400> 10
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 11
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG2 hinge

<400> 11
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1   5   10

<210> 12
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG3 hinge

<400> 12
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1   5   10   15
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
            20   25   30
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
        35   40   45
Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
    50   55   60

<210> 13
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 hinge

<400> 13
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1   5   10

<210> 14
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> IgA1 hinge

<400> 14
Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
1   5   10   15
Pro Ser Pro Ser Cys Cys His
            20

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> IgA2 hinge

<400> 15
Pro Val Pro Pro Pro Pro Pro Cys Cys His
1   5   10

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MMP2 substrate

<400> 16
Gly Pro Leu Gly Val Arg
1   5

<210> 17
<211> 2445
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1 Hinge Ipilimumab

<400> 17
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ctgggttcca ggttccactg gtgacgagcc caaatcttgt gacaaaactc acacatgccc 120

accgtgccca gttaacggcg gcggcggcag cggtcccctg ggtgtgagag cggcccagcc 180

ggccgaaatt gtgttgacgc agtctccagg caccctgtct ttgtctccag gggaaagagc 240

caccctctcc tgcagggcca gtcagagtgt tggcagcagc tacttagcct ggtaccagca 300

gaaacctggc caggctccca ggctcctcat ctatggtgca ttcagcaggg ccactggcat 360

cccagacagg ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact 420

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cccgccatct gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa 600

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ctcccaggag agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac 720

cctgacgctg agcaaagcag actacgagaa acacaaactc tacgcctgcg aagtcaccca 780

tcagggcctg agctcgcccg tcacaaagag cttcaacagg ggagagtgcc tcgagcgagc 840

aaaacgagca ccagtaaaac aaacactaaa cttcgaccta ctaaaactag caggagacgt 900

agaatcaaac ccaggaccag ccacaaccat ggagacagac acactcctgc tatgggtact 960

gctgctctgg gttccaggtt ccactggtga cgagcccaaa tcttgtgaca aaactcacac 1020

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atctcaggtg cagctggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag 1140

actctcctgt gcagcctctg gattcacctt cagtagctat actatgcact gggtccgcca 1200

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gtatctgcaa atgaacagcc tgagagctga ggacacggct atatattact gtgcgaggac 1380

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gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc 2220

cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct 2280

ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca 2340

gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca 2400

gaagagcctc tccctgtctc cgggtaaata aatcgatggc gcgcc 2445

<210> 18
<211> 2427
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG2 Hinge Ipilimumab

<400> 18
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ctgggttcca ggttccactg gtgacgagcg caaatgttgt gtcgagtgcc caccgtgccc 120

agttaacggc ggcggcggca gcggtcccct gggtgtgaga gcggcccagc cggccgaaat 180

tgtgttgacg cagtctccag gcaccctgtc tttgtctcca ggggaaagag ccaccctctc 240

ctgcagggcc agtcagagtg ttggcagcag ctacttagcc tggtaccagc agaaacctgg 300

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gttcagtggc agtgggtctg ggacagactt cactctcacc atcagcagac tggagcctga 420

agattttgca gtgtattact gtcagcagta tggtagctca ccgtggacgt tcggccaagg 480

gaccaaggtg gaaatcaaac ggactgtggc tgcaccatct gtcttcatct tcccgccatc 540

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gagtgtcaca gagcaggaca gcaaggacag cacctacagc ctcagcagca ccctgacgct 720

gagcaaagca gactacgaga aacacaaact ctacgcctgc gaagtcaccc atcagggcct 780

gagctcgccc gtcacaaaga gcttcaacag gggagagtgc ctcgagcgag caaaacgagc 840

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cccaggacca gccacaacca tggagacaga cacactcctg ctatgggtac tgctgctctg 960

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cccaaaaccc aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt 1860

ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt 1920

gcataatgcc aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag 1980

cgtcctcacc gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc 2040

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agaaccacag gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag 2160

cctgacctgc ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa 2220

tgggcagccg gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt 2280

cttcctctac agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc 2340

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tccgggtaaa taaatcgatg gcgcgcc 2427

<210> 19
<211> 2727
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG3 Hinge Ipilimumab

<400> 19
gctagcaagc ttgttatcca ccatggagac agacacactc ctgctatggg tactgctgct 60

ctgggttcca ggttccactg gtgacgagct caaaacccca cttggtgaca caactcacac 120

atgcccacgg tgcccagagc ccaaatcttg tgacacacct cccccgtgcc cacggtgccc 180

agagcccaaa tcttgtgaca cacctccccc atgcccacgg tgcccagagc ccaaatcttg 240

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gggtgtgaga gcggcccagc cggccgaaat tgtgttgacg cagtctccag gcaccctgtc 360
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<223> MMP2 substrate

<400> 53
Pro Gln Gly Ile Ala Gly Gln Arg
1 5

<210> 54
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> IgD1 Hinge

<400> 54
Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln Ala
1 5 10 15
Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg Asn
20 25 30
Thr Glu Cys
35

<210> 55
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> IgD2 Hinge

<400> 55
Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu Glu Gln Glu
1   5   10   15
Glu Arg Glu Thr Lys Thr Pro Glu Cys
            20   25

<210> 56
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> IgD1 Hinge

<400> 56
tctccaaagg cacaggcctc ctccgtgccc actgcacaac cccaagcaga gggcagcctc 60

gccaaggcaa ccacagcccc agccaccacc cgtaacacag agtgt 105

<210> 57
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> IgD2 Hinge

<400> 57
agaggaggag aagagaagaa gaaggagaag gagaaagagg aacaagaaga gagagagaca 60

aagacaccag agtgt 75

<210> 58
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> infliximab heavy chain

<400> 58
Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
            20   25   30
Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
        35   40   45
Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
    50   55   60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
65   70   75   80
Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
                85   90   95
Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

```
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
```

<210> 59
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> Panitumumab heavy chain

<400> 59

```
Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30
Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
        35                  40                  45
Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
    50                  55                  60
Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65                  70                  75                  80
Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
            100                 105                 110
Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125
```

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
165 170 175
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
180 185 190
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
210 215 220
Lys Arg Val Val Asp Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
225 230 235 240
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
245 250 255
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
275 280 285
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
290 295 300
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
305 310 315 320
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
325 330 335
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
340 345 350
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
355 360 365
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
370 375 380
Gly
385

<210> 60
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> Trastuzumab heavy chain

<400> 60
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
1 5 10 15
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30
Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
35 40 45
Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser
85 90 95
Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

```
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Val Asp Lys Lys Val Glu Pro
    210                 215                 220
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
        355                 360                 365
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430
Ser Val Met His Glu Ala Leu
        435

<210> 61
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> adalimumab heavy chain

<400> 61
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1                 5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50                  55                  60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
```

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

<210> 62
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> denosumab heavy chain

<400> 62

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
```

```
    130                 135                 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220
Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300
Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335
Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445



<210> 63
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab heavy chain

<400> 63
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 64
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> tremelimumab heavy chain

<400> 64
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1                 5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95
Ala Arg Asp Pro Arg Gly Ala Thr Leu Tyr Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140
Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190
Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205
Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220
Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

<210> 65
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> efalizumab heavy chain

<400> 65

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Thr Gly His
            20                  25                  30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Tyr Asn Gln Lys Phe
    50                  55                  60
```

```
Lys Asp Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Ile Tyr Phe Tyr Gly Thr Thr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

<210> 66
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> ustekinumab heavy chain

<400> 66

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

```
        35                  40                  45
Gly Ile Met Ser Pro Val Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
    50                  55                  60
Gln Gly Gln Val Thr Met Ser Val Asp Lys Ser Ile Thr Thr Ala Tyr
65                  70                  75                  80
Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Arg Arg Pro Gly Gln Gly Tyr Phe Asp Phe Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 67
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1 Hinge+ Ipilimumab light chain

<400> 67
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ggcagcggtc ccctgggtgt gagagcggcc cagccggccg aaattgtgtt gacgcagtct 120

ccaggcaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag ggccagtcag 180

agtgttggca gcagctactt agcctggtac cagcagaaac ctggccaggc tcccaggctc 240

ctcatctatg gtgcattcag cagggccact ggcatcccag acaggttcag tggcagtggg 300

tctgggacag acttcactct caccatcagc agactggagc ctgaagattt tgcagtgtat 360

tactgtcagc agtatggtag ctcaccgtgg acgttcggcc aagggaccaa ggtggaaatc 420

aaacggactg tggctgcacc atctgtcttc atcttcccgc catctgatga gcagttgaaa 480

tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta 540

cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 600

gacagcaagg acagcaccta cagcctcagc agcaccctga cgctgagcaa agcagactac 660

gagaaacaca aactctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca 720

aagagcttca acaggggaga gtgc 744

<210> 68
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1 Hinge+ Ipilimumab heavy chain

<400> 68
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ggcggcagcg gtcccctggg tgtgagaaga tctcaggtgc agctggtgga gtctgggga 120

ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcctctgg attcaccttc 180

agtagctata ctatgcactg ggtccgccag gctccaggca aggggctgga gtgggtgaca 240

tttatatcat atgatggaaa caataaatac tacgcagact ccgtgaaggg ccgattcacc 300

atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 360

gacacggcta tatattactg tgcgaggacc ggctggctgg ggcctttga ctactggggc 420

cagggaaccc tggtcaccgt ctcctcagcc tccaccaagg gaccatcggt cttccccctg 480

gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 540

tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 600

accttcccgg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 660

ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacaa gcccagcaac 720

accaaggtcg acaagaaagt tgagcccaaa tcttgtgaca aaactcacac atgcccaccg 780

tgcccagcac ccgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag 840

gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 900

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 960

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aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1320

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1380

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaataa 1440

<210> 69
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG2 Hinge+ Ipilimumab light chain

<400> 69
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cccctgggtg tgagagcggc ccagccggcc gaaattgtgt tgacgcagtc tccaggcacc 120

ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 180

agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggct cctcatctat 240

ggtgcattca gcagggccac tggcatccca gacaggttca gtggcagtgg gtctgggaca 300

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgta ttactgtcag 360

cagtatggta gctcaccgtg gacgttcggc caagggacca aggtggaaat caaacggact 420

gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 480

gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 540

gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 600

gacagcacct acagcctcag cagcaccctg acgctgagca aagcagacta cgagaaacac 660

aaactctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 720

aacaggggag agtgc 735

<210> 70
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG2 Hinge+ Ipilimumab heavy chain

<400> 70
gagcgcaaat gttgtgtcga gtgcccaccg tgcccaggcg gccgcggcgg cggcggcagc 60

ggtcccctgg gtgtgagaag atctcaggtg cagctggtgg agtctggggg aggcgtggtc 120

cagcctggga ggtccctgag actctcctgt gcagcctctg gattcacctt cagtagctat 180

actatgcact gggtccgcca ggctccaggc aaggggctgg agtgggtgac atttatatca 240

tatgatggaa acaataaata ctacgcagac tccgtgaagg gccgattcac catctccaga 300

gacaattcca agaacacgct gtatctgcaa atgaacagcc tgagagctga ggacacggct 360

atatattact gtgcgaggac cggctggctg gggccctttg actactgggg ccagggaacc 420

ctggtcaccg tctcctcagc ctccaccaag ggaccatcgg tcttcccccc ggcaccctcc 480

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 540

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtc 720

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780

cccgaactcc tgggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 840

atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 960

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1020

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1080

atcgagaaaa ccatctccaa agccaagggg cagccccgag aaccacaggt gtacaccctg 1140

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1260

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gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380

ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaata a 1431

<210> 71
<211> 885
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG3 Hinge+ Ipilimumab light chain

<400> 71
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tcttgtgaca cacctccccc gtgcccacgg tgcccagagc ccaaatcttg tgacacacct 120

cccccatgcc cacggtgccc agagcccaaa tcttgtgaca cacctccccc gtgcccaagg 180

tgcccagtta acggcggcgg cggcagcggt cccctgggtg tgagagcggc ccagccggcc 240

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 300

ctctcctgca gggccagtca gagtgttggc agcagctact tagcctggta ccagcagaaa 360

cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 420

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 480

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 540

caagggacca aggtggaaat caaacggact gtggctgcac catctgtctt catcttcccg 600

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 660

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 720

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 780

acgctgagca aagcagacta cgagaaacac aaactctacg cctgcgaagt cacccatcag 840

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgc 885

<210> 72
<211> 1581
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG3 Hinge+ Ipilimumab heavy chain

<400> 72
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tcttgtgaca cacctccccc gtgcccacgg tgcccagagc ccaaatcttg tgacacacct 120

cccccatgcc cacggtgccc agagcccaaa tcttgtgaca cacctccccc gtgcccaagg 180

tgcccaggcg gccgcggcgg cggcggcagc ggtcccctgg gtgtgagaag atctcaggtg 240

cagctggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag actctcctgt 300

gcagcctctg gattcacctt cagtagctat actatgcact gggtccgcca ggctccaggc 360

aaggggctgg agtgggtgac atttatatca tatgatggaa acaataaata ctacgcagac 420

tccgtgaagg gccgattcac catctccaga gacaattcca agaacacgct gtatctgcaa 480

atgaacagcc tgagagctga ggacacggct atatattact gtgcgaggac cggctggctg 540

gggccctttg actactgggg ccagggaacc ctggtcaccg tctcctcagc ctccaccaag 600

ggaccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 660

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 720

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aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaagggg 1260

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1320

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1380

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1440

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1500

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1560

tccctgtctc cgggtaaata a 1581

<210> 73
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG4 Hinge+ Ipilimumab light chain

<400> 73
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cccctgggtg tgagagcggc ccagccggcc gaaattgtgt tgacgcagtc tccaggcacc 120

ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 180

agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggct cctcatctat 240

ggtgcattca gcagggccac tggcatccca gacaggttca gtggcagtgg gtctgggaca 300

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgta ttactgtcag 360

cagtatggta gctcaccgtg gacgttcggc caagggacca aggtggaaat caaacggact 420

gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 480

gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 540

gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 600

gacagcacct acagcctcag cagcaccctg acgctgagca aagcagacta cgagaaacac 660

aaactctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 720

aacaggggag agtgc 735

<210> 74
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG4 Hinge+ Ipilimumab heavy chain

<400> 74
gagtccaaat atggtccccc atgcccatca tgcccaggcg gccgcggcgg cggcggcagc 60

ggtcccctgg gtgtgagaag atctcaggtg cagctggtgg agtctggggg aggcgtggtc 120

cagcctggga ggtccctgag actctcctgt gcagcctctg gattcacctt cagtagctat 180

actatgcact gggtccgcca ggctccaggc aaggggctgg agtgggtgac atttatatca 240

tatgatggaa acaataaata ctacgcagac tccgtgaagg gccgattcac catctccaga 300

gacaattcca agaacacgct gtatctgcaa atgaacagcc tgagagctga ggacacggct 360

atatattact gtgcgaggac cggctggctg gggccctttg actactgggg ccagggaacc 420

ctggtcaccg tctcctcagc ctccaccaag ggaccatcgg tcttcccccc ggcaccctcc 480

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 540

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtc 720

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780

cccgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 840

atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900

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cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1020

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1080

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cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1260

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gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380

ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaata a 1431

<210> 75
<211> 768
<212> DNA
<213> Artificial Sequence

<220>
<223> IgA1 Hinge+ Ipilimumab light chain

<400> 75
ccagttccct caactccacc taccccatct ccctcaactc cacctacccc atctccctca 60

tgctgccacg ttaacggcgg cggcggcagc ggtcccctgg gtgtgagagc ggcccagccg 120

gccgaaattg tgttgacgca gtctccaggc accctgtctt tgtctccagg ggaaagagcc 180

accctctcct gcagggccag tcagagtgtt ggcagcagct acttagcctg gtaccagcag 240

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gagcctgaag attttgcagt gtattactgt cagcagtatg gtagctcacc gtggacgttc 420

ggccaaggga ccaaggtgga aatcaaacgg actgtggctg caccatctgt cttcatcttc 480

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 540

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 600

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 660

ctgacgctga gcaaagcaga ctacgagaaa cacaaactct acgcctgcga agtcacccat 720

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgc 768

<210> 76
<211> 768
<212> DNA
<213> Artificial Sequence

<220>
<223> IgA1 Hinge+ Ipilimumab heavy chain

<400> 76
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gagcctgaag attttgcagt gtattactgt cagcagtatg gtagctcacc gtggacgttc 420

ggccaaggga ccaaggtgga aatcaaacgg actgtggctg caccatctgt cttcatcttc 480

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 540

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 600

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 660

ctgacgctga gcaaagcaga ctacgagaaa cacaaactct acgcctgcga agtcacccat 720

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgc 768

<210> 77
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> IgA2 Hinge+ Ipilimumab light chain

<400> 77
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ggtgtgagag cggcccagcc ggccgaaatt gtgttgacgc agtctccagg caccctgtct 120

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ggtagctcac cgtggacgtt cggccaaggg accaaggtgg aaatcaaacg gactgtggct 420

gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 480

gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 540

aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 600

acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaactc 660

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 720

ggagagtgc 729

<210> 78
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> IgA2 Hinge+ Ipilimumab heavy chain

<400> 78
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ggtgtgagag cggcccagcc ggccgaaatt gtgttgacgc agtctccagg caccctgtct 120

ttgtctccag gggaaagagc caccctctcc tgcagggcca gtcagagtgt tggcagcagc 180

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ttcagcaggg ccactggcat cccagacagg ttcagtggca gtgggtctgg gacagacttc 300

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gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 480

gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 540

aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 600

acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaactc 660

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 720

ggagagtgc 729