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<170> PatentIn version 3.5

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<212> PRT
<213> Homo sapiens
<223> MEDI4736 VL; Sequence 77 from PCT/US2010/058007

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

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

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

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

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

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

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<212> PRT
<213> Homo sapiens
<223> MEDI4736 VH; Sequence 72 from PCT/US2010/058007

<400> 4

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1 5 10 15

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<212> PRT
<213> Homo sapiens
<223> MEDI4736 VH CDR1; Sequence 73 from PCT/US2010/058007

<400> 5

Arg Tyr Trp Met Ser
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<210> 6
<211> 17
<212> PRT
<213> Homo sapiens
<223> MEDI4736 VH CDR2;Sequence 74 from PCT/US2010/058007

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Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 7
<211> 12
<212> PRT
<213> Homo sapiens
<223> MEDI4736 VH CDR3;Sequence 75 from PCT/US2010/058007

<400> 7

Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr
1 5 10

<210> 8
<211> 12
<212> PRT
<213> Homo sapiens

<223> MEDI4736 VL CDR1;Sequence 78 from PCT/US2010/058007

<400> 8

Arg Ala Ser Gln Arg Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 9
<211> 7
<212> PRT
<213> Homo sapiens
<223> MEDI4736 VL CDR2;Sequence 79 from PCT/US2010/058007

<400> 9

Asp Ala Ser Ser Arg Ala Thr
1 5

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens
<223> MEDI4736 VL CDR3;Sequence 80 from PCT/US2010/058007

<400> 10

Gln Gln Tyr Gly Ser Leu Pro Trp Thr
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<213> Artificial sequence
<223> Synthetic oligonucleotide (murine STAT3 ASO)

<400> 11
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<223> Synthetic oligonucleotide (murine control ASO)

<400> 12
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<210> 13
<211> 139
<212> PRT
<213> Homo sapiens
<223> Tremelimumab VL

<400> 13

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

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
50 55 60

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

Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys
85 90 95

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
100 105 110

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
115 120 125

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135

<210> 14
<211> 167
<212> PRT
<213> Homo sapiens
<223> Tremelimumab VH

<400> 14

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

Gly Lys Gly Leu Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn
35 40 45

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

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
65 70 75 80

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro Arg Gly Ala Thr Leu
85 90 95

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

Ala Leu Thr Ser Gly Val His
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<210> 15
<211> 10
<212> PRT
<213> Homo sapiens
<223> Tremelimumab VH CDR1

<400> 15

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

<210> 16
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<212> PRT
<213> Homo sapiens
<223> Tremelimumab VH CDR2

<400> 16

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
1 5 10 15

<210> 17
<211> 16
<212> PRT
<213> Homo sapiens
<223> Tremelimumab VH CDR3

<400> 17

Asp Pro Arg Gly Ala Thr Leu Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
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<210> 18
<211> 11
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<213> Homo sapiens
<223> Tremelimumab VL CDR1

<400> 18

Arg Ala Ser Gln Ser Ile Asn Ser Tyr Leu Asp
1 5 10

<210> 19
<211> 7
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Ala Ala Ser Ser Leu Gln Ser
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<213> Homo sapiens
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<400> 20

Gln Gln Tyr Tyr Ser Thr Pro Phe Thr
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<210> 21
<211> 223
<212> PRT
<213> Homo sapiens
<223> CTLA-4 polypeptide - GenBank Accession No. AAL07473.1

<400> 21

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Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60

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

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110

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Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
        115                 120                 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
    130                 135                 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145                 150                 155                 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
                165                 170                 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
            180                 185                 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
        195                 200                 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
    210                 215                 220
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<213> Homo sapiens
<223> OX40 polypeptide

<400> 22

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Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
        35                  40                  45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
    50                  55                  60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65                  70                  75                  80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
                85                  90                  95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
            100                 105                 110
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Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
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Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
260 265 270

Thr Leu Ala Lys Ile
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<210> 23
<211> 183
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<213> Homo sapiens
<223> OX40 ligand

<400> 23

Met Glu Arg Val Gln Pro Leu Glu Glu Asn Val Gly Asn Ala Ala Arg
1 5 10 15

Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val Ala Ser Val Ile Gln
20 25 30

Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser
35 40 45

Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val
50 55 60

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

Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn
85 90 95

Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu
100 105 110

Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln
115 120 125

Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr
130 135 140

Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu
145 150 155 160

Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn
165 170 175

Pro Gly Glu Phe Cys Val Leu
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<210> 24
<211> 410
<212> PRT
<213> Artificial sequence
<223> OX40 ligand protein; corresponds to SEQ ID NO: 8 in U.S. Patent 7,959,925

<400> 24

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35 40 45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn

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65                  70                  75                  80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                85                  90                  95

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

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        115                 120                 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    130                 135                 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145                 150                 155                 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                165                 170                 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            180                 185                 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        195                 200                 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    210                 215                 220

Ser Leu Ser Pro Gly Lys Glu Leu Leu Gly Gly Gly Ser Ile Lys Gln
225                 230                 235                 240

Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
                245                 250                 255

Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly His Gly
            260                 265                 270

Gly Gly Ser Asn Ser Gln Val Ser His Arg Tyr Pro Arg Phe Gln Ser
        275                 280                 285

Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu
    290                 295                 300

Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val
305                 310                 315                 320

Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe
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325 330 335

Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro
340 345 350

Leu Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala
355 360 365

Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn
370 375 380

Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile
385 390 395 400

His Gln Asn Pro Gly Glu Phe Cys Val Leu
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<213> Homo sapiens
<223> humanised anti-OX40 antibody VL
<400> 25

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 Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

<210> 26
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<213> Homo sapiens
<223> humanised anti-OX40 antibody VL
<400> 26

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1               5                  10                  15

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

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

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

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

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

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


<210>  27
<211>  121
<212>  PRT
<213>  Homo sapiens
<223>  humanised anti-OX40 antibody VH
<400>  27

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

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

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

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

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

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

Arg Tyr Lys Tyr Asp Tyr Asp Gly Gly His Ala Met Asp Tyr Trp Gly
            100                 105                 110
```

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 28
<211> 451
<212> PRT
<213> Homo sapiens
<223> humanised anti-Ox40 antibody heavy chain

<400> 28

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

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

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

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

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

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

Arg Tyr Lys Tyr Asp Tyr Asp Gly Gly His Ala Met 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 Arg 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 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

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> 29
<211> 214
<212> PRT
<213> Homo sapiens
<223> humanised anti-OX40 antibody Light chain

<400> 29

```
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 Asp Ile Ser Asn Tyr
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 30
<211> 412
<212> PRT
<213> Homo sapiens
<223> humanised anti-OX40 antibody

<400> 30

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Ala Pro Leu Ala Thr 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 Glu Leu Leu Gly Gly Gly Ser Ile
225                 230                 235                 240

Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
                245                 250                 255

Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly
            260                 265                 270

His Gly Gly Gly Ser Asn Ser Gln Val Ser His Arg Tyr Pro Arg Phe
        275                 280                 285

Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe
    290                 295                 300

Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn
305                 310                 315                 320

Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly
                325                 330                 335

Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu
            340                 345                 350

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

Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr
    370                 375                 380

Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile
385                 390                 395                 400

Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu
                405                 410
```

<210> 31
<211> 1206
<212> DNA
<213> Homo sapiens
<223> DNA Sequence of huIgG4FcPTF2OX40L (5′ to 3′ Open Reading Frame)

<400> 31

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gagagcaagt acggccctcc ctgcccccct tgccctgccc ccgagttcct gggcggacct       60

agcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagcag aacccccgag      120
```

gtgacctgcg tggtggtgga cgtgtcccag gaggaccccg aggtccagtt taattggtac 180

gtggacggcg tggaagtgca taacgccaag accaagccca gagaggagca gttcaacagc 240

acctacagag tggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 300

tacaagtgca aggtctccaa caagggcctg cctagcagca tcgagaagac catcagcaag 360

gccaagggcc agccacggga gccccaggtc tacaccctgc cacctagcca agaggagatg 420

accaagaacc aggtgtccct gacctgtctg gtgaaaggct tctatcccag cgatatcgcc 480

gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 540

gacagcgacg gcagcttctt cctgtactcc agactgaccg tggacaagtc cagatggcag 600

gagggcaacg tcttcagctg ctccgtgatg cacgaggccc tgcacaacca ctacacccag 660

aagtccctga gcctgagcct gggcaaggac caggataaga tcgaggctct gtcctccaag 720

gtgcagcagc tggaacggtc catcggcctg aaggacctgg ccatggctga cctggaacag 780

aaagtgctgg aaatggaagc ctccacacag gtgtcacaca gataccccg gatccagtcc 840

attaaggtgc agttcaccga gtacaagaaa gagaagggct ttatcctgac ctcccagaaa 900

gaggacgaga tcatgaaggt gcagaacaac tccgtgatca tcaactgcga cgggttctac 960

ctgatctccc tgaagggcta cttcagccag gaagtgaaca tctccctgca ctaccagaag 1020

gacgaggaac ccctgttcca gctgaagaaa gtgcggagcg tgaactccct gatggtggcc 1080

tctctgacct acaaggacaa ggtgtacctg aacgtgacca ccgacaacac ctccctggac 1140

gacttccacg tgaacggcgg cgagctgatc ctgatccacc agaaccctgg cgagttctgc 1200

gtgctg 1206

<210> 32
<211> 402
<212> PRT
<213> Homo Sapiens
<223> Amino Acid Sequence of huIgG4FcPTF2OX40L (N to C terminus)

<400> 32

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 Asp Gln Asp Lys Ile Glu Ala Leu Ser Ser Lys
225 230 235 240

Val Gln Gln Leu Glu Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala
245 250 255

Asp Leu Glu Gln Lys Val Leu Glu Met Glu Ala Ser Thr Gln Val Ser
260 265 270

His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr
275 280 285

Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile
290 295 300

Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr
305 310 315 320

Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu

325 330 335

His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys Val Arg
340 345 350

Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp Lys Val
355 360 365

Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe His Val
370 375 380

Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu Phe Cys
385 390 395 400

Val Leu

<210> 33
<211> 1206
<212> DNA
<213> Homo sapiens
<223> DNA Sequence of huIgG4FcPTF2OX40L F180A (5′ to 3′ Open Reading Frame)

<400> 33
gagagcaagt acggccctcc ctgcccccct tgccctgccc ccgagttcct gggcggacct 60

agcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagcag aacccccgag 120

gtgacctgcg tggtggtgga cgtgtcccag gaggaccccg aggtccagtt taattggtac 180

gtggacggcg tggaagtgca taacgccaag accaagccca gagaggagca gttcaacagc 240

acctacagag tggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 300

tacaagtgca aggtctccaa caagggcctg cctagcagca tcgagaagac catcagcaag 360

gccaagggcc agccacggga gccccaggtc tacaccctgc cacctagcca agaggagatg 420

accaagaacc aggtgtccct gacctgtctg gtgaaaggct tctatcccag cgatatcgcc 480

gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 540

gacagcgacg gcagcttctt cctgtactcc agactgaccg tggacaagtc cagatggcag 600

gagggcaacg tcttcagctg ctccgtgatg cacgaggccc tgcacaacca ctacacccag 660

aagtccctga gcctgagcct gggcaaggac caggataaga tcgaggctct gtcctccaag 720

gtgcagcagc tggaacggtc catcggcctg aaggacctgg ccatggctga cctggaacag 780

aaagtgctgg aaatggaagc ctccacacag gtgtcacaca gataccccg gatccagtcc 840

attaaggtgc agttcaccga gtacaagaaa gagaagggct ttatcctgac ctcccagaaa 900

gaggacgaga tcatgaaggt gcagaacaac tccgtgatca tcaactgcga cgggttctac 960

ctgatctccc tgaagggcta cttcagccag gaagtgaaca tctccctgca ctaccagaag 1020

gacgaggaac ccctgttcca gctgaagaaa gtgcggagcg tgaactccct gatggtggcc 1080

tctctgacct acaaggacaa ggtgtacctg aacgtgacca ccgacaacac ctccctggac 1140

gacttccacg tgaacggcgg cgagctgatc ctgatccacc agaaccctgg cgaggcctgc 1200

gtgctg 1206

<210> 34
<211> 1206
<212> PRT
<213> Homo Sapiens
<223> Amino Acid Sequence of huIgG4PFcTF2OX40L F180A (N to C terminus)

<400> 34

Gly Ala Gly Ala Gly Cys Ala Ala Gly Thr Ala Cys Gly Gly Cys Cys
1 5 10 15

Cys Thr Cys Cys Cys Thr Gly Cys Cys Cys Cys Cys Cys Thr Thr Gly
20 25 30

Cys Cys Cys Thr Gly Cys Cys Cys Cys Cys Gly Ala Gly Thr Thr Cys
35 40 45

Cys Thr Gly Gly Gly Cys Gly Gly Ala Cys Cys Thr Ala Gly Cys Gly
50 55 60

Thr Gly Thr Thr Cys Cys Thr Gly Thr Thr Cys Cys Cys Cys Cys Cys
65 70 75 80

Cys Ala Ala Gly Cys Cys Cys Ala Ala Gly Gly Ala Cys Ala Cys Cys
85 90 95

Cys Thr Gly Ala Thr Gly Ala Thr Cys Ala Gly Cys Ala Gly Ala Ala
100 105 110

Cys Cys Cys Cys Cys Gly Ala Gly Gly Thr Gly Ala Cys Cys Thr Gly
115 120 125

Cys Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Cys Gly Thr Gly
130 135 140

Thr Cys Cys Cys Ala Gly Gly Ala Gly Gly Ala Cys Cys Cys Cys Gly
145 150 155 160

Ala Gly Gly Thr Cys Cys Ala Gly Thr Thr Thr Ala Ala Thr Thr Gly
165 170 175

Gly Thr Ala Cys Gly Thr Gly Gly Ala Cys Gly Gly Cys Gly Thr Gly
180 185 190

```
Gly Ala Ala Gly Thr Gly Cys Ala Thr Ala Ala Cys Gly Cys Cys Ala
        195                 200                 205

Ala Gly Ala Cys Cys Ala Ala Gly Cys Cys Cys Ala Gly Ala Gly Ala
    210                 215                 220

Gly Gly Ala Gly Cys Ala Gly Thr Thr Cys Ala Ala Cys Ala Gly Cys
225                 230                 235                 240

Ala Cys Cys Thr Ala Cys Ala Gly Ala Gly Thr Gly Gly Thr Gly Thr
                245                 250                 255

Cys Cys Gly Thr Gly Cys Thr Gly Ala Cys Cys Gly Thr Gly Cys Thr
            260                 265                 270

Gly Cys Ala Cys Cys Ala Gly Gly Ala Cys Thr Gly Gly Cys Thr Gly
        275                 280                 285

Ala Ala Cys Gly Gly Cys Ala Ala Gly Gly Ala Ala Thr Ala Cys Ala
    290                 295                 300

Ala Gly Thr Gly Cys Ala Ala Gly Gly Thr Cys Thr Cys Cys Ala Ala
305                 310                 315                 320

Cys Ala Ala Gly Gly Gly Cys Cys Thr Gly Cys Cys Thr Ala Gly Cys
                325                 330                 335

Ala Gly Cys Ala Thr Cys Gly Ala Gly Ala Ala Gly Ala Cys Cys Ala
            340                 345                 350

Thr Cys Ala Gly Cys Ala Ala Gly Gly Cys Cys Ala Ala Gly Gly Gly
        355                 360                 365

Cys Cys Ala Gly Cys Cys Ala Cys Gly Gly Gly Ala Gly Cys Cys Cys
    370                 375                 380

Cys Ala Gly Gly Thr Cys Thr Ala Cys Ala Cys Cys Cys Thr Gly Cys
385                 390                 395                 400

Cys Ala Cys Cys Thr Ala Gly Cys Cys Ala Ala Gly Ala Gly Gly Ala
                405                 410                 415

Gly Ala Thr Gly Ala Cys Cys Ala Ala Gly Ala Ala Cys Cys Ala Gly
            420                 425                 430

Gly Thr Gly Thr Cys Cys Cys Thr Gly Ala Cys Cys Thr Gly Thr Cys
        435                 440                 445
```

```
Thr Gly Gly Thr Gly Ala Ala Ala Gly Gly Cys Thr Thr Cys Thr Ala
    450                 455                 460

Thr Cys Cys Cys Ala Gly Cys Gly Ala Thr Ala Thr Cys Gly Cys Cys
465                 470                 475                 480

Gly Thr Gly Gly Ala Gly Thr Gly Gly Gly Ala Gly Ala Gly Cys Ala
                485                 490                 495

Ala Cys Gly Gly Cys Cys Ala Gly Cys Cys Cys Gly Ala Gly Ala Ala
            500                 505                 510

Cys Ala Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys Ala Cys Cys
        515                 520                 525

Cys Cys Cys Cys Cys Thr Gly Thr Gly Cys Thr Gly Gly Ala Cys Ala
    530                 535                 540

Gly Cys Gly Ala Cys Gly Gly Cys Ala Gly Cys Thr Thr Cys Thr Thr
545                 550                 555                 560

Cys Cys Thr Gly Thr Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly
                565                 570                 575

Ala Cys Cys Gly Thr Gly Gly Ala Cys Ala Ala Gly Thr Cys Cys Ala
            580                 585                 590

Gly Ala Thr Gly Gly Cys Ala Gly Gly Ala Gly Gly Gly Cys Ala Ala
        595                 600                 605

Cys Gly Thr Cys Thr Thr Cys Ala Gly Cys Thr Gly Cys Thr Cys Cys
    610                 615                 620

Gly Thr Gly Ala Thr Gly Cys Ala Cys Gly Ala Gly Gly Cys Cys Cys
625                 630                 635                 640

Thr Gly Cys Ala Cys Ala Ala Cys Cys Ala Cys Thr Ala Cys Ala Cys
                645                 650                 655

Cys Cys Ala Gly Ala Ala Gly Thr Cys Cys Cys Thr Gly Ala Gly Cys
            660                 665                 670

Cys Thr Gly Ala Gly Cys Cys Thr Gly Gly Gly Cys Ala Ala Gly Gly
        675                 680                 685

Ala Cys Cys Ala Gly Gly Ala Thr Ala Ala Gly Ala Thr Cys Gly Ala
    690                 695                 700
```

```
Gly Gly Cys Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Ala Gly
705                 710                 715                 720

Gly Thr Gly Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Cys
                725                 730                 735

Gly Gly Thr Cys Cys Ala Thr Cys Gly Gly Cys Cys Thr Gly Ala Ala
            740                 745                 750

Gly Gly Ala Cys Cys Thr Gly Gly Cys Cys Ala Thr Gly Gly Cys Thr
        755                 760                 765

Gly Ala Cys Cys Thr Gly Gly Ala Ala Cys Ala Gly Ala Ala Ala Gly
    770                 775                 780

Thr Gly Cys Thr Gly Gly Ala Ala Ala Thr Gly Gly Ala Ala Gly Cys
785                 790                 795                 800

Cys Thr Cys Cys Ala Cys Ala Cys Ala Gly Gly Thr Gly Thr Cys Ala
                805                 810                 815

Cys Ala Cys Ala Gly Ala Thr Ala Cys Cys Cys Cys Cys Gly Gly Ala
            820                 825                 830

Thr Cys Cys Ala Gly Thr Cys Cys Ala Thr Thr Ala Ala Gly Gly Thr
        835                 840                 845

Gly Cys Ala Gly Thr Thr Cys Ala Cys Cys Gly Ala Gly Thr Ala Cys
    850                 855                 860

Ala Ala Gly Ala Ala Ala Gly Ala Gly Ala Ala Gly Gly Gly Cys Thr
865                 870                 875                 880

Thr Thr Ala Thr Cys Cys Thr Gly Ala Cys Cys Thr Cys Cys Cys Ala
                885                 890                 895

Gly Ala Ala Ala Gly Ala Gly Gly Ala Cys Gly Ala Gly Ala Thr Cys
            900                 905                 910

Ala Thr Gly Ala Ala Gly Gly Thr Gly Cys Ala Gly Ala Ala Cys Ala
        915                 920                 925

Ala Cys Thr Cys Cys Gly Thr Gly Ala Thr Cys Ala Thr Cys Ala Ala
    930                 935                 940

Cys Thr Gly Cys Gly Ala Cys Gly Gly Gly Thr Thr Cys Thr Ala Cys
945                 950                 955                 960
```

```
Cys Thr Gly Ala Thr Cys Thr Cys Cys Cys Thr Gly Ala Ala Gly Gly
                965                 970                 975

Gly Cys Thr Ala Cys Thr Thr Cys Ala Gly Cys Cys Ala Gly Gly Ala
            980                 985                 990

Ala Gly Thr Gly Ala Ala Cys Ala  Thr Cys Thr Cys Cys  Cys Thr Gly
        995                 1000                1005

Cys Ala  Cys Thr Ala Cys Cys  Ala Gly Ala Ala Gly  Gly Ala Cys
    1010                1015                1020

Gly Ala  Gly Gly Ala Ala Cys  Cys Cys Cys Thr Gly  Thr Thr Cys
    1025                1030                1035

Cys Ala  Gly Cys Thr Gly Ala  Ala Gly Ala Ala Ala  Gly Thr Gly
    1040                1045                1050

Cys Gly  Gly Ala Gly Cys Gly  Thr Gly Ala Ala Cys  Thr Cys Cys
    1055                1060                1065

Cys Thr  Gly Ala Thr Gly Gly  Thr Gly Gly Cys Cys  Thr Cys Thr
    1070                1075                1080

Cys Thr  Gly Ala Cys Cys Thr  Ala Cys Ala Ala Gly  Gly Ala Cys
    1085                1090                1095

Ala Ala  Gly Gly Thr Gly Thr  Ala Cys Cys Thr Gly  Ala Ala Cys
    1100                1105                1110

Gly Thr  Gly Ala Cys Cys Ala  Cys Cys Gly Ala Cys  Ala Ala Cys
    1115                1120                1125

Ala Cys  Cys Thr Cys Cys Cys  Thr Gly Gly Ala Cys  Gly Ala Cys
    1130                1135                1140

Thr Thr  Cys Cys Ala Cys Gly  Thr Gly Ala Ala Cys  Gly Gly Cys
    1145                1150                1155

Gly Gly  Cys Gly Ala Gly Cys  Thr Gly Ala Thr Cys  Cys Thr Gly
    1160                1165                1170

Ala Thr  Cys Cys Ala Cys Cys  Ala Gly Ala Ala Cys  Cys Cys Thr
    1175                1180                1185

Gly Gly  Cys Gly Ala Gly Gly  Cys Cys Thr Gly Cys  Gly Thr Gly
    1190                1195                1200
```

Cys Thr Gly
1205

<210> 35
<211> 1200
<212> DNA
<213> Homo sapiens
<223> DNA Sequence of huIgG1TF2OX40L (5′ to 3′ Open Reading Frame)

<400> 35
gataagaccc acacctgtcc cccttgtcct gcccctgaac tgctgggcgg accttccgtg 60

ttcctgttcc ccccaaagcc caaggacacc ctgatgatct cccggacccc cgaagtgacc 120

tgcgtggtgg tggatgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa ctccacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggattggc tgaacggcaa agagtacaag 300

tgcaaggtgt ccaacaaggc cctgcctgcc cccatcgaaa agaccatctc caaggccaag 360

ggccagcccc gggaacccca ggtgtacaca ctgcccccta gccgggaaga gatgaccaag 420

aaccaggtgt ccctgacctg tctcgtgaag ggcttctacc cctccgatat cgccgtggaa 480

tgggagtcca acggccagcc tgagaacaac tacaagacca ccccccctgt gctggactcc 540

gacggctcat tcttcctgta ctccaagctg acagtggaca agtcccggtg gcagcagggc 600

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 660

ctgtccctga gccccggcaa ggaccaggat aagatcgagg ctctgtcctc caaggtgcag 720

cagctggaac ggtccatcgg cctgaaggac ctggccatgg ctgacctgga acagaaagtg 780

ctggaaatgg aagcctccac acaggtgtca cacagatacc cccggatcca gtccattaag 840

gtgcagttca ccgagtacaa gaaagagaag ggctttatcc tgacctccca gaaagaggac 900

gagatcatga aggtgcagaa caactccgtg atcatcaact gcgacgggtt ctacctgatc 960

tccctgaagg gctacttcag ccaggaagtg aacatctccc tgcactacca gaaggacgag 1020

gaacccctgt tccagctgaa gaaagtgcgg agcgtgaact ccctgatggt ggcctctctg 1080

acctacaagg acaaggtgta cctgaacgtg accaccgaca acacctccct ggacgacttc 1140

cacgtgaacg gcggcgagct gatcctgatc caccagaacc ctggcgagtt ctgcgtgctg 1200

<210> 36
<211> 400
<212> PRT
<213> Homo sapiens
<223> Amino Acid Sequence of huIgG1FcTF2OX40L (N to C terminus)

<400> 36

Asp Lys Thr His Thr Cys Pro Pro 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 Glu Glu Met 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 Asp Gln Asp Lys Ile Glu Ala Leu Ser Ser Lys Val Gln
225                 230                 235                 240

Gln Leu Glu Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala Asp Leu
                245                 250                 255

Glu Gln Lys Val Leu Glu Met Glu Ala Ser Thr Gln Val Ser His Arg
```

```
            260                 265                 270

Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys
        275                 280                 285

Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys
    290                 295                 300

Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile
305                 310                 315                 320

Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr
                325                 330                 335

Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val
            340                 345                 350

Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu
        355                 360                 365

Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly
    370                 375                 380

Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu
385                 390                 395                 400
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<210> 37
<211> 1248
<212> DNA
<213> Mus musculis
<223> DNA Sequence of mouse construct mIgG1mTF2mOX40L (5′ to 3′ Open Reading Frame)

<400> 37

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gtgcctagag attgcggctg caagccctgc atctgcaccg tgcccgaggt gtccagcgtg       60

ttcatcttcc cacccaagcc caaggacgtg ctgaccatca ccctgacccc caaagtgacc      120

tgcgtggtgg tggacatcag caaggacgac cccgaggtgc agttcagttg gttcgtggac      180

gacgtggaag tgcacaccgc ccagacccag cccagagagg aacagttcaa cagcaccttc      240

agaagcgtgt ccgagctgcc catcatgcac caggactggc tgaacggcaa agaattcaag      300

tgcagagtga acagcgccgc cttccctgcc cccatcgaga aaaccatcag caagaccaag      360

ggcagaccca aggcccccca ggtgtacacc atccccccac ccaaagaaca gatggccaag      420

gacaaggtgt ccctgacctg catgatcacc gatttcttcc cagaggacat caccgtggaa      480

tggcagtgga acggccagcc cgccgagaac tacaagaaca cccagcccat catggacacc      540

gacggcagct acttcgtgta cagcaagctg aacgtgcaga agtccaactg ggaggccggc      600

aacaccttca cctgtagcgt gctgcacgag ggcctgcaca accaccacac cgagaagtcc      660
```

ctgagccaca gccccggcaa gcggctggac caggacaaga tcgaggccct gagcaacaag 720

gtgcagcagc tggaacggtc tatcggcctg aaggacctgg ctatggccga cctggaacag 780

aaagtgtctg agctggaagt gtccaccagc agccccgcca aggaccctcc catccagaga 840

ctgagaggcg ccgtgaccag atgcgaggac ggccagctgt tcatcagcag ctacaagaac 900

gagtaccaga ccatggaagt gcagaacaac agcgtggtca tcaagtgcga cggcctgtac 960

atcatctacc tcaagggcag cttcttccag gaagtgaaga tcgacctgca cttcagagag 1020

gaccacaacc ccatcagcat ccccatgctg aacgacggca gacggatcgt gttcaccgtg 1080

gtggctagcc tggccttcaa ggacaaagtg tatctgaccg tgaacgcccc cgacaccctg 1140

tgcgagcatc tgcagatcaa cgacggcgag ctgatcgtgg tgcagctgac ccccggctac 1200

tgtgcccctg agggcagcta ccacagcacc gtgaaccagg tgcccctg 1248

<210> 38
<211> 416
<212> PRT
<213> Mus musculis
<223> Amino Acid Sequence of mouse construct mIgG1FcmTF2mOX40L (N to C terminus)

<400> 38

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
1 5 10 15

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
20 25 30

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
35 40 45

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
50 55 60

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
65 70 75 80

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
115 120 125

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
130 135 140

```
Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
145                 150                 155                 160

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
                165                 170                 175

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
            180                 185                 190

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
        195                 200                 205

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
    210                 215                 220

Pro Gly Lys Arg Leu Asp Gln Asp Lys Ile Glu Ala Leu Ser Asn Lys
225                 230                 235                 240

Val Gln Gln Leu Glu Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala
                245                 250                 255

Asp Leu Glu Gln Lys Val Ser Glu Leu Glu Val Ser Thr Ser Ser Pro
            260                 265                 270

Ala Lys Asp Pro Pro Ile Gln Arg Leu Arg Gly Ala Val Thr Arg Cys
        275                 280                 285

Glu Asp Gly Gln Leu Phe Ile Ser Ser Tyr Lys Asn Glu Tyr Gln Thr
    290                 295                 300

Met Glu Val Gln Asn Asn Ser Val Val Ile Lys Cys Asp Gly Leu Tyr
305                 310                 315                 320

Ile Ile Tyr Leu Lys Gly Ser Phe Phe Gln Glu Val Lys Ile Asp Leu
                325                 330                 335

His Phe Arg Glu Asp His Asn Pro Ile Ser Ile Pro Met Leu Asn Asp
            340                 345                 350

Gly Arg Arg Ile Val Phe Thr Val Val Ala Ser Leu Ala Phe Lys Asp
        355                 360                 365

Lys Val Tyr Leu Thr Val Asn Ala Pro Asp Thr Leu Cys Glu His Leu
    370                 375                 380

Gln Ile Asn Asp Gly Glu Leu Ile Val Val Gln Leu Thr Pro Gly Tyr
385                 390                 395                 400
```

Cys Ala Pro Glu Gly Ser Tyr His Ser Thr Val Asn Gln Val Pro Leu
405 410 415