SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Combination therapy of antibodies against human CSF-1R and uses thereof

<130> 30886 WO

<150> EP12158519.4
<151> 2012-03-08

<160> 91

<170> PatentIn version 3.5

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Asp Gln Arg Leu Tyr Phe Asp Val
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Gly Ala Ser Asn Arg Tyr Thr

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

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

Asp Ile Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met
50 55 60

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

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

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

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<400> 8

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

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

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

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

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

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

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

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Asp Pro Arg Leu Tyr Phe Asp
1 5

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Val Ile Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Gly Phe Met Ser
1 5 10 15

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<400> 11

Ser Phe Asp Ile Ser
1 5

<210> 12
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<400> 12

Gly Gln Thr Phe Ser Tyr Pro Thr
1 5

<210> 13
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<400> 13

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 14
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<400> 14

Lys Ala Ser Glu Asp Val Val Thr Tyr Val Ser
1 5 10

<210> 15
<211> 116
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<213> *Mus musculus*

<400> 15

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

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

Asp Ile Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Gly Phe Met
50 55 60

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

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

Arg Asp Pro Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

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<400> 16

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

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

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

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

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

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

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

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<400> 17

Asp Gln Arg Leu Tyr Phe Asp Val
1 5

<210> 18
<211> 16
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, hMab 2F11-c11

<400> 18

Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met Ser
1 5 10 15

<210> 19
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, hMab 2F11-c11

<400> 19

Thr Tyr Asp Ile Ser
1 5

<210> 20
<211> 8

<212> PRT
<213> Artificial

<220>
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<400> 20

Gly Gln Ser Phe Ser Tyr Pro Thr
1 5

<210> 21
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<400> 21

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 22
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<213> Artificial

<220>
<223> light chain CDR1, hMab 2F11-c11

<400> 22

Arg Ala Ser Glu Asp Val Asn Thr Tyr Val Ser
1 5 10

<210> 23
<211> 116
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, hMab 2F11-c11

<400> 23

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

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

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

Gly Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met
50 55 60

Ser Arg Val Thr Ile Thr Lys Asp Glu Ser Thr Ser Thr Ala Tyr Met
65 70 75 80

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

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 24
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, hMab 2F11-c11

<400> 24

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 Glu Asp Val Asn Thr Tyr
20 25 30

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

Tyr Gly Ala Ser Asn Arg Tyr Thr 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 Gly Gln Ser Phe Ser Tyr Pro Thr
85 90 95

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

<210> 25
<211> 8
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, hMab 2F11-d8

<400> 25

Asp Gln Arg Leu Tyr Phe Asp Val
1 5

<210> 26
<211> 16

<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, hMab 2F11-d8

<400> 26

Val Ile Trp Thr Asp Gly Gly Ala Asn Tyr Ala Gln Lys Phe Gln Gly
1 5 10 15

<210> 27
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, hMab 2F11-d8

<400> 27

Thr Tyr Asp Ile Ser
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, hMab 2F11-d8

<400> 28

Gly Gln Ser Phe Ser Tyr Pro Thr
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, hMab 2F11-d8

<400> 29

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 30
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, hMab 2F11-d8

<400> 30

Lys Ala Ser Glu Asp Val Asn Thr Tyr Val Ser
1 5 10

<210> 31
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<220>
<223> heavy chain variable domain, hMab 2F11-d8

<400> 31

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

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

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

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

Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met
65 70 75 80

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

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 32
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, hMab 2F11-d8

<400> 32

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

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

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

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

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

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

<210> 33
<211> 8
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, hMab 2F11-e7

<400> 33

Asp Gln Arg Leu Tyr Phe Asp Val
1 5

<210> 34
<211> 16
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, hMab 2F11-e7

<400> 34

Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Ala Gln Lys Leu Gln Gly
1 5 10 15

<210> 35
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<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, hMab 2F11-e7

<400> 35

Ser Tyr Asp Ile Ser
1 5

<210> 36
<211> 8
<212> PRT
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<220>
<223> light chain CDR3, hMab 2F11-e7

<400> 36

Gln Gln Ser Phe Ser Tyr Pro Thr
1 5

<210> 37
<211> 7
<212> PRT
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<220>
<223> light chain CDR2, hMab 2F11-e7

<400> 37

Ala Ala Ser Asn Arg Tyr Thr
1 5

<210> 38
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, hMab 2F11-e7

<400> 38

Arg Ala Ser Glu Asp Val Asn Thr Tyr Val Ser
1 5 10

<210> 39
<211> 116
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, hMab 2F11-e7

<400> 39

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

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

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

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

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

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

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 40
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, hMab 2F11-e7

<400> 40

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 Glu Asp Val Asn Thr Tyr
20 25 30

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

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

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

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

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

<210> 41
<211> 8
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, hMab 2F11-f12

<400> 41

Asp Gln Arg Leu Tyr Phe Asp Val
1 5

<210> 42
<211> 16
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, hMab 2F11-f12

<400> 42

Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met Ser
1 5 10 15

<210> 43
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, hMab 2F11-f12

<400> 43

Thr Tyr Asp Ile Ser
1 5

<210> 44
<211> 8
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, hMab 2F11-f12

<400> 44

Gly Gln Ser Phe Ser Tyr Pro Thr
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, hMab 2F11-f12

<400> 45

Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 46
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, hMab 2F11-f12

<400> 46

Arg Ala Ser Glu Asp Val Asn Thr Tyr Val Ser
1 5 10

<210> 47
<211> 116
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, hMab 2F11-f12

<400> 47

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

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

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

Gly Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met
    50                  55                  60

Ser Arg Val Thr Ile Thr Lys Asp Glu Ser Thr Ser Thr Ala Tyr Met
65                  70                  75                  80

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

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
            100                 105                 110

Thr Val Ser Ser
        115
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<210> 48
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, hMab 2F11-f12

<400> 48

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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 Glu Asp Val Asn Thr Tyr
            20                  25                  30

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

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 49
<211> 8
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, hMab 2F11-g1

<400> 49

Asp Gln Arg Leu Tyr Phe Asp Val
1 5

<210> 50
<211> 16
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, hMab 2F11-g1

<400> 50

Val Ile Trp Thr Asp Gly Gly Thr Asn Tyr Asn Ser Pro Leu Lys Ser
1 5 10 15

<210> 51
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, hMab 2F11-g1

<400> 51

Thr Tyr Asp Ile Ser
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, hMab 2F11-g1

<400> 52

Gly Gln Ser Phe Ser Tyr Pro Thr
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, hMab 2F11-g1

<400> 53

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 54
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, hMab 2F11-g1

<400> 54

Arg Ala Ser Glu Asp Val Asn Thr Tyr Leu Ala
1 5 10

<210> 55
<211> 116
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, hMab 2F11-g1

<400> 55

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

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

Asp Ile Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gln Arg Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 56
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, hMab 2F11-g1

<400> 56

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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 Glu Asp Val Asn Thr Tyr
20 25 30

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

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

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

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

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

<210> 57
<211> 107
<212> PRT
<213> Homo sapiens

<400> 57

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 58
<211> 330
<212> PRT
<213> Homo sapiens

<400> 58

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                  10                  15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
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Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 59
<211> 330
<212> PRT
<213> Artificial

<220>
<223> human heavy chain constant region derived from IgG1 mutated on L234A and L235A

<400> 59

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 60
<211> 327
<212> PRT
<213> Homo sapiens

<400> 60

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 61
<211> 327
<212> PRT
<213> Artificial

<220>
<223> human heavy chain constant region derived from IgG4 mutated onS228P

<400> 61

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
```

225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 62
<211> 972
<212> PRT
<213> *Homo sapiens*

<400> 62

Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
20 25 30

Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
35 40 45

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
50 55 60

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

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

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
100 105 110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
115 120 125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
130 135 140

```
Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145                 150                 155                 160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
                165                 170                 175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
            180                 185                 190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
        195                 200                 205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
    210                 215                 220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225                 230                 235                 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
                245                 250                 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
            260                 265                 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
        275                 280                 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
    290                 295                 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305                 310                 315                 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
                325                 330                 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
            340                 345                 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
        355                 360                 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
    370                 375                 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385                 390                 395                 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
                405                 410                 415
```

```
Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
            420                 425                 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
        435                 440                 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
    450                 455                 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465                 470                 475                 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
                485                 490                 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
            500                 505                 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
        515                 520                 525

Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
    530                 535                 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545                 550                 555                 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
                565                 570                 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
            580                 585                 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
        595                 600                 605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
    610                 615                 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625                 630                 635                 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
                645                 650                 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
            660                 665                 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
        675                 680                 685
```

```
Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
    690                 695                 700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705                 710                 715                 720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
                725                 730                 735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
            740                 745                 750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
        755                 760                 765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
    770                 775                 780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785                 790                 795                 800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
                805                 810                 815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
            820                 825                 830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
        835                 840                 845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
    850                 855                 860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865                 870                 875                 880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
                885                 890                 895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
            900                 905                 910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
        915                 920                 925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
    930                 935                 940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945                 950                 955                 960
```

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
965 970

<210> 63
<211> 972
<212> PRT
<213> Artificial

<220>
<223> mutant CSF-1R L301S Y969F

<400> 63

Met Gly Pro Gly Val Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
20 25 30

Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
35 40 45

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
50 55 60

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

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

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
100 105 110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
115 120 125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
130 135 140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145 150 155 160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
165 170 175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
180 185 190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
195 200 205

```
Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
    210                 215                 220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225                 230                 235                 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
                245                 250                 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
            260                 265                 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
        275                 280                 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Ser Asn Leu Ser
    290                 295                 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305                 310                 315                 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
                325                 330                 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
            340                 345                 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
        355                 360                 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
    370                 375                 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385                 390                 395                 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
                405                 410                 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
            420                 425                 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
        435                 440                 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
    450                 455                 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465                 470                 475                 480
```

```
Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
                485                 490                 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
            500                 505                 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
        515                 520                 525

Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
    530                 535                 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545                 550                 555                 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
                565                 570                 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
            580                 585                 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
        595                 600                 605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
    610                 615                 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625                 630                 635                 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
                645                 650                 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
            660                 665                 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
        675                 680                 685

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
    690                 695                 700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705                 710                 715                 720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
                725                 730                 735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
            740                 745                 750
```

```
Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
        755                 760                 765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
    770                 775                 780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785                 790                 795                 800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
                805                 810                 815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
            820                 825                 830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
        835                 840                 845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
    850                 855                 860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865                 870                 875                 880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
                885                 890                 895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
            900                 905                 910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
        915                 920                 925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
    930                 935                 940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945                 950                 955                 960

Gln Pro Leu Leu Gln Pro Asn Asn Phe Gln Phe Cys
                965                 970
```

<210> 64
<211> 493
<212> PRT
<213> Artificial

<220>
<223> human CSF-1R Extracellular Domain

<400> 64

```
Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
1               5                  10                  15
```

```
Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
            20                  25                  30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
        35                  40                  45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
    50                  55                  60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65                  70                  75                  80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
                85                  90                  95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
            100                 105                 110

Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
        115                 120                 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
    130                 135                 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145                 150                 155                 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
                165                 170                 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
            180                 185                 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
        195                 200                 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
    210                 215                 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225                 230                 235                 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
                245                 250                 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
            260                 265                 270

Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln
        275                 280                 285
```

```
Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys Val
    290                 295                 300

Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr Leu
305                 310                 315                 320

Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala Thr
                325                 330                 335

Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg Leu
            340                 345                 350

Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro Gly
        355                 360                 365

Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro Glu
    370                 375                 380

Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu Cys
385                 390                 395                 400

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

Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp Asp
            420                 425                 430

Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val Thr
        435                 440                 445

Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr Tyr
    450                 455                 460

Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe Ile
465                 470                 475                 480

Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
                485                 490
```

<210> 65
<211> 388
<212> PRT
<213> Artificial

<220>
<223> human CSF-1R fragment delD4

<400> 65

```
Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
1               5                   10                  15
```

```
Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
            20                  25                  30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
        35                  40                  45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
    50                  55                  60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65                  70                  75                  80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
                85                  90                  95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
            100                 105                 110

Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
        115                 120                 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
    130                 135                 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145                 150                 155                 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
                165                 170                 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
            180                 185                 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
        195                 200                 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
    210                 215                 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225                 230                 235                 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
                245                 250                 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
            260                 265                 270

Phe Phe Arg Tyr Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn
        275                 280                 285
```

Gly Ser Gly Thr Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn
290 295 300

Val Thr Trp Leu Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala
305 310 315 320

Gln Val Leu Gln Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln
325 330 335

Glu Pro Phe His Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr
340 345 350

Leu Glu His Asn Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly
355 360 365

Ser Gly Ser Trp Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His
370 375 380

Pro Pro Asp Glu
385

<210> 66
<211> 292
<212> PRT
<213> Artificial

<220>
<223> *human CSF-1R fragment D1-D3*

<400> 66

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

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

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
35 40 45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
50 55 60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65 70 75 80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
85 90 95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
100 105 110

Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
115 120 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
130 135 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145 150 155 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
165 170 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
180 185 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
195 200 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
210 215 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225 230 235 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
245 250 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
260 265 270

Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln
275 280 285

Asn Leu Ile Gln
290

<210> 67
<211> 21
<212> PRT
<213> Artificial

<220>
<223> signal peptide

<400> 67

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

Trp His Gly Gln Gly
20

<210> 68
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 68
cacctccatg ttcttccggt acccccccaga ggtaag 36

<210> 69
<211> 8
<212> PRT
<213> Mus musculus

<400> 69

Asp Leu Arg Leu Tyr Phe Asp Val
1 5

<210> 70
<211> 16
<212> PRT
<213> Mus musculus

<400> 70

Val Ile Trp Ser Gly Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met Ser
1 5 10 15

<210> 71
<211> 10
<212> PRT
<213> Mus musculus

<400> 71

Gly Phe Ser Leu Thr Ser Tyr Asp Ile Ser
1 5 10

<210> 72
<211> 8
<212> PRT
<213> Mus musculus

<400> 72

Gly Gln Ser Phe Thr Tyr Pro Thr
1 5

<210> 73
<211> 7
<212> PRT
<213> Mus musculus

<400> 73

Gly Ser Ser Asn Arg Tyr Thr
1 5

<210> 74
<211> 11
<212> PRT
<213> Mus musculus

<400> 74

Lys Ala Ser Glu Asp Val Gly Thr Tyr Val Ser
1 5 10

<210> 75
<211> 116
<212> PRT
<213> Mus musculus

<400> 75

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

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

Asp Ile Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Gly Thr Asn Tyr Asn Ser Pro Phe Met
50 55 60

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

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

Arg Asp Leu Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 76
<211> 106
<212> PRT
<213> Mus musculus

<400> 76

Lys Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Val Ser Val Gly
1 5 10 15

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

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

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

eolf-seql

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

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

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

<210> 77
<211> 8
<212> PRT
<213> Mus musculus

<400> 77

Asp Pro Arg Leu Tyr Phe Asp Val
1 5

<210> 78
<211> 16
<212> PRT
<213> Mus musculus

<400> 78

Val Ile Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Gly Phe Met Ser
1 5 10 15

<210> 79
<211> 10
<212> PRT
<213> Mus musculus

<400> 79

Gly Ser Ser Leu Asp Ser Phe Asp Ile Ser
1 5 10

<210> 80
<211> 8
<212> PRT
<213> Mus musculus

<400> 80

Gly Gln Thr Phe Ser Tyr Pro Thr
1 5

<210> 81
<211> 7
<212> PRT
<213> Mus musculus

<400> 81

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 82

<211> 11
<212> PRT
<213> Mus musculus

<400> 82

Lys Ala Ser Glu Asp Val Val Thr Tyr Val Ser
1 5 10

<210> 83
<211> 116
<212> PRT
<213> Mus musculus

<400> 83

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

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

Asp Ile Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Gly Phe Met
50 55 60

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

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

Arg Asp Pro Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 84
<211> 106
<212> PRT
<213> Mus musculus

<400> 84

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 85
<211> 218
<212> PRT
<213> Artificial

<220>
<223> human CSF-1R fragment domains D4-D5

<400> 85

Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln Asn Leu Ile
1 5 10 15

Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys Val Met Val Glu
20 25 30

Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr Leu Gly Pro Phe
35 40 45

Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala Thr Thr Lys Asp
50 55 60

Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg Leu Lys Pro Ser
65 70 75 80

Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro Gly Gly Trp Arg
85 90 95

Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro Glu Val Ser Val
100 105 110

Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu Cys Ala Ala Ser
115 120 125

Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu Gln Cys Ser Gly His Thr
130 135 140

Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp Asp Asp Pro Tyr
145 150 155 160

Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val Thr Val Gln Ser
165 170 175

```
Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr Tyr Glu Cys Arg
            180                 185                 190

Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe Ile Pro Ile Ser
        195                 200                 205

Ala Gly Ala His Thr His Pro Pro Asp Glu
    210                 215
```

<210> 86
<211> 554
<212> PRT
<213> homo sapiens

<400> 86

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                   10                  15

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

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35                  40                  45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50                  55                  60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130                 135                 140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145                 150                 155                 160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
                165                 170                 175

Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
            180                 185                 190
```

Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
195 200 205

Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
210 215 220

Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225 230 235 240

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

Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
260 265 270

Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
275 280 285

Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
290 295 300

Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305 310 315 320

Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
325 330 335

Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
340 345 350

Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro
355 360 365

Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro
370 375 380

Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
385 390 395 400

Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser Asn Pro
405 410 415

Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
420 425 430

Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
435 440 445

Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
450 455 460

```
Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
465                 470                 475                 480

His Glu Arg Gln Ser Glu Gly Ser Phe Ser Pro Gln Leu Gln Glu Ser
                485                 490                 495

Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
            500                 505                 510

Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
        515                 520                 525

Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
    530                 535                 540

Gln Asp Asp Arg Gln Val Glu Leu Pro Val
545                 550
```

<210> 87
<211> 242
<212> PRT
<213> homo sapiens

<400> 87

```
Met Pro Arg Gly Phe Thr Trp Leu Arg Tyr Leu Gly Ile Phe Leu Gly
1               5                   10                  15

Val Ala Leu Gly Asn Glu Pro Leu Glu Met Trp Pro Leu Thr Gln Asn
            20                  25                  30

Glu Glu Cys Thr Val Thr Gly Phe Leu Arg Asp Lys Leu Gln Tyr Arg
        35                  40                  45

Ser Arg Leu Gln Tyr Met Lys His Tyr Phe Pro Ile Asn Tyr Lys Ile
    50                  55                  60

Ser Val Pro Tyr Glu Gly Val Phe Arg Ile Ala Asn Val Thr Arg Leu
65                  70                  75                  80

Gln Arg Ala Gln Val Ser Glu Arg Glu Leu Arg Tyr Leu Trp Val Leu
                85                  90                  95

Val Ser Leu Ser Ala Thr Glu Ser Val Gln Asp Val Leu Leu Glu Gly
            100                 105                 110

His Pro Ser Trp Lys Tyr Leu Gln Glu Val Glu Thr Leu Leu Leu Asn
        115                 120                 125

Val Gln Gln Gly Leu Thr Asp Val Glu Val Ser Pro Lys Val Glu Ser
    130                 135                 140
```

```
Val Leu Ser Leu Leu Asn Ala Pro Gly Pro Asn Leu Lys Leu Val Arg
145                 150                 155                 160

Pro Lys Ala Leu Leu Asp Asn Cys Phe Arg Val Met Glu Leu Leu Tyr
                165                 170                 175

Cys Ser Cys Cys Lys Gln Ser Ser Val Leu Asn Trp Gln Asp Cys Glu
            180                 185                 190

Val Pro Ser Pro Gln Ser Cys Ser Pro Glu Pro Ser Leu Gln Tyr Ala
        195                 200                 205

Ala Thr Gln Leu Tyr Pro Pro Pro Pro Trp Ser Pro Ser Ser Pro Pro
    210                 215                 220

His Ser Thr Gly Ser Val Arg Pro Val Arg Ala Gln Gly Glu Gly Leu
225                 230                 235                 240

Leu Pro
```

<210> 88
<211> 126
<212> PRT
<213> Homo sapiens

<400> 88

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

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

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

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

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

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

Ala Arg Asp Gln Pro Leu Gly Tyr Cys Thr Asn Gly Val Cys Ser Tyr
            100                 105                 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 89

<211> 107
<212> PRT
<213> Homo sapiens

<400> 89

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ile Phe Pro Leu
85 90 95

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

<210> 90
<211> 113
<212> PRT
<213> Artificial

<220>
<223> humanized S2C6 heavy chain variabel domain variant

<400> 90

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 Tyr
20 25 30

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

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

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

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

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Ala Arg Glu Gly Ile Tyr Trp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser

<210> 91
<211> 113
<212> PRT
<213> Artificial

<220>
<223> humanized S2C6 light chain variabel domain variant

<400> 91

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 Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Leu Leu Ile Tyr Thr Val Ser Asn Arg Phe 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 Phe Cys Ser Gln Thr
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg