SEQUENCE LISTING

<110> CSL Innovation Pty Ltd

<120> PROTEIN FORMULATIONS AND USES THEREOF

<130> 530550PCT

<150> AU2020904684
<151> 2020-12-16

<160> 18

<170> PatentIn version 3.5

<210> 1
<211> 319
<212> PRT
<213> artificial

<220>
<223> amino acids 25-335 of Homo sapiens G-CSFR (hG-CSFR) with a C-terminal polyhistidine tag

<400> 1

Glu Cys Gly His Ile Ser Val Ser Ala Pro Ile Val His Leu Gly Asp
1 5 10 15

Pro Ile Thr Ala Ser Cys Ile Ile Lys Gln Asn Cys Ser His Leu Asp
20 25 30

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

Gly Arg Gln Gln Arg Leu Ser Asp Gly Thr Gln Glu Ser Ile Ile Thr
50 55 60

Leu Pro His Leu Asn His Thr Gln Ala Phe Leu Ser Cys Ala Leu Asn
65 70 75 80

Trp Gly Asn Ser Leu Gln Ile Leu Asp Gln Val Glu Leu Arg Ala Gly
85 90 95

Tyr Pro Pro Ala Ile Pro His Asn Leu Ser Cys Leu Met Asn Leu Thr
100 105 110

Thr Ser Ser Leu Ile Cys Gln Trp Glu Pro Gly Pro Glu Thr His Leu
115 120 125

Pro Thr Ser Phe Thr Leu Lys Ser Phe Lys Ser Arg Gly Asn Cys Gln
130 135 140

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

```
His Cys Ser Ile Pro Arg Lys His Leu Leu Leu Tyr Gln Asn Met Gly
                165                 170                 175

Ile Trp Val Gln Ala Glu Asn Ala Leu Gly Thr Ser Met Ser Pro Gln
            180                 185                 190

Leu Cys Leu Asp Pro Met Asp Val Val Lys Leu Glu Pro Pro Met Leu
        195                 200                 205

Arg Thr Met Asp Pro Ser Pro Glu Ala Ala Pro Pro Gln Ala Gly Cys
    210                 215                 220

Leu Gln Leu Ser Trp Glu Pro Trp Gln Pro Gly Leu His Ile Asn Gln
225                 230                 235                 240

Lys Cys Glu Leu Arg His Lys Pro Gln Arg Gly Glu Ala Ser Trp Ala
                245                 250                 255

Leu Val Gly Pro Leu Pro Leu Glu Ala Leu Gln Tyr Glu Leu Cys Gly
            260                 265                 270

Leu Leu Pro Ala Thr Ala Tyr Thr Leu Gln Ile Arg Cys Ile Arg Trp
        275                 280                 285

Pro Leu Pro Gly His Trp Ser Asp Trp Ser Pro Ser Leu Glu Leu Arg
    290                 295                 300

Thr Thr Glu Arg Ala Pro Thr His His His His His His His His
305                 310                 315
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<210> 2
<211> 118
<212> PRT
<213> artificial

<220>
<223> VH of C1.2

<400> 2

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

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

Ser Ser Ile Ser Ser Ser Gly Gly Val Thr Pro Tyr Ala Asp Ser Val
```

```
    50                  55                  60

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

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

Ala Met Leu Gly Glu Leu Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 3
<211> 107
<212> PRT
<213> artificial

<220>
<223> VL of C1.2

<400> 3

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser 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 Ala Ser Asn Leu Gln Asn Gly Ile 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 His Cys Gln Gln Ser Tyr Ser Thr Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Asn Val Glu Ile Arg
            100                 105
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<210> 4
<211> 118
<212> PRT
<213> artificial

<220>
<223> VH of C1.2G

<400> 4

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

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

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

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

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

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

Ala Lys Leu Gly Glu Leu Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 5
<211> 107
<212> PRT
<213> artificial

<220>
<223> VL of C1.2G

<400> 5

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser 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 Ala Ser Asn Leu Gln Asn 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 Tyr Ser Thr Pro Leu

85 90 95

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

<210> 6
<211> 5
<212> PRT
<213> artificial

<220>
<223> HCDR1 of C1.2

<400> 6

Leu Tyr Trp Met Gly
1 5

<210> 7
<211> 17
<212> PRT
<213> artificial

<220>
<223> C1.2 HCDR2

<400> 7

Ser Ile Ser Ser Ser Gly Gly Val Thr Pro Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 8
<211> 9
<212> PRT
<213> artificial

<220>
<223> C1.2 HCDR3

<400> 8

Leu Gly Glu Leu Gly Trp Phe Asp Pro
1 5

<210> 9
<211> 11
<212> PRT
<213> artificial

<220>
<223> C1.2 LCDR1

<400> 9

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

<210> 10
<211> 6
<212> PRT
<213> artificial

<220>
<223> C1.2 LCDR2

<400> 10

Ala Ser Asn Leu Gln Asn
1 5

<210> 11
<211> 9
<212> PRT
<213> artificial

<220>
<223> C1.2 LCDR3

<400> 11

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 12
<211> 8
<212> PRT
<213> artificial

<220>
<223> consensus sequence of HCDR3 of C1.2

<220>
<221> VARIANT
<222> (5)..(5)
<223> X is an amino acid selected from the group consisting of tryptophan, glutamine, methionine, serine, phenylalanine, glutamic acid and histidine

<220>
<221> VARIANT
<222> (6)..(6)
<223> X iis an amino acid selected from the group consisting of phenylalanine, tyrosine, methionine, serine, glycine and isoleucine

<220>
<221> VARIANT
<222> (7)..(7)
<223> X is an amino acid selected from the group consisting of aspartic acid, methionine, glutamine, serine, leucine, valine, arginine and histidine

<220>
<221> VARIANT
<222> (8)..(8)
<223> X is an amino acid selected from the group consisting of proline gltuamic acid, alanine, leucine, phenylalanine, tyronis,

threonine, asparagine, aspartic acid, serine , glycine, arginine, lysine

<400> 12

Leu Gly Glu Leu Xaa Xaa Xaa Xaa
1 5

<210> 13
<211> 9
<212> PRT
<213> artificial

<220>
<223> consensus sequence of LCDR3 of C1.2

<220>
<221> VARIANT
<222> (1)..(1)
<223> X is an amino acid selected from the group consisting of glutamine, glutamic acid, histidine, alanine or serine

<220>
<221> VARIANT
<222> (2)..(2)
<223> X is an amino acid selected from the group consisting of glutamine, valine, phenylalanine, asparagine and glutamic acid

<220>
<221> VARIANT
<222> (3)..(3)
<223> X ian amino acid selected from the group consisting of serine or glycine

<220>
<221> VARIANT
<222> (4)..(4)
<223> X is an amino acid selected from the group consisting of tryptophan, methionine, phenylalanine, tyrosine, isoleucine and leucine

<220>
<221> VARIANT
<222> (5)..(5)
<223> X is an amino acid selected from the group consisting of glutamic acid, methionine, glutamine, tryptophan, serine, valine, asparagine, glycine, alanine, arganine, histidine, tyrosine, lysine or threonine

<220>
<221> VARIANT
<222> (6)..(6)
<223> X is an amino acid selected from the group consisting of tyrosine, methionine, isoleucine or threonine

<220>
<221> VARIANT
<222> (7)..(7)
<223> X is an amino acid selected from the group consisting of proline, alanine, histidine, glycine and lysine

<220>
<221> VARIANT

<222> (8)..(8)
<223> X is an amino acid selected from the group consisting of leucine, glutamine, methionine, alanine, phenylalanine, isoleucine, lysine, histidine and glycine

<220>
<221> VARIANT
<222> (9)..(9)
<223> X is an amino acid selected from the group consisting of threonine, phenylalanine, tyrosine, methionine, lysine, serine, histidine, proline, tryptophan, isoleucine, glutamine, glycine and valine

<400> 13

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 14
<211> 445
<212> PRT
<213> artificial

<220>
<223> C1.2G heavy chain IgG4 with S241P mutation

<400> 14

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

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

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

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

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

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

Ala Lys Leu Gly Glu Leu Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr
100 105 110

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

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

```
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
```

```
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 15
<211> 214
<212> PRT
<213> artificial

<220>
<223> C1.2G with kappa light chain

<400> 15

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser 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 Ala Ser Asn Leu Gln Asn 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 Tyr Ser Thr Pro Leu
                85                  90                  95

Thr Phe Gly Gly 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> 16
<211> 836
<212> PRT
<213> Homo sapiens

<400> 16

```
Met Ala Arg Leu Gly Asn Cys Ser Leu Thr Trp Ala Ala Leu Ile Ile
1               5                   10                  15


Leu Leu Leu Pro Gly Ser Leu Glu Glu Cys Gly His Ile Ser Val Ser
            20                  25                  30


Ala Pro Ile Val His Leu Gly Asp Pro Ile Thr Ala Ser Cys Ile Ile
        35                  40                  45


Lys Gln Asn Cys Ser His Leu Asp Pro Glu Pro Gln Ile Leu Trp Arg
    50                  55                  60


Leu Gly Ala Glu Leu Gln Pro Gly Gly Arg Gln Gln Arg Leu Ser Asp
65                  70                  75                  80


Gly Thr Gln Glu Ser Ile Ile Thr Leu Pro His Leu Asn His Thr Gln
                85                  90                  95


Ala Phe Leu Ser Cys Cys Leu Asn Trp Gly Asn Ser Leu Gln Ile Leu
            100                 105                 110


Asp Gln Val Glu Leu Arg Ala Gly Tyr Pro Pro Ala Ile Pro His Asn
        115                 120                 125


Leu Ser Cys Leu Met Asn Leu Thr Thr Ser Ser Leu Ile Cys Gln Trp
    130                 135                 140


Glu Pro Gly Pro Glu Thr His Leu Pro Thr Ser Phe Thr Leu Lys Ser
145                 150                 155                 160


Phe Lys Ser Arg Gly Asn Cys Gln Thr Gln Gly Asp Ser Ile Leu Asp
                165                 170                 175


Cys Val Pro Lys Asp Gly Gln Ser His Cys Cys Ile Pro Arg Lys His
            180                 185                 190
```

```
Leu Leu Leu Tyr Gln Asn Met Gly Ile Trp Val Gln Ala Glu Asn Ala
        195                 200                 205

Leu Gly Thr Ser Met Ser Pro Gln Leu Cys Leu Asp Pro Met Asp Val
    210                 215                 220

Val Lys Leu Glu Pro Pro Met Leu Arg Thr Met Asp Pro Ser Pro Glu
225                 230                 235                 240

Ala Ala Pro Pro Gln Ala Gly Cys Leu Gln Leu Cys Trp Glu Pro Trp
                245                 250                 255

Gln Pro Gly Leu His Ile Asn Gln Lys Cys Glu Leu Arg His Lys Pro
            260                 265                 270

Gln Arg Gly Glu Ala Ser Trp Ala Leu Val Gly Pro Leu Pro Leu Glu
        275                 280                 285

Ala Leu Gln Tyr Glu Leu Cys Gly Leu Leu Pro Ala Thr Ala Tyr Thr
    290                 295                 300

Leu Gln Ile Arg Cys Ile Arg Trp Pro Leu Pro Gly His Trp Ser Asp
305                 310                 315                 320

Trp Ser Pro Ser Leu Glu Leu Arg Thr Thr Glu Arg Ala Pro Thr Val
                325                 330                 335

Arg Leu Asp Thr Trp Trp Arg Gln Arg Gln Leu Asp Pro Arg Thr Val
            340                 345                 350

Gln Leu Phe Trp Lys Pro Val Pro Leu Glu Glu Asp Ser Gly Arg Ile
        355                 360                 365

Gln Gly Tyr Val Val Ser Trp Arg Pro Ser Gly Gln Ala Gly Ala Ile
    370                 375                 380

Leu Pro Leu Cys Asn Thr Thr Glu Leu Ser Cys Thr Phe His Leu Pro
385                 390                 395                 400

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

Ser Arg Pro Thr Pro Val Val Phe Ser Glu Ser Arg Gly Pro Ala Leu
            420                 425                 430

Thr Arg Leu His Ala Met Ala Arg Asp Pro His Ser Leu Trp Val Gly
        435                 440                 445
```

```
Trp Glu Pro Pro Asn Pro Trp Pro Gln Gly Tyr Val Ile Glu Trp Gly
    450                 455                 460

Leu Gly Pro Pro Ser Ala Ser Asn Ser Asn Lys Thr Trp Arg Met Glu
465                 470                 475                 480

Gln Asn Gly Arg Ala Thr Gly Phe Leu Leu Lys Glu Asn Ile Arg Pro
                485                 490                 495

Phe Gln Leu Tyr Glu Ile Ile Val Thr Pro Leu Tyr Gln Asp Thr Met
            500                 505                 510

Gly Pro Ser Gln His Val Tyr Ala Tyr Ser Gln Glu Met Ala Pro Ser
        515                 520                 525

His Ala Pro Glu Leu His Leu Lys His Ile Gly Lys Thr Trp Ala Gln
    530                 535                 540

Leu Glu Trp Val Pro Glu Pro Pro Glu Leu Gly Lys Ser Pro Leu Thr
545                 550                 555                 560

His Tyr Thr Ile Phe Trp Thr Asn Ala Gln Asn Gln Ser Phe Ser Ala
                565                 570                 575

Ile Leu Asn Ala Ser Ser Arg Gly Phe Val Leu His Gly Leu Glu Pro
            580                 585                 590

Ala Ser Leu Tyr His Ile His Leu Met Ala Ala Ser Gln Ala Gly Ala
        595                 600                 605

Thr Asn Ser Thr Val Leu Thr Leu Met Thr Leu Thr Pro Glu Gly Ser
    610                 615                 620

Glu Leu His Ile Ile Leu Gly Leu Phe Gly Leu Leu Leu Leu Leu Thr
625                 630                 635                 640

Cys Leu Cys Gly Thr Ala Trp Leu Cys Cys Ser Pro Asn Arg Lys Asn
                645                 650                 655

Pro Leu Trp Pro Ser Val Pro Asp Pro Ala His Ser Ser Leu Gly Ser
            660                 665                 670

Trp Val Pro Thr Ile Met Glu Glu Asp Ala Phe Gln Leu Pro Gly Leu
        675                 680                 685

Gly Thr Pro Pro Ile Thr Lys Leu Thr Val Leu Glu Glu Asp Glu Lys
    690                 695                 700
```

```
Lys Pro Val Pro Trp Glu Ser His Asn Ser Ser Glu Thr Cys Gly Leu
705                 710                 715                 720


Pro Thr Leu Val Gln Thr Tyr Val Leu Gln Gly Asp Pro Arg Ala Val
                725                 730                 735


Ser Thr Gln Pro Gln Ser Gln Ser Gly Thr Ser Asp Gln Val Leu Tyr
            740                 745                 750


Gly Gln Leu Leu Gly Ser Pro Thr Ser Pro Gly Pro Gly His Tyr Leu
        755                 760                 765


Arg Cys Asp Ser Thr Gln Pro Leu Leu Ala Gly Leu Thr Pro Ser Pro
    770                 775                 780


Lys Ser Tyr Glu Asn Leu Trp Phe Gln Ala Ser Pro Leu Gly Thr Leu
785                 790                 795                 800


Val Thr Pro Ala Pro Ser Gln Glu Asp Asp Cys Val Phe Gly Pro Leu
                805                 810                 815


Leu Asn Phe Pro Leu Leu Gln Gly Ile Arg Val His Gly Met Glu Ala
            820                 825                 830


Leu Gly Ser Phe
        835


<210>  17
<211>  319
<212>  PRT
<213>  artificial

<220>
<223>  Ig and CRH domains of Macaca fascicularis G-CSFR (cynoG-CSFR)
       with a C-terminal polyhistidine tag

<400>  17

Glu Cys Gly His Ile Ser Val Ser Ala Pro Ile Val His Leu Gly Asp
1               5                   10                  15


Pro Ile Thr Ala Ser Cys Ile Ile Lys Gln Asn Cys Ser His Leu Asp
            20                  25                  30


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


Gly Arg Gln Gln Arg Leu Ser Asp Gly Ser Gln Gln Ser Thr Ile Thr
    50                  55                  60


Leu Pro His Leu Asn His Thr Arg Ala Phe Leu Ser Cys Ala Leu Asn
65                  70                  75                  80
```

```
Trp Gly Asn Ser Leu Gln Ile Leu Asp Gln Val Glu Leu Arg Ala Gly
                85                  90                  95

Tyr Pro Pro Ala Val Pro Arg Asn Leu Ser Cys Leu Met Asn Leu Thr
            100                 105                 110

Thr Ser Ser Leu Ile Cys Gln Trp Glu Pro Gly Pro Glu Thr His Leu
        115                 120                 125

Pro Thr Ser Phe Thr Leu Lys Ser Phe Lys Ser Arg Gly Asn Cys Gln
    130                 135                 140

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

His Cys Ser Ile Pro Arg Arg His Leu Leu Leu Tyr Gln Asn Met Gly
                165                 170                 175

Ile Trp Val Gln Ala Glu Asn Ala Leu Gly Thr Ser Met Ser Pro Gln
            180                 185                 190

Leu Cys Leu Glu Pro Met Asp Val Val Lys Leu Glu Pro Pro Met Leu
        195                 200                 205

Arg Thr Met Asp Pro Ser Pro Glu Ala Ala Pro Pro Gln Ala Gly Cys
    210                 215                 220

Leu Gln Leu Ser Trp Glu Pro Trp Gln Pro Ala Leu His Ile Asn Gln
225                 230                 235                 240

Lys Cys Glu Leu Arg His Lys Pro Gln Ser Gly Glu Ala Ser Trp Ala
                245                 250                 255

Leu Val Gly Pro Leu Pro Leu Glu Ala Leu Arg Tyr Glu Leu Cys Gly
            260                 265                 270

Leu Leu Pro Ala Thr Ala Tyr Thr Leu Gln Ile Arg Cys Ile Arg Trp
        275                 280                 285

Pro Leu Pro Gly His Trp Ser Asn Trp Ser Pro Ser Leu Glu Leu Arg
    290                 295                 300

Thr Thr Glu Arg Ala Pro Thr His His His His His His His His
305                 310                 315
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<210> 18
<211> 444
<212> PRT

<213> artificial

<220>
<223> C1.2G heavy chain IgG4 with S241P mutation and lacking C-terminal lysine residue

<400> 18

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


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


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


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


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


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


Ala Lys Leu Gly Glu Leu Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110


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


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


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


Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175


Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190


Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205


Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220


Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
```

```
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440
```