SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Glycosylated repeat-motif-molecule conjugates

<130> 26437

<150> EP09013887.6
<151> 2009-11-05

<160> 66

<170> PatentIn version 3.5

<210> 1
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 1

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> proline or alanine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> alanine or valine

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> histidine or asparagine

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> isoleucine or valine

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> leucine or isoleucine

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> aspartic acid or asparagine

<400> 1

Asp Gly Asn Thr Xaa Leu His Leu Ala Xaa Glu Asn Gly Xaa Leu Glu
1 5 10 15

Xaa Val Lys Leu Leu Xaa Glu Ala Gly Ala Xaa Ile Asn Ala
20 25 30

<210> 2
<211> 33
<212> PRT
<213> Artificial Sequence

<220>

<223> consensus sequence 2

<400> 2

Asp Ser Asp Gly Asn Thr Pro Leu His Leu Ala Ala Glu Asn Gly Gln
1 5 10 15

Leu Glu Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn Ala
20 25 30

Arg

<210> 3
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 3

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> aspartic acid or threonine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> leucine or isoleucine

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> aspartic acid or asparagine

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> valine or isoleucine

<400> 3

Xaa Lys Asn Gly Leu Thr Pro Leu His Xaa Ala Ala Gln Glu Gly His
1 5 10 15

Leu Glu Val Val Lys Leu Leu Leu Glu Asn Gly Ala Xaa Xaa Asn Ala
20 25 30

Lys

<210> 4
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 4

<220>
<221> MISC_FEATURE

<222> (1)..(33)
<223> Xaa denoting variable position

<400> 4

Asp Xaa Xaa Gly Xaa Thr Pro Leu His Leu Ala Ala Xaa Xaa Gly His
1 5 10 15

Leu Glu Ile Val Glu Val Leu Leu Lys Xaa Gly Ala Asp Val Asn Ala
20 25 30

Xaa

<210> 5
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 5

<400> 5

Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu
1 5 10 15

Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
20 25 30

Gly

<210> 6
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 6

<220>
<221> MISC_FEATURE
<222> (1)..(33)
<223> Xaa denoting variable position

<400> 6

Asp Xaa Xaa Gly Xaa Thr Pro Leu His Leu Ala Ala Xaa Xaa Gly Pro
1 5 10 15

Xaa Pro Ala Val Pro Xaa Leu Leu Pro Xaa Gly Ala Asp Val Asn Ala
20 25 30

Xaa

<210> 7
<211> 33
<212> PRT

<213> Artificial Sequence

<220>
<223> consensus sequence 7

<220>
<221> MISC_FEATURE
<222> (1)..(33)
<223> Xaa denoting variable position

<400> 7

Asp Xaa Xaa Gly Xaa Thr Pro Leu His Leu Ala Xaa Xaa Xaa Gly Xaa
1 5 10 15

Xaa Xaa Val Val Xaa Leu Leu Leu Xaa Xaa Gly Ala Asp Val Asn Ala
20 25 30

Xaa

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

<220>
<223> consensus sequence 8

<220>
<221> MISC_FEATURE
<222> (1)..(33)
<223> Xaa denoting variable position

<400> 8

Asp Xaa Xaa Gly Xaa Thr Pro Leu His Leu Ala Xaa Xaa Xaa Gly Xaa
1 5 10 15

Xaa Xaa Ile Val Xaa Val Leu Leu Xaa Xaa Gly Ala Asp Val Asn Ala
20 25 30

Xaa

<210> 9
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence 9

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> Xaa denotes amino acid selected from A, D, E, F, H, I, K, L, M, N, Q, R, S, T, V, W and Y

<220>
<221> MISC_FEATURE

<222> (26)..(26)
<223> Xaa denotes amino acid selected from H, N and Y

<220>
<221> MISC_FEATURE
<222> (27)..(33)
<223> Xaa denotes amino acid selected from A, D, E, F, H, I, K, L, M, N, Q, R, S, T, V, W and Y

<400> 9

Asp Xaa Xaa Gly Xaa Thr Pro Leu His Leu Ala Ala Xaa Xaa Gly His
1 5 10 15

Leu Glu Ile Val Glu Val Leu Leu Lys Xaa Gly Ala Asp Val Asn Ala
20 25 30

Xaa

<210> 10
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> model repeat-motif-molecule H10-2-G3 with C-terminal hexa-histidine-tag

<400> 10

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His His
115 120 125

His His
130

<210> 11
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> model repeat-motif-molecule H10-2-G3 with C-terminally conjugated IgG1 Fc-part

<400> 11

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                245                 250                 255

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        275                 280                 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
    290                 295                 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305                 310                 315                 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                325                 330                 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            340                 345                 350
```

<210> 12
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag

<400> 12

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125
```

```
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His
145                 150                 155                 160

His His His
```

<210> 13
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> model repeat-motif-molecule 9-26 with C-terminally conjugated IgG1 Fc-part

<400> 13

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys
145                 150                 155                 160

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
```

180 185 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
195 200 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
210 215 220

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225 230 235 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
245 250 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
260 265 270

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
290 295 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305 310 315 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
340 345 350

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
355 360 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
370 375 380

Lys
385

<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 1

<400> 14

Gly Gly Gly Gly Ser
1 5

<210> 15

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

<220>
<223> linker 2

<400> 15

Gln Gln Gln Gln Gly
1 5

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 3

<400> 16

Ser Ser Ser Ser Gly
1 5

<210> 17
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 4

<400> 17

Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
1 5 10 15

Gly

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

<220>
<223> linker 5

<400> 18

Gly Gln Gln Gln Gln Gly Gln Gln Gln Gln Gly Gln Gln Gln Gln Gly
1 5 10 15

Asn Asn

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 6

<400> 19

Leu Ser Leu Ser Pro Gly Lys
1 5

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 7

<400> 20

Leu Ser Pro Asn Arg Gly Glu Cys
1 5

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 8

<400> 21

Leu Ser Leu Ser Gly Gly
1 5

<210> 22
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 9

<400> 22

Leu Ser Leu Ser Pro Gly Gly
1 5

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 10

<400> 23

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 11

<400> 24

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 25
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 12

<400> 25

Gly Gly Gly Ser
1

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 13

<400> 26

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 27
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 14

<400> 27

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 28
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 15

<400> 28

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 29
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 16

<400> 29

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Ser
20

<210> 30
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 17

<400> 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 18

<400> 31

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 32
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 19

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 33
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 20

<400> 33

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 34
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated IgG1 Fc-part with two disulfide bonds in the hinge region

<400> 34

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Ser Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
245 250 255

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
275 280 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
290 295 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
325 330 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

<210> 35
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated IgG1 Fc-part with two disulfide bonds in the hinge region

<400> 35

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
50 55 60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65 70 75 80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly

```
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Ser Asp Lys
145                 150                 155                 160

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            180                 185                 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        195                 200                 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    210                 215                 220

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225                 230                 235                 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                245                 250                 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            260                 265                 270

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
    290                 295                 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305                 310                 315                 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
            340                 345                 350

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
        355                 360                 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    370                 375                 380
```

Lys
385

<210> 36
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated IgG1 Fc-part with CH3-knob-domain

<400> 36

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
245 250 255

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
260 265 270

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
275 280 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
290 295 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
325 330 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

<210> 37
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated IgG1 Fc-part with CH3-hole-domain

<400> 37

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
50 55 60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65 70 75 80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly

```
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys
145                 150                 155                 160

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            180                 185                 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        195                 200                 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    210                 215                 220

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225                 230                 235                 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                245                 250                 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            260                 265                 270

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
        275                 280                 285

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
    290                 295                 300

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305                 310                 315                 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
            340                 345                 350

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
        355                 360                 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    370                 375                 380
```

Lys
385

<210> 38
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated model repeat-motif-molecule 9-26.

<400> 38

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
245 250 255

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
275 280 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
290 295 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
325 330 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
355 360 365

Gly Gly Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
370 375 380

Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
385 390 395 400

Asn Ala Lys Asp Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala
405 410 415

Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp
420 425 430

Val Asn Ala His Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala
435 440 445

Lys Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala
450 455 460

Asp Val Asn Ala Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala
465 470 475 480

Ala Ala His Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly
485 490 495

Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
500 505 510

Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
515 520 525

<210> 39
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated IgG1 Fc-part with two disulfide bonds in the hinge region with C-terminally conjugated model repeat-motif-molecule 9-26

<400> 39

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Ser Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
245 250 255

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
275 280 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
290 295 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
325 330 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
355 360 365

Gly Gly Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
370 375 380

Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
385 390 395 400

Asn Ala Lys Asp Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala
405 410 415

Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp
420 425 430

Val Asn Ala His Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala
435 440 445

Lys Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala
450 455 460

Asp Val Asn Ala Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala
465 470 475 480

```
Ala Ala His Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly
                485                 490                 495

Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
            500                 505                 510

Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
        515                 520                 525
```

<210> 40
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag.

<400> 40

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
    50                  55                  60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65                  70                  75                  80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
            100                 105                 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu Gly
    130                 135                 140

Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
145                 150                 155                 160

Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Phe Tyr Gly
                165                 170                 175

Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu Glu Ile Val
            180                 185                 190
```

```
Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His Asp Trp Asn
        195                 200                 205

Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His Leu Glu Ile
    210                 215                 220

Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Ile Asp Asn
225                 230                 235                 240

Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly His Leu Glu
                245                 250                 255

Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Gln Asp
            260                 265                 270

Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu
        275                 280                 285

Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His His His His
    290                 295                 300
```

<210> 41
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated model repeat-motif-molecule H10-2-G3 with C-terminally conjugated hexa-histidine-tag

<400> 41

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110
```

```
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu
                165                 170                 175

Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
            180                 185                 190

Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Tyr
        195                 200                 205

Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu Glu Ile
    210                 215                 220

Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val Asp Ala
225                 230                 235                 240

Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His Leu Glu
                245                 250                 255

Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp
            260                 265                 270

Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly Asn Glu
        275                 280                 285

Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His His His His
    290                 295                 300
```

<210> 42
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> Dimeric model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag

<400> 42

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45
```

```
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu
                165                 170                 175

Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
            180                 185                 190

Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Phe Tyr
        195                 200                 205

Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu Glu Ile
    210                 215                 220

Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His Asp Trp
225                 230                 235                 240

Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His Leu Glu
                245                 250                 255

Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Ile Asp
            260                 265                 270

Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly His Leu
        275                 280                 285

Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Gln
    290                 295                 300

Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn
305                 310                 315                 320

Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His His His
```

325 330 335

His

<210> 43
<211> 330
<212> PRT
<213> Homo sapiens

<400> 43

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

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> 44
<211> 327
<212> PRT
<213> Homo sapiens

<400> 44

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> 45
<211> 107
<212> PRT
<213> Homo sapiens

<400> 45

```
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> 46
<211> 105
<212> PRT
<213> Human

<400> 46

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
20 25 30

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 47
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal capping repeat

<400> 47

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
20 25

<210> 48
<211> 28
<212> PRT

<213> Artificial Sequence

<220>
<223> C-terminal capping repeat

<400> 48

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

Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
20 25

<210> 49
<211> 602
<212> DNA
<213> Human cytomegalovirus

<400> 49
gttgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata 60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc 120

ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac ttggcagtac 240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg 300

cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360

tattagtcat cgctattagc atggtgatgc ggttttggca gtacatcaat gggcgtggat 420

agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt 480

tttggcacca aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc 540

aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctccg tttagtgaac 600

gt 602

<210> 50
<211> 122
<212> PRT
<213> Artificial

<220>
<223> VH

<400> 50

Gln 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 Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> VH

<400> 51

Gln 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 Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
100 105 110

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

<210> 52
<211> 124
<212> PRT
<213> Artificial

<220>
<223> VH

<400> 52

Gln 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 Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

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

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

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

Ala Arg Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp
            100                 105                 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 53
<211> 110
<212> PRT
<213> Artificial

<220>
<223> VL

<400> 53

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Val Tyr Asn Pro Pro
                85                  90                  95

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

<210> 54
<211> 110

<212> PRT
<213> Artificial

<220>
<223> VL

<400> 54

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

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

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

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

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

<210> 55
<211> 110
<212> PRT
<213> Artificial

<220>
<223> VL

<400> 55

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

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

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

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

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

<210> 56
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated hexa-histidine-tag amino acid sequence and introduced engineered glycosylation site at the beginning of the C-capping repeat.

<400> 56

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Thr Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His His
115 120 125

His His
130

<210> 57
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated IgG1 Fc-part and thereto C-terminally conjugated membrane anchor domain.

<400> 57

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys Thr
115 120 125

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
145 150 155 160

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
165 170 175

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
180 185 190

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
195 200 205

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
210 215 220

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
225 230 235 240

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
245 250 255

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
275 280 285

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
290 295 300

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
325 330 335

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Glu Leu
340 345 350

Gln Leu Glu Glu Ser Cys Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly
355 360 365

Leu Trp Thr Thr Ile Thr Ile Phe Ile Thr Leu Phe Leu Leu Ser Val
370 375 380

Cys Tyr Ser Ala Thr Val Thr Phe Phe Lys Val Lys Trp Ile Phe Ser
385 390 395 400

Ser Val Val Asp Leu Lys Gln Thr Ile Val Pro Asp Tyr Arg Asn Met
405 410 415

Ile Arg Gln Gly Ala
420

<210> 58
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag amino acid sequence and introduced engineered glycosylation site at the beginning of the C-capping repeat.

<400> 58

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
50 55 60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65 70 75 80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
100 105 110

```
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Thr Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly His His His
145                 150                 155                 160

His His His
```

<210> 59
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated IgG1 Fc-part and thereto C-terminally conjugated membrane anchor domain.

<400> 59

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Pro Lys Ser Cys Asp Lys
145                 150                 155                 160
```

```
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            180                 185                 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        195                 200                 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    210                 215                 220

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225                 230                 235                 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                245                 250                 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            260                 265                 270

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
    290                 295                 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305                 310                 315                 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
            340                 345                 350

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
        355                 360                 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Glu
    370                 375                 380

Leu Gln Leu Glu Glu Ser Cys Ala Glu Ala Gln Asp Gly Glu Leu Asp
385                 390                 395                 400

Gly Leu Trp Thr Thr Ile Thr Ile Phe Ile Thr Leu Phe Leu Leu Ser
                405                 410                 415

Val Cys Tyr Ser Ala Thr Val Thr Phe Phe Lys Val Lys Trp Ile Phe
            420                 425                 430

Ser Ser Val Val Asp Leu Lys Gln Thr Ile Val Pro Asp Tyr Arg Asn
        435                 440                 445
```

Met Ile Arg Gln Gly Ala
450

<210> 60
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated hexa-histidine-tag amino acid sequence and glycosylation tag in the C-terminal region.

<400> 60

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly Asn Gly Thr Glu
115 120 125

Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys Thr Gly Ser Gly His
130 135 140

His His His His His
145

<210> 61
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag amino acid sequence and glycosylation tag in the C-terminal region.

<400> 61

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
        35                  40                  45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
    50                  55                  60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65                  70                  75                  80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
            100                 105                 110

His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly Asn Gly Thr
145                 150                 155                 160

Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys Thr Gly Ser Gly
                165                 170                 175

His His His His His His
            180
```

<210> 62
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule H10-2-G3 with C-terminally conjugated hexa-histidine-tag amino acid sequence and glycosylation tag in the C-terminal region.

<400> 62

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30

Glu Tyr Gly Leu Thr Pro Leu Tyr Leu Ala Thr Ala His Gly His Leu
        35                  40                  45
```

Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Val
50 55 60

Asp Ala Ile Gly Phe Thr Pro Leu His Leu Ala Ala Phe Ile Gly His
65 70 75 80

Leu Glu Ile Ala Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Gly Asn Gly
100 105 110

Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly Asn Gly Thr Glu
115 120 125

Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Ala Thr Gly Ser Gly His
130 135 140

His His His His His
145

<210> 63
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Model repeat-motif-molecule 9-26 with C-terminally conjugated hexa-histidine-tag amino acid sequence and glycosylation tag in the C-terminal region.

<400> 63

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15

Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30

Phe Tyr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu
35 40 45

Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His
50 55 60

Asp Trp Asn Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His
65 70 75 80

Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95

Ile Asp Asn Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly
100 105 110

```
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125

Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140

Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Gly Ser Gly Asn Gly Thr
145                 150                 155                 160

Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Ala Thr Gly Ser Gly
                165                 170                 175

His His His His His His
            180
```

<210> 64
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> anticalin A-44 with hexa-his-tag

<400> 64

```
Ala Ser Asp Glu Glu Ile Gln Asp Val Ser Gly Thr Trp Tyr Leu Lys
1               5                   10                  15

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

Ile Pro Thr Thr Leu Thr Thr Leu Glu Gly Gly Asn Leu Glu Ala Lys
        35                  40                  45

Val Thr Met His Ile Lys Gly Arg Ser Gln Glu Val Lys Ala Val Leu
    50                  55                  60

Ser Lys Thr Asp Glu Pro Gly Ile Tyr Thr Ala Ile Gly Gly Ile His
65                  70                  75                  80

Val Ala Lys Ile Gly Arg Ser His Val Lys Asp His Tyr Ile Phe Tyr
                85                  90                  95

Ser Glu Gly Cys Leu Ser Gly Val Pro Val Pro Gly Val Trp Leu Val
            100                 105                 110

Gly Arg Asp Pro Lys Asn Asn Leu Glu Ala Leu Glu Asp Phe Glu Lys
        115                 120                 125

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

Gln Ser Glu Thr Ser Ser Pro Gly Ser Ala Gly Ser Gly His His His
145                 150                 155                 160
```

His His His

<210> 65
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> anticalin A-44 with Fc-tag (3 SS bridges)

<400> 65

```
Ala Ser Asp Glu Glu Ile Gln Asp Val Ser Gly Thr Trp Tyr Leu Lys
1               5                  10                  15

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

Ile Pro Thr Thr Leu Thr Thr Leu Glu Gly Gly Asn Leu Glu Ala Lys
        35                  40                  45

Val Thr Met His Ile Lys Gly Arg Ser Gln Glu Val Lys Ala Val Leu
    50                  55                  60

Ser Lys Thr Asp Glu Pro Gly Ile Tyr Thr Ala Ile Gly Gly Ile His
65                  70                  75                  80

Val Ala Lys Ile Gly Arg Ser His Val Lys Asp His Tyr Ile Phe Tyr
                85                  90                  95

Ser Glu Gly Cys Leu Ser Gly Val Pro Val Pro Gly Val Trp Leu Val
            100                 105                 110

Gly Arg Asp Pro Lys Asn Asn Leu Glu Ala Leu Glu Asp Phe Glu Lys
        115                 120                 125

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

Gln Ser Glu Thr Ser Ser Pro Gly Ser Ala Pro Lys Ser Cys Asp Lys
145                 150                 155                 160

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            180                 185                 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        195                 200                 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    210                 215                 220
```

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225 230 235 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
245 250 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
260 265 270

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
290 295 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305 310 315 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
340 345 350

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
355 360 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
370 375 380

Lys
385

<210> 66
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> anticalin A-44 with Fc-tag (3 SS bridges)

<400> 66

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

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

Ile Pro Thr Thr Leu Thr Thr Leu Glu Gly Gly Asn Leu Glu Ala Lys
35 40 45

Val Thr Met His Ile Lys Gly Arg Ser Gln Glu Val Lys Ala Val Leu
50 55 60

```
Ser Lys Thr Asp Glu Pro Gly Ile Tyr Thr Ala Ile Gly Gly Ile His
65                  70                  75                  80

Val Ala Lys Ile Gly Arg Ser His Val Lys Asp His Tyr Ile Phe Tyr
                85                  90                  95

Ser Glu Gly Cys Leu Ser Gly Val Pro Val Pro Gly Val Trp Leu Val
            100                 105                 110

Gly Arg Asp Pro Lys Asn Asn Leu Glu Ala Leu Glu Asp Phe Glu Lys
        115                 120                 125

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

Gln Ser Glu Thr Ser Ser Pro Gly Ser Ala Pro Lys Ser Ser Asp Lys
145                 150                 155                 160

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                165                 170                 175

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            180                 185                 190

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        195                 200                 205

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    210                 215                 220

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
225                 230                 235                 240

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                245                 250                 255

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            260                 265                 270

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
    290                 295                 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305                 310                 315                 320

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
            340                 345                 350
```

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
355 360 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
370 375 380

Lys
385