SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Polypeptide-polynucleotide-complex and its use in targeted effector moiety delivery

<130> 27203

<150> EP10196688.5
<151> 2010-12-23

<160> 77

<170> PatentIn version 3.5

<210> 1
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> VH (mAb 1.4.168)

<400> 1

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

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

Asp Tyr Pro Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu
        35                  40                  45

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

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

Leu Tyr Leu Gln Met Gly Ser Leu Gln Ser Glu Asp Ala Ala Met Tyr
                85                  90                  95

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

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

<210> 2
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> VL (mAb 1.4.168)

<400> 2

Gln Leu Val Leu Thr Gln Ser Ser Ser Ala Ser Phe Ser Leu Gly Ala
1 5 10 15

Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30

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

Glu Leu Lys Lys Asp Gly Ser His Thr Thr Gly Asp Gly Ile Pro Asp
50 55 60

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

Asn Ile Gln Pro Glu Asp Glu Ser Ile Tyr Ile Cys Gly Val Gly Asp
85 90 95

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

Thr Val Leu Gly
115

<210> 3
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH (mAb 8.1.2)

<400> 3

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

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

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

Gly Tyr Leu Asn Pro Tyr Asn Asp Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Arg Gly Ile Tyr Ala Tyr Asp His Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Leu Thr Val Ser Ser
115 120

<210> 4
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> VL (mAb 8.1.2)

<400> 4

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

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

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

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

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

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

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

<210> 5
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> 17mer ssDNA (covalently bound with 5' end to Fab')

<400> 5

agttctatcg tcgtcca 17

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> 19mer ssDNA (covalently bound with 3' end to Fab')

<400> 6
agtctattaa tgcttctgc 19

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

<220>
<223> complementary 19mer ssDNA (used as part of a linker)

<400> 7
gcagaagcat taatagact 19

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> complementary 17mer ssDNA (used as part of a linker)

<400> 8
tggacgacga tagaact 17

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

<220>
<223> fragment

<220>
<221> MISC_FEATURE
<222> (16)..(17)
<223> beta-alanine

<400> 9

Glu Arg Ala Glu Gln Gln Arg Ile Arg Ala Glu Arg Glu Lys Glu Xaa
1 5 10 15

Xaa Ser Leu Lys Asp Arg Ile Glu Lys Arg Arg Arg Ala Glu Arg Ala
20 25 30

Glu

<210> 10
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment

<220>
<221> MISC_FEATURE
<222> (15)..(16)
<223> amino-trioxa-octanoic-acid

<400> 10

Leu Lys Asp Arg Ile Glu Arg Arg Arg Ala Glu Arg Ala Glu Xaa Xaa
1 5 10 15

Glu Arg Ala Glu Gln Gln Arg Ile Arg Ala Glu Arg Glu Lys Glu
20 25 30

<210> 11
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> IGF-1R (1340-1366)

<400> 11

Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly Gly Arg Lys Asn
1 5 10 15

Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser Thr
20 25

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

<220>
<223> hInsR(1355-1382)

<400> 12

Tyr Glu Glu His Ile Pro Tyr Thr His Met Asn Gly Gly Lys Lys Asn
1 5 10 15

Gly Arg Ile Leu Thr Leu Pro Arg Ser Asn Pro
20 25

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 35-mer polynucleotide linker

<220>
<221> misc_feature
<222> (1)..(35)
<223> n is a, c, g, or t

<400> 13
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnn 35

<210> 14
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> 75-mer polynucleotide linker

<220>
<221> misc_feature
<222> (1)..(75)
<223> n is a, c, g, or t

<400> 14
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnn 75

<210> 15
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> 95-mer polynucleotide linker

<220>
<221> misc_feature
<222> (1)..(95)
<223> n is a, c, g, or t

<400> 15
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnn 95

<210> 16
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 4D5 Fab' heavy chain amino acid sequence

<400> 16

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val
    210                 215
```

<210> 17

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

<220>
<223> 4D5 Fab' light chain amino acid sequence

<400> 17

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


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


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


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


Ser Arg 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 His Tyr Thr Thr Pro Pro
                85                  90                  95


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


Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
        115                 120                 125


Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
    130                 135                 140


Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145                 150                 155                 160


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


Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180                 185                 190


Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
        195                 200                 205


Ala Pro Thr Glu Cys Ser
    210
```

<210> 18
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C4 Fab' heavy chain amino acid sequence

<400> 18

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


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


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


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


Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


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


Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140


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


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


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


Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
```

Ser Asn Thr Lys Val Asp Lys Lys Val
210 215

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

<220>
<223> 2C4 Fab' light chain amino acid sequence

<400> 19

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

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

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

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

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

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

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

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

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

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

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

Thr Glu Cys Ser
210

<210> 20
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2 ECD fragment

<400> 20

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

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

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125

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

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys

```
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

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

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430
```

eolf-seql

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625 630 635 640

Gly Cys Pro Ala Glu
645

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> fragment

<220>
<221> misc_feature
<223> X = propylene-phosphate introduced via phosphoramidite C3
(3-(4,4'-dimethoxytrityloxy)propyl-1-[(2-cyanoethyl)-(N,N-diisopr
opyl)]-phosphoramidite

<220>
<221> misc_feature
<223> Y = 5'-amino-modifier C6 introduced via
(6-(4-monomethoxytritylamino)hexyl-(2-cyanoethyl)-(N,N-diisopropy
l)-phosphoramidite

<220>
<221> misc_feature
<223> Z = 4[N-maleinimidomethyl]cyclohexane-1-carboxy introduced via
Sulfosuccinimidyl 4-[N-maleimidomethyl]cyclohexane-1-carboxylate

<220>
<221> misc_feature
<222> (20)..(24)
<223> n is a, c, g, or t

<400> 21
agtctattaa tgcttctgcn nnnn 24

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> fragment

<220>
<221> misc_feature
<223> X = propylene-phosphate introduced via Phosphoramidite C3
(3-(4,4'-Dimethoxytrityloxy)propyl-1-[(2-cyanoethyl)-(N,N-diisopr
opyl)]-phosphoramidite

<220>
<221> misc_feature
<223> Y = 5'-Amino-Modifier C6 introduced via
(6-(4-Monomethoxytritylamino)hexyl-(2-cyanoethyl)-(N,N-diisopropy
l)-phosphoramidite

<220>
<221> misc_feature
<223> Z = 4[N-maleinimidomethyl]cyclohexane-1-carboxy introduced via
Sulfosuccinimidyl 4-[N-maleimidomethyl]cyclohexane-1-carboxylate

<220>
<221> misc_feature
<222> (1)..(5)
<223> n is a, c, g, or t

<400> 22
nnnnnagttc tatcgtcgtc ca 22

<210> 23
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 1

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<400> 23
gcagaagcat taatagactn ggacgacgat agaact 36

<210> 24
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 2

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<400> 24
gcagaagcat taatagactt ttttnttttt ggacgacgat agaact 46

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 3

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<400> 25

gcagaagcat taatagactt ttttttttt ttttnttttt ttttttttt ggacgacgat 60

agaact 66

<210> 26
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HER2 antibody 4D5 heavy chain variable domain

<400> 26

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 27
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR1

<400> 27

Gly Phe Asn Ile Lys Asp Thr Tyr Ile His
1 5 10

<210> 28
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR2

<400> 28

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

Gly

<210> 29
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3

<400> 29

Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
1 5 10

<210> 30
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HER2 antibody 4D5 heavy light variable domain

<400> 30

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

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

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

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

Ser Arg 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 His Tyr Thr Thr Pro Pro
85 90 95

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

<210> 31
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1

<400> 31

Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp
1 5 10

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2

<400> 32

Ser Ala Ser Phe Leu Tyr Ser
1 5

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

<220>
<223> VL CDR3

<400> 33

Gln Gln His Tyr Thr Thr Pro Pro Thr
1 5

<210> 34
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HER2 antibody 2C4 heavy chain variable domain

<400> 34

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

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

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

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

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR1

<400> 35

```
Gly Phe Thr Phe Thr Asp Tyr Thr Met Asp
1               5                   10
```

<210> 36
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR2

<400> 36

```
Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe Lys
1               5                   10                  15

Gly
```

<210> 37
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3

<400> 37

Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
1 5 10

<210> 38
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HER2 antibody 2C4 light chain variable domain

<400> 38

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

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

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

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

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

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

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

<210> 39
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1

<400> 39

Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala
1 5 10

<210> 40
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2

<400> 40

Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR3

<400> 41

Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr
1 5

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> amino modified polynucleotide linker precursors

<220>
<221> misc_feature
<223> X= Fluorescein

Y=C7Aminolinker

Z=C3 spacer

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(24)
<223> n is a, c, g, or t

<400> 42
nagtctatta atgcttctgc nnnn 24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> amino modified polynucleotide linker precursors

<220>
<221> misc_feature
<223> X=Cy5

Y=C7Aminolinker

Z=C3 spacer

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(24)
<223> n is a, c, g, or t

<400> 43
nagtctatta atgcttctgc nnnn 24

<210> 44
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> amino modified polynucleotide linker precursors

<220>
<221> misc_feature
<223> X=Aminolinker

Y= Fluorescein

Z=C3 spacer

<220>
<221> misc_feature
<222> (1)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<400> 44
nnnnagttct atcgtcgtcc an 22

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> amino modified L-polynucleotide linker precursors

<220>
<221> misc_feature
<223> X=Fluorescein

Y= C7Aminolinker

Z=C3 spacer

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(24)
<223> n is a, c, g, or t

<400> 45
nagtctatta atgcttctgc nnnn 24

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> amino modified L-polynucleotide linker precursors

<220>
<221> misc_feature
<223> X= Aminolinker

Y= Fluorescein

Z=C3 spacer

<220>
<221> misc_feature
<222> (1)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<400> 46
nnnnagttct atcgtcgtcc an 22

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> ssDNA linker 1

<400> 47
gcagaagcat taatagactt ggacgacgat agaact 36

<210> 48
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> ssDNA linker 2

<400> 48
gcagaagcat taatagactt ttttttttt ttttttttt ttttttttt ttttttttt 60

ggacgacgat agaact 76

<210> 49
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ss-L-DNA linker 3

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<400> 49
gcagaagcat taatagactn tggacgacga tagaact 37

<210> 50
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ss-L-DNA linker 4

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<400> 50
gcagaagcat taatagactt ttttntttt tggacgacga tagaact 47

<210> 51

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

<220>
<223> biotinylated ss-L-DNA linker 5

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (40)..(40)
<223> n is a, c, g, or t

<400> 51
gcagaagcat taatagactt ttttttttt ttttttttn ttttttttt ttttttttt 60

tggacgacga tagaact 77

<210> 52
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ss-L-DNA linker 6

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (50)..(50)
<223> n is a, c, g, or t

<400> 52
gcagaagcat taatagactt ttttttttt ttttttttt ttttttttn ttttttttt 60

ttttttttt ttttttttt tggacgacga tagaact 97

<210> 53
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 7

<220>
<221> misc_feature
<223> n=biotin dT

<220>
<221> misc_feature
<222> (25)..(25)

<223> n is a, c, g, or t

<400> 53
gcagaagcat taatagactt ttttnttttt tggacgacga tagaact   47

<210> 54
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 8

<220>
<221> misc_feature
<223> n= biotin dT

<220>
<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t

<400> 54
gcagaagcat taatagactt ttttttttn ttttttttt tggacgacga tagaact   57

<210> 55
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 9

<220>
<221> misc_feature
<223> n= biotin dt

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<400> 55
gcagaagcat taatagactt ttttttttt ttttnttttt ttttttttt tggacgacga   60

tagaact   67

<210> 56
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 10

<220>
<221> misc_feature

<223> n=biotin dt

<220>
<221> misc_feature
<222> (40)..(40)
<223> n is a, c, g, or t

<400> 56
gcagaagcat taatagactt ttttttttt ttttttttn ttttttttt ttttttttt 60

ggacgacgat agaact 76

<210> 57
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 11

<220>
<221> misc_feature
<223> n=biotin dt

s=spacer C18

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<400> 57
gcagaagcat taatagacts nstggacgac gatagaact 39

<210> 58
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 12

<220>
<221> misc_feature
<223> n=biotin dt

s=spacer c18

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<400> 58
gcagaagcat taatagacts snsstggacg acgatagaac t 41

<210> 59
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ssDNA linker 13

<220>
<221> misc_feature
<223> n=biotin dt

s=spacer c18

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<400> 59
gcagaagcat taatagacts ssnssstgga cgacgataga act 43

<210> 60
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ss-L-DNA linker 14

<220>
<221> misc_feature
<223> n=biotin dt

s=spacer c18

<220>
<221> misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t

<400> 60
gcagaagcat taatagacts sssnssssstg gacgacgata gaact 45

<210> 61
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> digoxygenylated ss-L-DNA linker 15

<220>
<221> misc_feature
<223> n=digoxigenin dt

<220>
<221> misc_feature
<222> (40)..(40)
<223> n is a, c, g, or t

<400> 61
gcagaagcat taatagactt ttttttttt ttttttttn ttttttttt ttttttttt 60

tggacgacga tagaact 77

<210> 62
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> digoxygenylated ss-L-DNA linker 16

<220>
<221> misc_feature
<223> n=digoxigenin dt

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<400> 62
gcagaagcat taatagactn tggacgacga tagaact 37

<210> 63
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> biotinylated ss-L-DNA linker 17

<220>
<221> misc_feature
<223> n=biotin dt

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<400> 63
gcagaagcat taatagactn tggacgacga tagaact 37

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-tag

<400> 64

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 65
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Avi-tag

<400> 65

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
1 5 10 15

<210> 66
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 66

Ser Gly Gly Gly Ser
1 5

<210> 67
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> fMLP

<220>
<221> MISC_FEATURE
<223> X=f-met

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 67

Xaa Leu Phe
1

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> f-Met-Leu-Phe-o-methyl ester

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> f-met

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> o-methyl ester

<400> 68

Xaa Leu Phe Xaa
1

<210> 69
<211> 107
<212> PRT
<213> Homo sapiens

<400> 69

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> 70
<211> 105
<212> PRT
<213> Homo sapiens

<400> 70

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> 71
<211> 330
<212> PRT
<213> Homo sapiens

<400> 71

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> 72
<211> 330
<212> PRT
<213> Homo sapiens

<400> 72

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 Glu Glu
225                 230                 235                 240

Met 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
```

eolf-seql

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> 73
<211> 330
<212> PRT
<213> Homo sapiens

<400> 73

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 74
<211> 327
<212> PRT
<213> Homo sapiens

<400> 74

```
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> 75
<211> 327
<212> PRT
<213> Homo sapiens

<400> 75

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

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

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

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

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

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

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

Glu Phe Glu 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> 76
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> detection probe

<220>
<221> misc_feature
<223> Y = 5'-Amino-Modifier

Z = 3'-Aminomodifier C6

Cy5-dye at 5' and 3' terminus

<220>
<221> misc_feature
<222> (1)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(23)
<223> n is a, c, g, or t

<400> 76
nnatgcgagt accttagagt cnn 23

<210> 77
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> T20-linker

<400> 77
gcagaagcat taatagactt ttttttttt ttttttttg actctaaggt actcgcattt 60

ttttttttt ttttttttg gacgacgata gaact 95