SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Method for the production and selection of molecules comprising at least two different entities and uses thereof

<130> 31245 WO

<150> EP12184473.2
<151> 2012-09-14

<160> 52

<170> PatentIn version 3.5

<210> 1
<211> 5
<212> PRT
<213> Staphylococcus aureus

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X can be any amino acid residue

<400> 1

Leu Pro Xaa Thr Gly
1 5

<210> 2
<211> 4
<212> PRT
<213> Homo sapiens

<400> 2

Lys Asp Glu Leu
1

<210> 3
<211> 4
<212> PRT
<213> Saccharomyces cerevisiae

<400> 3

His Asp Glu Leu
1

<210> 4
<211> 9
<212> PRT
<213> Adenovirus type 2

<220>
<221> MISC_FEATURE
<222> (4)..(7)
<223> X can be any amino acid residue

<400> 4

Ser Phe Ile Xaa Xaa Xaa Xaa Met Pro
1 5

<210> 5
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<220>
<223> Arg-tag

<400> 5

Arg Arg Arg Arg Arg
1 5

<210> 6
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<220>
<223> Arg-tag 2

<400> 6

Arg Arg Arg Arg Arg Arg
1 5

<210> 7
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<220>
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<400> 7

His His His His His His
1 5

<210> 8
<211> 19
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<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 8

Lys Asp His Leu Ile His Asn Val His Lys Glu Phe His Ala His Ala
1 5 10 15

His Asn Lys

<210> 9
<211> 8
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<220>
<223> amino acid tag

<400> 9

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 10
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 10

Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1 5 10 15

Lys Asp Asp Asp Asp Lys
20

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag#

<400> 11

Ala Trp Arg His Pro Gln Phe Gly Gly
1 5

<210> 12
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 12

Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 13

Met Asp Val Glu Ala Trp Leu Gly Ala Arg
1 5 10

<210> 14
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 14

Met Asp Val Glu Ala Trp Leu Gly Ala Arg Val Pro Leu Val Glu Thr
1 5 10 15

<210> 15
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 15

Met Asp Glu Lys Thr Thr Gly Trp Arg Gly Gly His Val Val Glu Gly
1 5 10 15

Leu Ala Gly Glu Leu Glu Gln Leu Arg Ala Arg Leu Glu His His Pro
20 25 30

Gln Gly Gln Arg Glu Pro
35

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 16

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 17

Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1 5 10 15

<210> 18
<211> 26

<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 18

Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg
1 5 10 15

Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu
20 25

<210> 19
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid tag

<400> 19

Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr
1 5 10 15

Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser
20 25 30

Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
35 40 45

<210> 20
<211> 32
<212> PRT
<213> Butyrivibrio fibrisolvens

<400> 20

Met Asp Trp Asn Ala Asn Ile Ala Pro Gly Asn Ser Val Glu Phe Gly
1 5 10 15

Ile Gln Gly Ala Gly Ser Val Gly Asn Val Ile Asp Ile Thr Val Glu
20 25 30

<210> 21
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> chitin-binding-domain

<400> 21

Thr Asn Pro Gly Val Ser Ala Trp Gln Val Asn Thr Ala Tyr Thr Ala
1 5 10 15

Gly Gln Leu Val Thr Tyr Asn Gly Lys Thr Tyr Lys Cys Leu Gln Pro

20 25 30

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

Gln Leu Gln
50

<210> 22
<211> 209
<212> PRT
<213> Chondrus crispus

<400> 22

Met Pro Glu Ile Lys Leu Thr Tyr Phe Asp Met Arg Gly Arg Ala Glu
1 5 10 15

Ala Ser Arg Leu Ala Leu Val Val Gly Glu Ile Pro Phe Glu Asp Glu
20 25 30

Arg Val Val Phe Asp His Trp Lys Glu Ala Lys Pro Lys Thr Pro Tyr
35 40 45

Ala Ala Leu Pro Met Leu Thr Val Asp Gly Met Gln Val Ala Gln Ser
50 55 60

Asp Ala Ile Leu Arg Tyr Cys Gly Lys Leu Ala Gly Leu Tyr Pro Ser
65 70 75 80

Asp Pro Leu Glu Ala Ala Lys Val Asp Glu Val Gly Gly Val Ile Asp
85 90 95

Asp Val Thr His Ala Met Tyr Arg Tyr Arg Gly Asp Asp Lys Asp Lys
100 105 110

Leu Arg Glu Glu Arg Asp Lys Phe Ser Lys Val Asp Val Pro Arg Tyr
115 120 125

Val Gly Ala Leu Glu Lys Arg Leu Glu Ala Phe Gly Asp Gly Pro Trp
130 135 140

Ala Val Gly Gly Asn Met Thr Ile Ala Asp Leu His Ile Cys His Leu
145 150 155 160

Val Thr Asn Ile Arg Cys Gly Met Leu Asp Phe Val Asp Lys Asp Leu
165 170 175

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

His Pro Lys Val Thr Glu Trp Tyr Glu Lys Lys Pro Val Lys Met Phe
195 200 205

Ser

<210> 23
<211> 396
<212> PRT
<213> Escherichia coli

<400> 23

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
20 25 30

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

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
85 90 95

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

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
210 215 220

```
Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
225                 230                 235                 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
                245                 250                 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
            260                 265                 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
        275                 280                 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
    290                 295                 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
305                 310                 315                 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
                325                 330                 335

Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
            340                 345                 350

Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
        355                 360                 365

Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
    370                 375                 380

Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
385                 390                 395
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<210> 24
<211> 222
<212> PRT
<213> Homo sapiens

<400> 24

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Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
1               5                   10                  15

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            20                  25                  30

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        35                  40                  45

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    50                  55                  60
```

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
65 70 75 80

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
85 90 95

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
100 105 110

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
115 120 125

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
130 135 140

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

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

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
195 200 205

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 25
<211> 222
<212> PRT
<213> Homo sapiens

<400> 25

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
1 5 10 15

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
20 25 30

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
35 40 45

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

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
65 70 75 80

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys

85 90 95

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
100 105 110

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
115 120 125

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
130 135 140

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

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

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

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
195 200 205

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215 220

<210> 26
<211> 107
<212> PRT
<213> Homo sapiens

<400> 26

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Trp Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35 40 45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60

Glu Ser Thr Tyr Arg Trp Ser Val Leu Thr Val Leu His Gln Asp Trp
65 70 75 80

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
85 90 95

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 27
<211> 106
<212> PRT
<213> Homo sapiens

<400> 27

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> sortase motif with C-terminal GS linker

<400> 28

Leu Pro Glu Thr Gly Gly Ser
1 5

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> hexa-histidine - sortase motif- endoplasmic reticulum retention signal - tag

<400> 29

Gly Ser His His His His His His Gly Ser Leu Pro Glu Thr Gly Gly
1 5 10 15

Ser Lys Asp Glu Leu
20

<210> 30
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> mature scFab fragment of anti-transferrin receptor antibody 3D8 with C-terminal His-tag, sortase motif, and ER retention signal fusion protein

<400> 30

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

Glu Ile Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Gly Asn Trp
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220
```

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
225 230 235 240

Gly Gly Gly Ser Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
245 250 255

Leu Val Gln Pro Gly Asn Ser Leu Thr Leu Ser Cys Val Ala Ser Gly
260 265 270

Phe Thr Phe Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Lys
275 280 285

Lys Gly Leu Glu Trp Ile Ala Met Ile Tyr Tyr Asp Ser Ser Lys Met
290 295 300

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

Ser Lys Asn Thr Leu Tyr Leu Glu Met Asn Ser Leu Arg Ser Glu Asp
325 330 335

Thr Ala Met Tyr Tyr Cys Ala Val Pro Thr Ser His Tyr Val Val Asp
340 345 350

Val Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser Ala Ser Thr Lys
355 360 365

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
370 375 380

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
385 390 395 400

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
405 410 415

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
420 425 430

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
435 440 445

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
450 455 460

Lys Ser Cys Gly Ser His His His His His His Gly Ser Leu Pro Glu
465 470 475 480

Thr Gly Gly Ser Lys Asp Glu Leu
485

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

<220>
<223> linker polypeptide

<400> 31

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

<210> 32
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> mature scFab fragment of anti-transferrin receptor antibody 3D8 with N-terminal glycine-serine motif

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
1 5 10 15

Ser Pro Ala Ser Leu Ser Ala Ser Leu Glu Glu Ile Val Thr Ile Thr
20 25 30

Cys Gln Ala Ser Gln Asp Ile Gly Asn Trp Leu Ala Trp Tyr Gln Gln
35 40 45

Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile Tyr Gly Ala Thr Ser Leu
50 55 60

Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Gln
65 70 75 80

Phe Ser Leu Lys Ile Ser Arg Val Gln Val Glu Asp Ile Gly Ile Tyr
85 90 95

Tyr Cys Leu Gln Ala Tyr Asn Thr Pro Trp Thr Phe Gly Gly Gly Thr
100 105 110

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

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

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln

```
                165                 170                 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
            180                 185                 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
        195                 200                 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                245                 250                 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
            260                 265                 270

Ser Leu Thr Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
        275                 280                 285

Gly Met His Trp Ile Arg Gln Ala Pro Lys Lys Gly Leu Glu Trp Ile
    290                 295                 300

Ala Met Ile Tyr Tyr Asp Ser Ser Lys Met Asn Tyr Ala Asp Thr Val
305                 310                 315                 320

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

Leu Glu Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
            340                 345                 350

Ala Val Pro Thr Ser His Tyr Val Val Asp Val Trp Gly Gln Gly Val
        355                 360                 365

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
    370                 375                 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385                 390                 395                 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
                405                 410                 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
            420                 425                 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
```

435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
465 470 475

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

<220>
<223> oligoglycine

<400> 33

Gly Gly Gly
1

<210> 34
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> mature antibody Fc-region fragment with N-terminal triple glycine motif

<400> 34

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
1 5 10 15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20 25 30

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65 70 75 80

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

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

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

eolf-seql

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 35
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Pertuzumab heavy chain variable domain combined with a human heavy chain constant region of the subclass IgG1 containing a T366W mutation

<400> 35

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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 Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

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

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
```

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 36
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Pertuzumab light chain variable domain combined with a human kappa light chain constant region

<400> 36

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 Arg Thr Val Ala Ala
100 105 110

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

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145 150 155 160

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 37
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Trastuzumab heavy chain variable domain combined with a human heavy chain constant region of the subclass IgG1 containing a T366S, L368A, and Y407V mutation

<400> 37

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 Glu Pro Lys Ser Cys Asp
210 215 220

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

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 38
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Trastuzumab light chain variable domain combined with a human kappa light chain constant region

<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 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 Val Ala Ala
100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 39
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GGGSHHHHHHGSLPETGGSKDEL *amino acid sequence*

<400> 39

```
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 Glu Pro Lys Ser Cys Gly Gly
210 215 220

Gly Ser His His His His His His Gly Ser Leu Pro Glu Thr Gly Gly
225 230 235 240

Ser Lys Asp Glu Leu
245

<210> 40
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GSHHHHHHGSLPETGGSKDEL sequence

<400> 40

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

eolf-seql

```
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 Glu Pro Lys Ser Cys Gly Ser
    210                 215                 220

His His His His His His Gly Ser Leu Pro Glu Thr Gly Gly Ser Lys
225                 230                 235                 240

Asp Glu Leu
```

<210> 41
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal HHHHHHGSLPETGGSKDEL sequence

<400> 41

```
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 Glu Pro Lys Ser Cys His His
    210                 215                 220

His His His His Gly Ser Leu Pro Glu Thr Gly Gly Ser Lys Asp Glu
225                 230                 235                 240

Leu
```

<210> 42
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GGGSHHHHHHGSLPETGGSGSKDEL sequence

<400> 42

```
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 Glu Pro Lys Ser Cys Gly
    210                 215                 220

Gly Gly Ser His His His His His His Gly Ser Leu Pro Glu Thr Gly
225                 230                 235                 240

Gly Ser Gly Ser Lys Asp Glu Leu
                245
```

<210> 43
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GSHHHHHHGSLPETGGSGSKDEL sequence

<400> 43

```
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 Glu Pro Lys Ser Cys Gly
210 215 220

Ser His His His His His His Gly Ser Leu Pro Glu Thr Gly Gly Ser
225 230 235 240

Gly Ser Lys Asp Glu Leu
245

<210> 44
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal HHHHHHGSLPETGGSGSKDEL sequence

<400> 44

eolf-seql

```
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 Glu Pro Lys Ser Cys His
    210                 215                 220

His His His His His Gly Ser Leu Pro Glu Thr Gly Gly Ser Gly Ser
225                 230                 235                 240

Lys Asp Glu Leu
```

<210> 45
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A and Y407V mutation containing a N-terminal gggdkthtcppc sequence

<400> 45

```
Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
1               5                  10                  15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            20                  25                  30

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65                  70                  75                  80

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

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

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

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    130                 135                 140

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 46
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A and Y407V mutation containing a N-terminal gghtcppc sequence

<400> 46

Gly Gly His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
1 5 10 15

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
35 40 45

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
85 90 95

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

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

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

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
145 150 155 160

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
195 200 205

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

Gly Lys
225

<210> 47
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A and Y407V mutation containing a N-terminal ggcppc sequence

<400> 47

Gly Gly Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
1 5 10 15

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
35 40 45

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
65 70 75 80

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
85 90 95

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
100 105 110

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
130 135 140

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
145 150 155 160

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
165 170 175

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
195 200 205

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 48
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutation containing a N-terminal gggdkthtcppc sequence

<400> 48

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
1 5 10 15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20 25 30

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65 70 75 80

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
130 135 140

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

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

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

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

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

210 215 220

Ser Leu Ser Pro Gly Lys
225 230

<210> 49
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutations containing a N-terminal gghtcppc sequence

<400> 49

Gly Gly His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
1 5 10 15

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
35 40 45

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
85 90 95

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

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

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
130 135 140

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
195 200 205

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    210                 215                 220

Gly Lys
225
```

<210> 50
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutation containing a N-terminal ggcppc sequence

<400> 50

```
Gly Gly Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
1               5                   10                  15

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        35                  40                  45

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
65                  70                  75                  80

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                85                  90                  95

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            100                 105                 110

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

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
    130                 135                 140

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
145                 150                 155                 160

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                165                 170                 175

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
195 200 205

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 51
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> mature soluble sortase with ER retention signal

<400> 51

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

Ile Glu Ile Pro Asp Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro
20 25 30

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

Glu Ser Leu Asp Asp Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile
50 55 60

Asp Arg Pro Asn Tyr Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly
65 70 75 80

Ser Met Val Tyr Phe Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met
85 90 95

Thr Ser Ile Arg Asp Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu
100 105 110

Gln Lys Gly Lys Asp Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr
115 120 125

Asn Glu Lys Thr Gly Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr
130 135 140

Glu Val Lys Asp Glu Leu
145 150

<210> 52
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> mature soluble sortase with GSKDEL ER retention signal

<400> 52

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

Ile Glu Ile Pro Asp Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro
            20                  25                  30

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

Glu Ser Leu Asp Asp Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile
    50                  55                  60

Asp Arg Pro Asn Tyr Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly
65                  70                  75                  80

Ser Met Val Tyr Phe Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met
                85                  90                  95

Thr Ser Ile Arg Asp Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu
            100                 105                 110

Gln Lys Gly Lys Asp Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr
        115                 120                 125

Asn Glu Lys Thr Gly Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr
    130                 135                 140

Glu Val Lys Gly Ser Lys Asp Glu Leu
145                 150
```