

## SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG  
 <120> The Contorsbody - a single chain target binder  
 <130> P33504-W0  
 <150> EP16167920  
 <151> 2016-05-02  
 <160> 105  
 <170> PatentIn version 3.5  
 <210> 1  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Arg-tag  
 <400> 1  
 Arg Arg Arg Arg Arg  
 1 5  
  
 <210> 2  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Arg-tag 2  
 <400> 2  
 Arg Arg Arg Arg Arg Arg  
 1 5  
  
 <210> 3  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> His-tag  
 <400> 3

His His His His His His  
1 5

<210> 4  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino acid tag

<400> 4

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

His Asn Lys

<210> 5  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino acid tag

<400> 5

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 6  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino acid tag

<400> 6

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> 7  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino acid tag#

<400> 7

Ala Trp Arg His Pro Gln Phe Gly Gly  
 1 5

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

<220>  
 <223> amino acid tag

<400> 8

Trp Ser His Pro Gln Phe Glu Lys  
 1 5

<210> 9  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino acid tag

<400> 9

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

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

<220>  
 <223> amino acid tag

<400> 10

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

<210> 11

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid tag

<400> 11

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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> 12

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid tag

<400> 12

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

<210> 13

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid tag

<400> 13

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

<210> 14  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino acid tag

<400> 14

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> 15  
 <211> 47  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino acid tag

<400> 15

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> 16  
 <211> 32  
 <212> PRT  
 <213> Butyrivibrio fibrisolvens

<400> 16

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> 17  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> chitin-binding-domain

<400> 17

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> 18  
 <211> 209  
 <212> PRT  
 <213> Chondrus crispus

<400> 18

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> 19

<211> 396

<212> PRT

<213> Escherichia coli

<400> 19

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

<210> 20  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 20

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

&lt;210&gt; 21

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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> 22  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 22

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> 23  
 <211> 10  
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> X=S or P

<400> 23

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Thr | His | Thr | Cys | Pro | Xaa | Cys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 24

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (5)..(5)

<223> X=S or P

<400> 24

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Cys | Pro | Xaa | Cys | Pro |
| 1   |     |     | 5   |     |     |     |

<210> 25

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> X=S or P

<400> 25

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Cys | Pro | Xaa | Cys | Pro |
| 1   |     |     | 5   |     |

<210> 26

<211> 330

<212> PRT

<213> Homo sapiens

&lt;400&gt; 26

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> 27  
 <211> 330  
 <212> PRT  
 <213> Homo sapiens

<400> 27

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

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> 28  
 <211> 326  
 <212> PRT  
 <213> Homo sapiens

<400> 28

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 Asn Phe Gly Thr Gln Thr  
 65 70 75 80

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 100 105 110

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

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

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

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
 180 185 190

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys  
 325

<210> 29  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 29

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro  
 100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg  
 115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys  
 130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro  
 145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr  
 195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His  
 225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
 260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
 275 280 285

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

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

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile  
 340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln  
                   355                                  360                                  365

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
       370                                  375

<210> 30  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<400> 30

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> | 31           |
| <211> | 226          |
| <212> | PRT          |
| <213> | Homo sapiens |

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (131)..(131)

&lt;223&gt; X=E or D

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (133)..(133)

&lt;223&gt; X=M or L

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (136)..(136)

&lt;223&gt; Xaa can be any naturally occurring amino acid

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (138)..(138)

&lt;223&gt; Xaa can be any naturally occurring amino acid

&lt;400&gt; 31

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

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

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

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

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

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

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115

120

125

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

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

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

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

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

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

Pro Gly  
 225

<210> 32  
 <211> 226  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG1 isotype with a hole mutation

<400> 32

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
 225

<210> 33  
 <211> 226  
 <212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 isotype with a knob mutation

<400> 33

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

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

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

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

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

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180

185

190

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

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

Pro Gly  
 225

<210> 34

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 isotype with the mutations  
 L234A, L235A

<400> 34

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
 225

<210> 35  
 <211> 226  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG1 isotype with a L234A, L235A  
 and hole mutation

<400> 35

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
 225

<210> 36  
 <211> 226  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG1 isotype with a L234A, L235A  
 and knob mutation

<400> 36

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
 225

<210> 37  
 <211> 226  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG1 isotype with a L234A, L235A  
 and P329G mutation

<400> 37

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

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

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85

90

95

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

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

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

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

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

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

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

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

Pro Gly  
 225

<210> 38

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 isotype with a L234A, L235A,  
 P329G and hole mutation

<400> 38

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
225

<210> 39  
<211> 226  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variant human Fc-region of the IgG1 isotype with a L234A, L235A, P329G and knob mutation

<400> 39

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly  
225

<210> 40

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 subclass with the mutations  
L234A, L235A, P329G, Y349C, T366S, L368A and Y407V

<400> 40

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly Ala Pro Ile Glu Lys Thr Ile Ser  
100 105 110

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

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

<210> 41

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 subclass with a L234A, L235A, P329G and S354C, T366W mutation

<400> 41

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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  |
| 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 Gly 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 |
| Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp 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 |
| 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             |     |     |     |

210

215

220

&lt;210&gt; 42

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; variant human Fc-region of the IgG1 subclass with a L234A, L235A, P329G and S354C, T366S, L368A and Y407V mutation

&lt;400&gt; 42

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

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

<210> 43

$\langle 211 \rangle$     221

<212> PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> variant human Fc-region of the IgG1 subclass with a L234A, L235A, P329G and Y349C, T366W mutation

<400> 43

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly Ala Pro Ile Glu Lys Thr Ile Ser  
                   100                  105                  110

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp 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  
       210                  215                  220

<210> 44

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 subclass with the mutations  
       I253A, H310A and H435A

<400> 44

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 Ala 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 Ala 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 Ala Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
      210                         215                         220

<210> 45

<211> 221

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> variant human Fc-region of the IgG1 subclass with the mutations  
H310A, H433A and Y436A

&lt;400&gt; 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Ala | 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 Ala  
           195                                  200                                  205

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

<210> 46

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG1 subclass with the mutations  
 M252Y, S254T and T256E

<400> 46

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 Tyr Ile Thr Arg Glu 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  
 210 215 220

<210> 47  
 <211> 228  
 <212> PRT  
 <213> Homo sapiens

<400> 47

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe  
 1 5 10 15

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

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

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

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

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

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

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
                     180                    185                    190

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

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

Leu Ser Leu Gly  
                     225

<210> 48  
 <211> 228  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG4 isotype with a S228P and  
                     L235E mutation

<400> 48

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
 1 5 10 15

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

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

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

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

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

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

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
 180 185 190

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

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

Leu Ser Leu Gly  
 225

<210> 49  
 <211> 228  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variant human Fc-region of the IgG4 isotype with a S228P, L235E  
 and P329G mutation

<400> 49

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
 1 5 10 15

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

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

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

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

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

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

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

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

130

135

140

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
 180 185 190

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

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

Leu Ser Leu Gly  
 225

<210> 50

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG4 isotype with a S228P and  
 L235E mutation

<400> 50

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
 1 5 10 15

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

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

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

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

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

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

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu  
180 185 190

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

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

Leu Ser Leu Gly  
225

<210> 51

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> variant human Fc-region of the IgG4 isotype with a S228P, L235E and P329G mutation

<400> 51

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
1 5 10 15

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

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

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

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

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

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

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
180 185 190

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

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

Leu Ser Leu Gly  
 225

<210> 52  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 52

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> 53  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 53

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> 54

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 54

Gly Gly Gly Ser  
1

<210> 55

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 55

Gly Gly Gly Gly Ser  
1 5

<210> 56

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 56

Gln Gln Gln Ser  
1

<210> 57

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 57

Gln Gln Gln Gln Ser  
1 5

<210> 58

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 58

Ser Ser Ser Gly  
1

<210> 59

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 59

Ser Ser Ser Ser Gly  
1 5

<210> 60

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 60

Gly Gly Gly Ser Gly Gly Gly Ser  
1 5

<210> 61

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 61

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

<210> 62

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 62

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

<210> 63  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptidic linker

<400> 63

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

Gly Gly Gly Ser  
 20

<210> 64  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptidic linker

<400> 64

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

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

<220>  
 <223> peptidic linker

<400> 65

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

<210> 66  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> peptidic linker

<400> 66

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

Gly Gly Gly Ser  
20

<210> 67

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 67

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

Gly

<210> 68

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 68

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

Gly Ser

<210> 69

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 69

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

Gly Gly Gly Ser Gly Gly  
20

<210> 70

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic linker

<400> 70

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25 30

<210> 71

<211> 118

<212> PRT

<213> Mus musculus

<400> 71

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

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

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

Ala Met Ile Tyr Tyr Asp Ser Ser Lys Met Asn Tyr Ala Asp Thr Val  
 50 55 60

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

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

Ala Val Pro Thr Ser His Tyr Val Val Asp Val Trp Gly Gln Gly Val  
 100 105 110

Ser Val Thr Val Ser Ser  
 115

<210> 72  
 <211> 107  
 <212> PRT  
 <213> Mus musculus

<400> 72

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 Leu Glu Leu Lys

100

105

<210> 73  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-TfR mAb 8D3 VL variant L104V L106I

<400> 73

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  
 100 105

<210> 74  
 <211> 122  
 <212> PRT  
 <213> *Oryctolagus cuniculus*

<400> 74

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

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

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

Tyr Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Ser Trp Ala Lys Gly  
 50 55 60

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

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

Gly Thr Ser Tyr Pro Asp Tyr Gly Asp Ala Asn Gly Phe Asp Pro Trp  
 100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 75  
 <211> 110  
 <212> PRT  
 <213> *Oryctolagus cuniculus*

<400> 75

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

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

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

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

Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val Glu Cys

65 70 75 80

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Cys Tyr Ser Ser Ser Asn

85 90 95

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Asn | Thr | Phe | Gly | Gly | Gly | Thr | Glu | Val | Val | Val | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |

|       |                       |
|-------|-----------------------|
| <210> | 76                    |
| <211> | 7                     |
| <212> | PRT                   |
| <213> | Oryctolagus cuniculus |

<400> 76

Gly Phe Ser Leu Ser Ser Tyr  
1 5

|       |                       |
|-------|-----------------------|
| <210> | 77                    |
| <211> | 5                     |
| <212> | PRT                   |
| <213> | Oryctolagus cuniculus |

<400> 77

Trp Ser Gly Gly Ser  
1 5

```
<210> 78
<211> 17
<212> PRT
<213> Oryctolagus cuniculus
```

<400> 78

Arg Tyr Gly Thr Ser Tyr Pro Asp Tyr Gly Asp Ala Asn Gly Phe Asp  
1 5 10 15

Pro

|       |                     |
|-------|---------------------|
| <210> | 79                  |
| <211> | 17                  |
| <212> | PRT                 |
| <213> | Artificial Sequence |

&lt;220&gt;

&lt;223&gt; 299-000 HVR-H3 DASG

&lt;400&gt; 79

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Gly | Thr | Ser | Tyr | Pro | Asp | Tyr | Gly | Asp | Ala | Ser | Gly | Phe | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Pro

&lt;210&gt; 80

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; 299-000 HVR-H3 DAQG

&lt;400&gt; 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Gly | Thr | Ser | Tyr | Pro | Asp | Tyr | Gly | Asp | Ala | Gln | Gly | Phe | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Pro

&lt;210&gt; 81

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; 299-000 HVR-L1 RAA

&lt;400&gt; 81

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Ser | Gln | Ser | Ile | Ser | Ser | Tyr | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

&lt;210&gt; 82

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Oryctolagus cuniculus

&lt;400&gt; 82

Arg Ala Ser Thr Leu Ala Ser  
1 5

<210> 83  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> 299-000 HVR-L3 NYA

<400> 83

Gln Gln Asn Tyr Ala Ser Ser Asn Val Asp Asn Thr  
1 5 10

<210> 84  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-TfR mAb 567 VH (=humanized 299 VH\_basic)

<400> 84

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

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

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

Tyr Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Ser Trp Ala Lys Gly  
50 55 60

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

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

Gly Thr Ser Tyr Pro Asp Tyr Gly Asp Ala Asn Gly Phe Asp Pro Trp  
 100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 85  
 <211> 110  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-TfR mAb 567 VL (=humanized 299 VL\_basic)

<400> 85

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

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

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

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

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

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Ser Asn  
 85 90 95

Val Asp Asn Thr Phe Gly Gly Gly Thr Glu Val Val Val Lys  
 100 105 110

<210> 86  
 <211> 122  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; anti-TfR mAb 932 VH (=humanized 299 VH\_mutated)

&lt;400&gt; 86

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

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

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

Tyr Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Ser Trp Ala Lys Ser  
 50 55 60

Arg Val Thr Ile Ser Lys Thr Ser Thr Thr Val Ser Leu Lys Leu Ser  
 65 70 75 80

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

Gly Thr Ser Tyr Pro Asp Tyr Gly Asp Ala Asn Gly Phe Asp Pro Trp  
 100 105 110

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

&lt;210&gt; 87

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; anti-TfR mAb 932 VL (=humanized 299 VL\_mutated)

&lt;400&gt; 87

Ala Ile Gln Leu 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 Ser Ile Ser Ser Tyr

20

25

30

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

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

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

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

Val Asp Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105 110

<210> 88

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 299-023 VH humanization variant\_DASG

<400> 88

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

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

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

Tyr Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Ser Trp Ala Lys Ser  
 50 55 60

Arg Val Thr Ile Ser Lys Thr Ser Thr Thr Val Ser Leu Lys Leu Ser  
 65 70 75 80

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

Gly Thr Ser Tyr Pro Asp Tyr Gly Asp Ala Ser Gly Phe Asp Pro Trp  
                     100                    105                    110

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

<210> 89  
 <211> 119  
 <212> PRT  
 <213> Mus musculus

<400> 89

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

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

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

Gly Arg Ile Asp Pro Ala Asn Gly Asp Thr Lys Cys Asp Pro Lys Phe  
                     50                    55                    60

Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
 65                    70                    75                    80

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

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

Thr Thr Leu Thr Val Ser Ser  
                     115

<210> 90  
 <211> 108  
 <212> PRT  
 <213> Mus musculus

<400> 90

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

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

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

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

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

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

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

<210> 91  
 <211> 118  
 <212> PRT  
 <213> Mus musculus

<400> 91

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

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

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

Gly Arg Ile Asn Pro His Asn Gly Gly Thr Asp Tyr Ala Gln Lys Phe  
 50 55 60

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

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

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

Leu Val Thr Val Ser Ser  
 115

<210> 92  
 <211> 106  
 <212> PRT  
 <213> Mus musculus

<400> 92

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 Ser Ser Ile Arg Tyr Ile  
 20 25 30

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Asn Ser Tyr Pro Trp Thr  
 85 90 95

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

<210> 93  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> human transferrin receptor fragment

<400> 93

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

<210> 94  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> human transferrin receptor fragment

<400> 94

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

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

<220>  
 <223> human transferrin receptor fragment

<400> 95

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

<210> 96  
 <211> 693  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; anti-Her2 circular fusion polypeptide

&lt;400&gt; 96

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 Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro  
 225 230 235 240

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 245 250 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 260 265 270

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 275 280 285

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 290 295 300

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 305 310 315 320

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 325 330 335

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 340 345 350

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 355 360 365

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 370 375 380

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 385 390 395 400

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 405 410 415

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 420 425 430

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 435 440 445

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly  
 450 455 460

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 465 470 475 480

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 485 490 495

Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 500 505 510

Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val  
 515 520 525

Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr  
 530 535 540

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
 545 550 555 560

His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 565 570 575

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 580 585 590

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 595 600 605

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 610 615 620

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 625 630 635 640

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 645 650 655

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 660 665 670

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Gly His  
 675 680 685

His His His His His  
 690

<210> 97

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-cMet circular fusion polypeptide

<400> 97

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 Thr Ser Glu Asn Ile Tyr Ser Tyr  
 20 25 30

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

Tyr Asn Ala Lys Thr Leu Ala Glu 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 | His | His | Tyr | Gly | Thr | Pro | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | 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 | Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val |

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 275                                                             |     | 280 |     | 285 |
| Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln | 290 | 295 | 300 |     |
| Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln | 305 | 310 | 315 | 320 |
| Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala | 325 | 330 | 335 |     |
| Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro | 340 | 345 | 350 |     |
| Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr | 355 | 360 | 365 |     |
| Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser | 370 | 375 | 380 |     |
| Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr | 385 | 390 | 395 | 400 |
| Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr | 405 | 410 | 415 |     |
| Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe | 420 | 425 | 430 |     |
| Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys | 435 | 440 | 445 |     |
| Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly | 450 | 455 | 460 |     |
| Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro | 465 | 470 | 475 | 480 |
| Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr |     |     |     |     |

485

490

495

Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu  
 500 505 510

Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Leu Pro  
 515 520 525

Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln  
 530 535 540

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 545 550 555 560

Tyr Cys Ala Pro Ser Tyr Tyr Tyr Gly Gly Lys His Val Ala Leu Phe  
 565 570 575

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
 580 585 590

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 595 600 605

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 610 615 620

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 625 630 635 640

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
 645 650 655

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
 660 665 670

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 675 680 685

Pro Lys Ser Cys

690

<210> 98  
 <211> 693  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-CD20 circular fusion polypeptide (1)

<400> 98

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

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

Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile  
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys  
 225 230 235 240

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu  
 245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
 260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
 275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys  
 290 295 300

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
 305 310 315 320

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
 325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
 340 345 350

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
 355 360 365

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
 385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly  
 405 410 415

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
 420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
 435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly  
 450 455 460

Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Ser Gln Ser Pro Ala  
 465 470 475 480

Ile Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala  
 485 490 495

Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser  
 500 505 510

Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val  
 515 520 525

Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr  
 530 535 540

Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
 545 550 555 560

Trp Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
 565 570 575

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
                   580                  585                  590

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
           595                  600                  605

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
       610                  615                  620

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 625                  630                  635                  640

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
                   645                  650                  655

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
                   660                  665                  670

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Gly His  
       675                  680                  685

His His His His His  
       690

<210> 99  
 <211> 697  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-CD20 circular fusion polypeptide (2)

<400> 99

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

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

Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Arg Ile Phe Pro Gly Asp Gly Asp Thr Asp Tyr Asn Gly Lys Phe  
 50 55 60

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

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

Ala Arg Asn Val Phe Asp Gly Tyr Trp Leu Val 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 Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro  
 225 230 235 240

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Thr | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Lys | Val | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | Gly | Gly | Gly | Gly | Ser |

450

455

460

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu  
 465 470 475 480

Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys  
 485 490 495

Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln  
 500 505 510

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu  
 515 520 525

Val Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 530 535 540

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr  
 545 550 555 560

Tyr Cys Ala Gln Asn Leu Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr  
 565 570 575

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His

660

665

670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
           675                          680                          685

Gly Ser Gly His His His His His His  
       690                          695

&lt;210&gt; 100

&lt;211&gt; 689

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; anti-cMet circular fusion polypeptide VH-out-knob

&lt;400&gt; 100

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

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

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

Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Leu Pro Ser Leu  
   50                  55                  60

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

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

Ala Pro Ser Tyr Tyr Tyr Gly Gly Lys His Val Ala Leu Phe Ala Tyr  
           100                  105                  110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
           115                  120                  125

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

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

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

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

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
 210 215 220

Ser Cys Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys  
 225 230 235 240

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 275 280 285

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 305 310 315 320

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
                   340                  345                  350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
           355                  360                  365

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp  
       370                  375                  380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 385                  390                  395                  400

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
           420                  425                  430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
       435                  440                  445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
       450                  455                  460

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr  
 465                  470                  475                  480

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
                   485                  490                  495

Thr Cys Arg Thr Ser Glu Asn Ile Tyr Ser Tyr Leu Ala Trp Tyr Gln  
           500                  505                  510

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val Tyr Asn Ala Lys Thr  
       515                  520                  525

Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
       530                  535                  540

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 545 550 555 560

Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Phe Thr Phe Gly Gln Gly  
 565 570 575

Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile  
 580 585 590

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

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys  
 610 615 620

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu  
 625 630 635 640

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu  
 645 650 655

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 660 665 670

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
 675 680 685

Cys

<210> 101

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-cMet circular fusion polypeptide VH-in-knob

<400> 101

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 Thr Ser Glu Asn Ile Tyr Ser Tyr | 20  | 25  | 30  |
| Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val | 35  | 40  | 45  |
| Tyr Asn Ala Lys Thr Leu Ala Glu 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  |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Phe | 85  | 90  | 95  |
| Thr Phe Gly Gln Gly Thr Lys Leu 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 |
| 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 225 | Gly 225 | Gly 225 | Gly 225 | Ser 230 | Asp 230 | Lys 230 | Thr 230 | His 230 | Thr 230 | Cys 235 | Pro 235 | Pro 235 | Cys 235 | Pro 235 | Ala 240 |
| Pro 245 | Glu 245 | Leu 245 | Leu 245 | Gly 245 | Gly 245 | Pro 245 | Ser 245 | Val 245 | Phe 250 | Leu 250 | Phe 250 | Pro 250 | Pro 250 | Lys 255 | Pro 255 |
| Lys 260 | Asp 260 | Thr 260 | Leu 260 | Met 260 | Ile 260 | Ser 260 | Arg 260 | Thr 265 | Pro 265 | Glu 265 | Val 265 | Thr 265 | Cys 270 | Val 270 | Val 270 |
| Val 275 | Asp 275 | Val 275 | Ser 275 | His 275 | Glu 275 | Asp 275 | Pro 280 | Glu 280 | Val 280 | Lys 280 | Phe 280 | Asn 285 | Trp 285 | Tyr 285 | Val 285 |
| Asp 290 | Gly 290 | Val 290 | Glu 290 | Val 290 | His 290 | Asn 295 | Ala 295 | Lys 295 | Thr 295 | Lys 295 | Pro 300 | Arg 300 | Glu 300 | Glu 300 | Gln 300 |
| Tyr 305 | Asn 305 | Ser 305 | Thr 305 | Tyr 305 | Arg 310 | Val 310 | Val 310 | Ser 310 | Val 310 | Leu 315 | Thr 315 | Val 315 | Leu 315 | His 315 | Gln 320 |
| Asp 325 | Trp 325 | Leu 325 | Asn 325 | Gly 325 | Lys 325 | Glu 325 | Tyr 325 | Lys 330 | Cys 330 | Lys 330 | Val 330 | Ser 330 | Asn 335 | Lys 335 | Ala 335 |
| Leu 340 | Pro 340 | Ala 340 | Pro 340 | Ile 340 | Glu 340 | Lys 340 | Thr 340 | Ile 345 | Ser 345 | Lys 345 | Ala 345 | Lys 345 | Gly 350 | Gln 350 | Pro 350 |
| Arg 355 | Glu 355 | Pro 355 | Gln 355 | Val 355 | Tyr 355 | Thr 355 | Leu 360 | Pro 360 | Pro 360 | Cys 360 | Arg 360 | Asp 365 | Glu 365 | Leu 365 | Thr 365 |
| Lys 370 | Asn 370 | Gln 370 | Val 370 | Ser 370 | Leu 370 | Trp 375 | Cys 375 | Leu 375 | Val 375 | Lys 375 | Gly 380 | Phe 380 | Tyr 380 | Pro 380 | Ser 380 |
| Asp 385 | Ile 385 | Ala 385 | Val 385 | Glu 385 | Trp 390 | Glu 390 | Ser 390 | Asn 390 | Gly 390 | Gln 395 | Pro 395 | Glu 395 | Asn 395 | Asn 395 | Tyr 400 |
| Lys 405 | Thr 405 | Thr 405 | Pro 405 | Pro 405 | Val 405 | Leu 405 | Asp 405 | Ser 410 | Asp 410 | Gly 410 | Ser 410 | Phe 410 | Phe 410 | Leu 415 | Tyr 415 |
| Ser 415 | Lys 415 | Leu 415 | Thr 415 | Val 415 | Asp 415 | Lys 415 | Ser 415 | Arg 415 | Trp 415 | Gln 415 | Gln 415 | Gly 415 | Asn 415 | Val 415 | Phe 415 |

420

425

430

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 435 440 445

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly  
 450 455 460

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
 465 470 475 480

Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr  
 485 490 495

Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu  
 500 505 510

Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Leu Pro  
 515 520 525

Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln  
 530 535 540

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 545 550 555 560

Tyr Cys Ala Pro Ser Tyr Tyr Tyr Gly Gly Lys His Val Ala Leu Phe  
 565 570 575

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
 580 585 590

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 595 600 605

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 610 615 620

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His

625                      630                      635                      640

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
                                 645                      650                      655

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
                                 660                      665                      670

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
                                 675                      680                      685

Pro Lys Ser Cys  
                                 690

<210> 102  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-cMet circular fusion polypeptide VH-out-hole

<400> 102

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

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

Phe Ile Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
                                 35                      40                      45

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

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Gly Gly Gly Gly Ser  
 210 215 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys  
 225 230 235 240

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu  
 245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
 260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
 275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys  
 290 295 300

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
 305 310 315 320

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
 325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
 340 345 350

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser  
 355 360 365

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys  
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
 385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly  
 405 410 415

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
 420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
 435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly  
 450 455 460

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala  
 465 470 475 480

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala  
 485 490 495

Ser Ser Ser Val Ser His Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Gln  
 500 505 510

Ala Pro Arg Leu Trp Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val  
           515                                  520                                  525

Pro Ala Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr  
       530                                  535                                  540

Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys His Gln  
 545                                  550                                  555                                  560

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
                                   580                                  585                                  590

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
                   595                                  600                                  605

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
       610                                  615                                  620

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 625                                  630                                  635                                  640

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Ser Leu Ser Lys Ala Asp  
                                   645                                  650                                  655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
                                   660                                  665                                  670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
           675                                  680                                  685

<210> 103  
 <211> 686  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-cMet circular fusion polypeptide VH-out-hole-CH-CL-crossed

&lt;400&gt; 103

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

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

Phe Ile Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

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

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

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

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

Thr Val Ser Ser Ser Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
 115 120 125

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

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 165 170 175

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

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln

195

200

205

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys  
 225 230 235 240

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 275 280 285

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 305 310 315 320

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 340 345 350

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser  
 370 375 380

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|            |            |            | 405        |            |            |            |            | 410        |            |            |            |            | 415        |            |            |
| Asp        | Ser        | Asp        | Gly<br>420 | Ser        | Phe        | Phe        | Leu        | Val<br>425 | Ser        | Lys        | Leu        | Thr        | Val<br>430 | Asp        | Lys        |
| Ser        | Arg        | Trp<br>435 | Gln        | Gln        | Gly        | Asn        | Val<br>440 | Phe        | Ser        | Cys        | Ser        | Val<br>445 | Met        | His        | Glu        |
| Ala        | Leu        | His        | Asn        | His        | Tyr        | Thr        | Gln<br>455 | Lys        | Ser        | Leu        | Ser<br>460 | Leu        | Ser        | Pro        | Gly        |
| Lys<br>465 | Gly        | Gly        | Gly        | Gly        | Ser<br>470 | Gly        | Gly        | Gly        | Gly        | Ser<br>475 | Glu        | Ile        | Val        | Leu        | Thr<br>480 |
| Gln        | Ser        | Pro        | Ala        | Thr<br>485 | Leu        | Ser        | Leu        | Ser        | Pro<br>490 | Gly        | Glu        | Arg        | Ala        | Thr<br>495 | Leu        |
| Ser        | Cys        | Arg        | Ala<br>500 | Ser        | Ser        | Ser        | Val        | Ser<br>505 | His        | Leu        | Tyr        | Trp        | Tyr<br>510 | Gln        | Gln        |
| Lys        | Pro        | Gly<br>515 | Gln        | Ala        | Pro        | Arg        | Leu<br>520 | Trp        | Ile        | Tyr        | Asp        | Thr<br>525 | Ser        | Asn        | Leu        |
| Ala<br>530 | Ser        | Gly        | Val        | Pro        | Ala        | Arg<br>535 | Phe        | Ser        | Gly        | Ser        | Arg<br>540 | Ser        | Gly        | Thr        | Asp        |
| Phe<br>545 | Thr        | Leu        | Thr        | Ile        | Ser<br>550 | Ser        | Leu        | Glu        | Pro        | Glu<br>555 | Asp        | Phe        | Ala        | Val        | Tyr<br>560 |
| Phe        | Cys        | His        | Gln        | Arg<br>565 | Thr        | Asn        | Tyr        | Pro        | Trp<br>570 | Thr        | Phe        | Gly        | Gln        | Gly<br>575 | Thr        |
| Lys        | Leu        | Glu        | Ile<br>580 | Lys        | Ser        | Ser        | Ala        | Ser<br>585 | Thr        | Lys        | Gly        | Pro        | Ser<br>590 | Val        | Phe        |
| Pro        | Leu<br>595 | Ala        | Pro        | Ser        | Ser        | Lys        | Ser<br>600 | Thr        | Ser        | Gly        | Gly        | Thr<br>605 | Ala        | Ala        | Leu        |
| Gly        | Cys        | Leu        | Val        | Lys        | Asp        | Tyr        | Phe        | Pro        | Glu        | Pro        | Val        | Thr        | Val        | Ser        | Trp        |

610                                      615                                      620

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
625                                      630                                      635                                      640

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
645                                      650                                      655

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
660                                      665                                      670

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675                                      680                                      685

<210> 104  
<211> 683  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-cMet circular fusion polypeptide VH-out-hole-VH-VL-crossed

<400> 104

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser His Leu  
20                                      25                                      30

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

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

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

Asp Phe Ala Val Tyr Phe Cys His Gln Arg Thr Asn Tyr Pro Trp Thr  
85                                      90                                      95

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

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

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 195 200 205

Lys Ser Cys Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu  
450 455 460

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile  
465 470 475 480

Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ala Tyr Phe Ile Asn Trp  
485 490 495

Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Tyr  
500 505 510

Pro Tyr Asn Gly Asn Thr Phe Tyr Asp Gln Ser Phe Gln Gly Gln Val  
           515                          520                          525

Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser  
       530                          535                          540

Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Trp Asp  
 545                          550                          555                          560

Tyr Asn Tyr Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
                           565                          570                          575

Ser Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
                           580                          585                          590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
           595                          600                          605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
       610                          615                          620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 625                          630                          635                          640

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
                           645                          650                          655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
                           660                          665                          670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
       675                          680

<210> 105  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> MISC\_FEATURE  
 <222> (131)..(131)  
 <223> X=E or D

<220>  
 <221> MISC\_FEATURE  
 <222> (133)..(133)  
 <223> X=M or L

<400> 105

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

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

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

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

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

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

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

Glu Lys Thr Ile Ser Lys Ala Lys  
 115 120