

SEQUENCE LISTING

<110> Affimed GmbH

<120> BISPECIFIC EGFR/CD16 ANTIGEN-BINDING PROTEIN

<130> A 3317PCT

<150> EP18161871.1

<151> 2018-03-14

<160> 45

<170> BiSSAP 1.3.6

<210> 1

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> vh domain

<400> 1

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Val	Ser	Ser	Gly
			20					25					30		
Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
			35				40					45			
Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser
	50				55					60					
Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe
65				70				75						80	
Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
			85					90					95		
Cys	Ala	Arg	Asn	Pro	Ile	Ser	Ile	Pro	Ala	Phe	Asp	Ile	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Met	Val	Thr	Val	Ser	Ser								
		115				120									

<210> 2

<211> 108

<212> PRT

<213> artificial sequence

<220>

<223> vl domain

<400> 2

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

Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	Ser	Val
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Tyr	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Gly
65					70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Thr	Ser	Ser	Asp	His
			85						90					95	
Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu				
			100					105							

<210> 3
 <211> 8
 <212> PRT
 <213> homo sapiens

<400> 3
 Ser Phe Phe Pro Pro Gly Tyr Gln
 1 5

<210> 4
 <211> 192
 <212> PRT
 <213> homo sapiens

<400> 4

Gly	Met	Arg	Thr	Glu	Asp	Leu	Pro	Lys	Ala	Val	Val	Phe	Leu	Glu	Pro
1				5					10				15		
Gln	Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln
			20					25					30		
Gly	Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu
		35					40					45			
Ser	Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr
	50					55					60				
Val	Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu
65					70				75						80
Ser	Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln
			85						90					95	
Ala	Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys
			100					105					110		
His	Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn
		115					120					125			
Gly	Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro
	130					135					140				
Lys	Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Phe
145					150					155					160
Gly	Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Ile	Thr	Gln
			165						170					175	
Gly	Leu	Ala	Val	Ser	Thr	Ile	Ser	Ser	Phe	Phe	Pro	Pro	Gly	Tyr	Gln
			180					185					190		

<210> 5
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 5
Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 6
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 6
Ile Asn Pro Ser Gly Gly Ser Thr
1 5

<210> 7
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 7
Ala Arg Gly Ser Ala Tyr Tyr Tyr Asp Phe Ala Asp Tyr
1 5 10

<210> 8
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 8
Asn Ile Gly Ser Lys Asn
1 5

<210> 9
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 9
Gln Asp Asn Lys Arg
1 5

<210> 10
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 10
Gln Val Trp Asp Asn Tyr Ser Val Leu
1 5

<210> 11
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 11
Ile Glu Pro Met Tyr Gly Ser Thr
1 5

<210> 12
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> vh

<400> 12
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Ile	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	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	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120								

<210> 13
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> v1

Ser	Tyr	Val	Leu	Thr	Gln	Pro	Ser	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln
1				5					10					15	
Thr	Ala	Thr	Ile	Ser	Cys	Gly	Gly	His	Asn	Ile	Gly	Ser	Lys	Asn	Val
			20					25					30		
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Gln	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr	Gln	Ala	Met
65					70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Asn	Tyr	Ser	Val	Leu
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu						
			100					105							

<210> 14
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> vh

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	
Ser	Leu	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly	Ala	Ile	Glu	Pro	Met	Tyr	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe
50						55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	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	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120								

<210> 15

<211> 328

<212> PRT

<213> artificial sequence

<220>

<223> silenced Fc

<400> 15

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	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr
65					70					75					80
Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys
			85						90					95	
Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
			100					105					110		
Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
		115					120					125			
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
	130					135					140				
Val	Val	Ala	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
145					150					155					160
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
			165						170					175	
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
		180						185					190		
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
		195					200					205			
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
	210					215					220				
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met
225					230					235					240
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
			245						250					255	
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn

				260				265				270					
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu		
				275				280				285					
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val		
				290				295				300					
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln		
305						310					315				320		
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly										
				325													

<210> 16
 <211> 106
 <212> PRT
 <213> homo sapiens

<400> 16																	
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser		
1				5					10					15			
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp		
			20					25					30				
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro		
		35					40					45					
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn			
	50					55				60							
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys		
65					70					75					80		
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val		
				85					90					95			
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser								
			100					105									

<210> 17
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> linker

<400> 17									
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
1				5					10

<210> 18
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> linker

<400> 18

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

<210> 19

<211> 15

<212> PRT

<213> homo sapiens

<400> 19

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 20

<211> 216

<212> PRT

<213> artificial sequence

<220>

<223> silenced Fc

<400> 20

Ala Pro Glu Phe Glu 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
Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205
Lys Ser Leu Ser Leu Ser Pro Gly
210 215

<210> 21
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 21
Gly Gly Ser Val Ser Ser Gly Ser Tyr Tyr
1 5 10

<210> 22
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 22
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 23
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 23
Ala Arg Asn Pro Ile Ser Ile Pro Ala Phe Asp Ile
1 5 10

<210> 24
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 24
Asn Ile Gly Ser Lys Ser
1 5

<210> 25

<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 25
Tyr Asp Ser Asp
1

<210> 26
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> cdr

<400> 26
Gln Val Trp Asp Thr Ser Ser Asp His Val Leu
1 5 10

<210> 27
<211> 489
<212> PRT
<213> artificial sequence

<220>
<223> tandem diabody

<400> 27
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 Gly Ser Val Ser Ser Gly
20 25 30
Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Asn Pro Ile Ser Ile Pro Ala Phe Asp Ile Trp Gly Gln
100 105 110
Gly Thr Met Val Thr Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
115 120 125
Ser Ser Tyr Val Leu Thr Gln Pro Ser Ser Val Ser Val Ala Pro Gly
130 135 140
Gln Thr Ala Thr Ile Ser Cys Gly Gly His Asn Ile Gly Ser Lys Asn

145					150				155				160
Val	His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Val	Ile
				165					170				175
Tyr	Gln	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Gly
			180					185				190	
Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Ala
		195					200				205		
Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Asn	Val
	210				215					220			
Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gly	Gly
225				230					235				240
Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Gly
			245					250					255
Glu	Ser	Leu	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Ser
		260					265					270	
Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Trp
	275					280					285		
Met	Gly	Ile	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Lys
	290				295					300			
Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Val
305				310					315				320
Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Tyr
			325					330				335	
Cys	Ala	Arg	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Gly
		340					345			350			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Ser	Gly	Gly
	355					360			365				
Gly	Ser	Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Ala
	370				375				380				
Gly	Lys	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Lys
385				390					395				400
Ser	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val
		405						410				415	
Ile	Tyr	Tyr	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Ser
		420					425				430		
Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Glu
	435					440					445		
Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser
	450				455					460			
Asp	His	Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Ala
465				470					475				480
Ala	Gly	Ser	His	His	His	His	His	His					
			485										

<210> 28

<211> 705

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain

<400> 28

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu	1	5	10	15
Ser	Leu	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	20	25	30	
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	35	40	45	
Gly	Ile	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe	50	55	60	
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	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	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Tyr	Trp	Gly	Gln	100	105	110	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	130	135	140	
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	145	150	155	160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	165	170	175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	180	185	190	
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	195	200	205	
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	210	215	220	
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	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	Ala	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	Tyr	340	345	350	
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	355	360	365	
Thr	Cys	Leu	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	Tyr	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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 450 455 460
 Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
 465 470 475 480
 Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly Ser Tyr Tyr Trp Ser
 485 490 495
 Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile
 500 505 510
 Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val
 515 520 525
 Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser
 530 535 540
 Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Pro
 545 550 555 560
 Ile Ser Ile Pro Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
 565 570 575
 Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 580 585 590
 Gly Ser Gly Gly Ser Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser
 595 600 605
 Val Ala Pro Gly Lys Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
 610 615 620
 Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 625 630 635 640
 Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
 645 650 655
 Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
 660 665 670
 Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp
 675 680 685
 Thr Ser Ser Asp His Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val
 690 695 700
 Leu
 705

<210> 29
 <211> 212
 <212> PRT
 <213> artificial sequence

<220>
 <223> light chain

<400> 29
 Ser Tyr Val Leu Thr Gln Pro Ser Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Thr Ile Ser Cys Gly Gly His Asn Ile Gly Ser Lys Asn Val
 20 25 30
 His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
 35 40 45
 Gln Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50		55		60
Asn Ser Gly Asn Thr	Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met			
65	70	75	80	
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Tyr Ser Val Leu				
	85	90	95	
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala				
	100	105	110	
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn				
	115	120	125	
Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val				
	130	135	140	
Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu				
145	150	155	160	
Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser				
	165	170	175	
Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser				
	180	185	190	
Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro				
	195	200	205	
Thr Glu Cys Ser				
210				

<210> 30

<211> 734

<212> PRT

<213> artificial sequence

<220>

<223> Bi-scFv-Fc

<400> 30

Ser Tyr Val Leu Thr Gln Pro Ser Ser Val Ser Val Ala Pro Gly Gln				
1	5	10	15	
Thr Ala Thr Ile Ser Cys Gly Gly His Asn Ile Gly Ser Lys Asn Val				
	20	25	30	
His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Val Leu Val Ile Tyr				
	35	40	45	
Gln Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser				
	50	55	60	
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met				
65	70	75	80	
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Tyr Ser Val Leu				
	85	90	95	
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Ser Gly Gly Ser				
	100	105	110	
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gln				
	115	120	125	
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser				
	130	135	140	
Leu Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr				
145	150	155	160	
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly				
	165	170	175	

Ile	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe	Gln	
			180					185					190			
Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr	Met	
		195					200					205				
Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
	210					215					220					
Arg	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Tyr	Trp	Gly	Gln	Gly	
225					230					235					240	
Thr	Leu	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	
				245					250					255		
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	
			260					265					270			
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	
		275					280					285				
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Ala	Val	Ser	His	Glu	Asp	Pro	Glu	
	290					295					300					
Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	
305					310					315					320	
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	
				325					330					335		
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	
			340				345						350			
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	
		355					360					365				
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	
	370					375				380						
Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	
385					390					395					400	
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	
				405					410					415		
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	
			420					425					430			
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	
		435					440					445				
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	
	450					455					460					
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Gly	Gly	
465					470					475					480	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	
				485					490					495		
Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	
			500					505					510			
Ser	Gly	Gly	Ser	Val	Ser	Ser	Gly	Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	
		515					520					525				
Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser	
	530					535					540					
Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	
545					550					555					560	
Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	
				565					570					575		
Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Pro	Ile	Ser	Ile	
			580					585					590			
Pro	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	
		595					600					605				

Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	
610						615					620					
Gly	Ser	Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	
625					630					635					640	
Gly	Lys	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	
				645					650					655		
Ser	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	
			660					665					670			
Ile	Tyr	Tyr	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	
		675					680					685				
Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	
690					695						700					
Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Thr	Ser	Ser	
705					710					715					720	
Asp	His	Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu			
			725						730							

<210> 31
 <211> 121
 <212> PRT
 <213> artificial sequence

<220>
 <223> vh

<400> 31																
Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Ile	Asp	Leu	Ser	Asn	Tyr	
			20					25					30			
Ala	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
		35				40						45				
Gly	Ile	Ile	Trp	Ala	Ser	Gly	Thr	Thr	Phe	Tyr	Ala	Thr	Trp	Ala	Lys	
50						55					60					
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	Leu	
65					70					75					80	
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
			85					90						95		
Arg	Thr	Val	Pro	Gly	Tyr	Ser	Thr	Ala	Pro	Tyr	Phe	Asp	Leu	Trp	Gly	
			100					105					110			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120									

<210> 32
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> vl

<400> 32

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Val	Ser	Ala	Ser	Val	Gly
1				5				10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ser	Ser	Pro	Ser	Val	Trp	Ser	Asn
			20				25					30			
Phe	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu
		35				40					45				
Ile	Tyr	Glu	Ala	Ser	Lys	Leu	Thr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser
	50				55					60					
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln
65				70					75					80	
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gly	Gly	Tyr	Ser	Ser	Ile
			85					90					95		
Ser	Asp	Thr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys		
			100					105					110		

<210> 33
 <211> 20
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

<400> 33
 taatacgact cactataggg 20

<210> 34
 <211> 18
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

<400> 34
 tagaaggcac agtcgagg 18

<210> 35
 <211> 6
 <212> PRT
 <213> artificial sequence

<220>
 <223> linker

<400> 35
 Gly Gly Ser Gly Gly Ser
 1 5

<210> 36
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> linker

<400> 36
Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5

<210> 37
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 37
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15
Gly Ser Gly Gly Ser
20

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1

<400> 38
Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 39
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3

<400> 39
Ala Arg Gly Ser Ala Tyr Tyr Tyr Asp Phe Ala Asp Tyr
1 5 10

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1

<400> 40
Asn Ile Gly Ser Lys Asn
1 5

<210> 41
<400> 41
000

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3

<400> 42
Gln Val Trp Asp Asn Tyr Ser Val Leu
1 5

<210> 43
<211> 705
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 43
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ala Ile Glu Pro Met Tyr Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Gly Ser Ala Tyr Tyr Tyr Asp Phe Ala 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
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	165	170	175
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	180	185	190
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	195	200	205
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	210	215	220
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	225	230	235
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	Ala	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
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	Tyr	340	345	350
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	355	360	365
Thr	Cys	Leu	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
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	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	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	450	455	460
Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	465	470	475
Cys	Thr	Val	Ser	Gly	Gly	Ser	Val	Ser	Ser	Gly	Ser	Tyr	Tyr	Trp	Ser	485	490	495
Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	500	505	510
Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	515	520	525
Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Lys	Leu	Ser	530	535	540

Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Pro
545					550					555					560
Ile	Ser	Ile	Pro	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr
				565					570					575	
Val	Ser	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly
			580					585					590		
Gly	Ser	Gly	Gly	Ser	Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser
		595				600					605				
Val	Ala	Pro	Gly	Lys	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile
	610					615					620				
Gly	Ser	Lys	Ser	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro
625					630					635					640
Val	Leu	Val	Ile	Tyr	Tyr	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu
				645					650					655	
Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser
			660					665					670		
Arg	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp
		675					680					685			
Thr	Ser	Ser	Asp	His	Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val
	690					695					700				
Leu															
705															

<210> 44

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain

<400> 44

Ser	Tyr	Val	Leu	Thr	Gln	Pro	Ser	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln
1				5					10					15	
Thr	Ala	Thr	Ile	Ser	Cys	Gly	Gly	His	Asn	Ile	Gly	Ser	Lys	Asn	Val
			20					25					30		
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Gln	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr	Gln	Ala	Met
65					70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Asn	Tyr	Ser	Val	Leu
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala
			100					105					110		
Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn
		115					120					125			
Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val
	130					135					140				
Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys	Ala	Gly	Val	Glu
145					150					155					160
Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser

				165				170					175			
Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His	Arg	Ser	Tyr	Ser	
			180					185					190			
Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys	Thr	Val	Ala	Pro	
		195					200					205				
Thr	Glu	Cys	Ser													
	210															

<210> 45

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain

<400> 45

Ser	Tyr	Val	Leu	Thr	Gln	Pro	Ser	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln	
1				5				10						15		
Thr	Ala	Thr	Ile	Ser	Cys	Gly	Gly	His	Asn	Ile	Gly	Ser	Lys	Asn	Val	
			20				25						30			
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Val	Leu	Val	Ile	Tyr	
		35					40					45				
Gln	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	
	50					55				60						
Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr	Gln	Ala	Met	
65				70					75						80	
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Asn	Tyr	Ser	Val	Leu	
			85					90						95		
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gly	Ser	Gly	Gly	Ser	
			100					105					110			
Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	
		115				120						125				
Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu	Ser	
	130					135					140					
Leu	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Tyr	
145				150					155						160	
Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	
				165				170						175		
Ala	Ile	Glu	Pro	Met	Tyr	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe	Gln	
			180					185					190			
Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr	Met	
	195						200					205				
Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
	210					215					220					
Arg	Gly	Ser	Ala	Tyr	Tyr	Tyr	Asp	Phe	Ala	Asp	Tyr	Trp	Gly	Gln	Gly	
225				230						235					240	
Thr	Leu	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	
				245					250					255		
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	
		260						265					270			
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	
		275					280					285				

Pro	Glu	Val	Thr	Cys	Val	Val	Val	Ala	Val	Ser	His	Glu	Asp	Pro	Glu
290						295					300				
Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
305					310					315					320
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
				325					330					335	
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
			340				345						350		
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile
		355					360					365			
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
	370					375					380				
Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
385					390					395					400
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
			405						410					415	
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
			420					425					430		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
		435					440					445			
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
						455					460				
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Gly	Gly
465					470					475					480
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly
				485					490					495	
Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val
			500					505					510		
Ser	Gly	Gly	Ser	Val	Ser	Ser	Gly	Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg
		515					520					525			
Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser
		530				535					540				
Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser
545					550					555					560
Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr
				565					570					575	
Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Pro	Ile	Ser	Ile
			580					585					590		
Pro	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser
		595					600					605			
Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly
					615						620				
Gly	Ser	Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro
625					630					635					640
Gly	Lys	Thr	Ala	Arg	Ile	Thr	Cys	Gly							

Asp	His	Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu
				725					730				