SEQUENCE LISTING

<110> Macrogenics, Inc.
Johnson, Leslie S.
Huang, Ling

<120> COVALENT DIABODIES AND USES THEREOF

<130> 1301.0007I2

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<150> 60/945,523
<151> 2007-06-21

<150> 60/019,051
<151> 2008-01-04

<160> 104

<170> PatentIn version 3.4

<210> 1
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 hinge

<400> 1
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1 5 10

<210> 2
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG2 hinge

<400> 2
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro
1 5 10

<210> 3
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3 hinge

<400> 3
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1 5 10 15
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45
Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
50 55 60

<210> 4

<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG4 hinge

<400> 4
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
 1   5   10

<210> 5
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 Fc domain

<400> 5
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
Val Val Asp 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 Asp Glu Leu
        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 Lys
    210   215

<210> 6
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG2 Fc domain

<400> 6
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30

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Val Asp Val Ser His Glu Asp Pro Glu Val Gln 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
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65                  70                  75                  80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85                  90                  95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
            100                 105                 110

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
        115                 120                 125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165                 170                 175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180                 185                 190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205
Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215


<210> 7
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3 Fc domain

<400> 7
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
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        35                  40                  45
Val Asp Gly Val Gln Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln
    50                  55                  60
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asn Trp Leu Asp 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 Thr 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 Ser Gly Gln Pro Glu Asn Asn
145                 150                 155                 160
Tyr Asn Thr Thr Pro Pro Met 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 Ile
            180                 185                 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        195                 200                 205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215


<210> 8
<211> 217
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<212> PRT
<213> Homo sapiens

<220>
<223> human IgG4 Fc domain

<400> 8
Ala Pro Glu Phe 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
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln 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 Phe 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
Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu 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 Leu Gly Lys
    210   215

<210> 9
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 1

<400> 9
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1   5   10   15
Glu Lys Val Thr Phe Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35   40   45
Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65   70   75   80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100   105   110
Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
        115   120   125
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130   135   140
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145   150   155   160
Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165   170   175

Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
180 185 190
Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
195 200 205
Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
210 215 220
Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225 230 235

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

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

<210> 11
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 2

<400> 11
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
115 120 125
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160
Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175
Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190
Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp
195 200 205
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220
Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240
Leu Gly Gly Cys

<210> 12
<211> 240

<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 3

<400> 12

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

<210> 13
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 4

<400> 13

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

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Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp
                165                 170                 175
Asp Lys Arg Tyr Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys
            180                 185                 190
Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro
        195                 200                 205
Val Asp Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe
    210                 215                 220
Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly
225                 230                 235                 240
Cys
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<210> 14
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 5

<400> 14

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Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1                5                  10                  15
Glu Lys Val Thr Phe Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45
Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110
Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
        115                 120                 125
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160
Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175
Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
            180                 185                 190
Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205
Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220
Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
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        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470


<210> 15
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 6

<400> 15
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
        115                 120                 125
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    130                 135                 140
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145                 150                 155                 160
Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
                165                 170                 175
Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
            180                 185                 190
Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp
        195                 200                 205
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
    210                 215                 220
Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225                 230                 235                 240
Leu Gly Gly Cys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335
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Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 7

<400> 16
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Phe Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110
Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
115 120 125
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
130 135 140
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145 150 155 160
Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
165 170 175
Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
180 185 190
Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
195 200 205
Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
210 215 220
Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Phe Asn Arg
225 230 235 240
Gly Glu Cys

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker plus C-terminus of human IgG-kappa chain

<400> 17
Leu Gly Gly Cys Phe Asn Arg Gly Glu Cys
1 5 10

<210> 18
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 8

<400> 18
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
115 120 125
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160
Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175
Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190
Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp
195 200 205
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220
Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240
Leu Gly Gly Cys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 19
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 9

<400> 19
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
115 120 125
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145 150 155 160
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220
Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly
225 230 235 240
Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
245 250 255
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe
260 265 270
Asp Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro
275 280 285
Pro Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro
290 295 300
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
305 310 315 320
Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser
325 330 335
Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
340 345 350
Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
355 360 365
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
370 375 380

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Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala
385                 390                 395                 400
Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr
                405                 410                 415
Tyr Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val
            420                 425                 430
Val Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser
        435                 440                 445
Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr
    450                 455                 460
Tyr Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
465                 470                 475                 480
Ser Leu Gly Gly Cys
                485
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<210> 20
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 10

<400> 20

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

<210> 21
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 11

<400> 21
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Phe Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95
Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110
Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
115 120 125
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
130 135 140
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145 150 155 160
Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
165 170 175
Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
180 185 190
Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
195 200 205
Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
210 215 220
Gln Gly Thr Leu Val Thr Val Ser Ser Val Glu Pro Lys Ser Cys Asp
225 230 235 240
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

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

<210> 22
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody Construct 12

<400> 22
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
115 120 125
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160
Gly Gln Cys Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175
Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190
Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp
195 200 205
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220
Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240
Phe Asn Arg Gly Glu Cys
245

<210> 23
<211> 6

<212> PRT
<213> Homo sapiens

<220>
<223> C-terminus of human IgG Kappa chain

<400> 23
Phe Asn Arg Gly Glu Cys
 1   5

<210> 24
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Heavy chain variable region - CDR1

<400> 24
Asn Tyr Trp Ile His
 1   5

<210> 25
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Heavy Chian Variable region - CDR1

<400> 25
Asp Ala Trp Met Asp
 1   5

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Heavy chain variable region - CDR2

<400> 26
Val Ile Asp Pro Ser Asp Thr Tyr Pro Asn Tyr Asn Lys Lys Phe Lys
 1   5   10   15
Gly

<210> 27
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Heavy Chian Variable region - CDR2

<400> 27
Glu Ile Arg Asn Lys Ala Asn Asn Leu Ala Thr Tyr Tyr Ala Glu Ser
 1   5   10   15
Val Lys Gly

<210> 28

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

<220>
<223> 2B6 Heavy chain variable region - CDR3

<400> 28
Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr
 1   5   10

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Heavy Chian Variable region - CDR3

<400> 29
Tyr Ser Pro Phe Ala Tyr
 1   5

<210> 30
<400> 30
000

<210> 31
<400> 31
000

<210> 32
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Light chain variable region - CDR1

<400> 32
Arg Thr Ser Gln Ser Ile Gly Thr Asn Ile His
 1   5   10

<210> 33
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Light Chian Variable region - CDR1

<400> 33
Arg Ala Ser Gln Glu Ile Ser Gly Tyr Leu Ser
 1   5   10

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Light chain variable region - CDR2

<400> 34
Asn Val Ser Glu Ser Ile Ser
1 5

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Light chain variable region - CDR2

<400> 35
Tyr Val Ser Glu Ser Ile Ser
1 5

<210> 36
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Light chain variable region - CDR2

<400> 36
Tyr Ala Ser Glu Ser Ile Ser
1 5

<210> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Light Chian Variable region - CDR2

<400> 37
Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 Light chain variable region - CDR3

<400> 38
Gln Gln Ser Asn Thr Trp Pro Phe Thr
1 5

<210> 39
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Light Chian Variable region - CDR3

<400> 39
Leu Gln Tyr Val Ser Tyr Pro Tyr Thr
1 5

<210> 40
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 heavy chain variable region

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

<210> 41
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B6 light chain variable region - Hu2B6VL-1

<400> 41
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1   5   10   15
Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35   40   45
Lys Asn Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65   70   75   80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 42
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 2B6 light chain variable region - Hu2B6VL-2

<400> 42
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1   5   10   15
Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile

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

<210> 43
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 2B6 light chain variable region - Hu2B6VL-3

<400> 43
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 44
<211> 107
<212> PRT
<213> mus sp.

<220>
<223> mouse 3H7 Light Chain Variable Region

<400> 44
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Arg Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60
Ser Trp Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Val Ser Tyr Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 45
Lys Lys Phe Ser Arg Ser Asp Pro Asn
1 5

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 46
Gln Lys Phe Ser Arg Leu Asp Pro Asn
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 47
Gln Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 48
Lys Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 49
Gln Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 50
Lys Lys Phe Ser His Leu Asp Pro Thr

1 5

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 51
Gln Lys Phe Ser Arg Leu Asp Pro Asn
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 52
Lys Lys Phe Ser Arg Ser Asp Pro Asn
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 53
Gln Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 54
Gln Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 55
Lys Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG binding site of the Fc-gamma-RIIB receptor

<400> 56
Lys Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh321F primer

<400> 57
cgagctagct ctagatgaga tcacagttct ctctac 36

<210> 58
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh318R primer

<400> 58
gcctccgcct ccggatccgc ctcctttgat ctccaccttg gtccctc 47

<210> 59
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh319F primer

<400> 59
ggaggcggat ccggaggcgg aggccaggtt cagctggtgc agtctgg 47

<210> 60
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh320R primer

<400> 60
tttgaattct agcagcctcc cagtgaggag acggtgaccg tgg 43

<210> 61
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh315R primer

<400> 61
gcctccgcct ccggatccgc ctcctttgat ctcaagcttg gtcccc 46

<210> 62
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh316F primer

<400> 62
ggaggcggat ccggaggcgg aggccaggtt accctgagag agtctggc 48

<210> 63
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Lgh317R primer

<400> 63
tttgaattcc tagcagcctc ccagtgagct cacagtgacc agagtcc 47

<210> 64
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh339R primer

<400> 64
ctcaacgcag cctcccagtg agctcac 27

<210> 65
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh340R primer

<400> 65
aacgcagcct cccagtgagg agacggtgac c 31

<210> 66
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh366R primer

<400> 66
tttgaattct atttacccgg agacagg 27

<210> 67
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh367F primer

<400> 67
ctgggaggct gcgcagagcc caaatcttgt gac 33

<210> 68
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh368R primer

<400> 68
gtcacaagat ttgggctctg cgcagcctcc cag 33

<210> 69
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh369R primer

<400> 69
tttgaattct aacactctcc cctgttgaag cagcctccca gtgaggagac 50

<210> 70
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A heavy chain variable region(Hu3G8VH-1)

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

<210> 71
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A heavy chain variable region(Hu3G8VH-5)

<400> 71
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val

65 70 75 80
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 72
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A heavy chain variable region(Hu3G8VH-22)

<400> 72
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Ile Asn Pro Ala Tyr Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser
115

<210> 73
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A light chain variable region(Hu3G8VL-1)

<400> 73
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 74
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A light chain variable region(Hu3G8VL-43)

<400> 74
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Ser Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 75
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A light chain variable region(Hu3G8VL-22)

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

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence of linker (SEQ ID NO. 10)

<400> 76
ggaggcggat ccggaggcgg aggc 24

<210> 77
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<223> DNA sequence of C-terminus of human IgG Kappa chain

<400> 77
ttcaacaggg gagagtgt 18

<210> 78
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Linker plus C-terminus of human IgG Kappa chain

<400> 78
ctgggaggct gcttcaacag gggagagtgt 30

<210> 79
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG hinge domain

<400> 79
Val Glu Pro Lys Ser Cys
1 5

<210> 80
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<223> Human IgG hinge domain

<400> 80
gttgagccca aatcttgt 18

<210> 81
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> VH domain of 3G8 antibody

<400> 81
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Arg Thr Ser
20 25 30
Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65 70 75 80
Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 82
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<223> VH domain of 3G8 antibody

<400> 82

caggttaccc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60
acttgttctt tctctgggtt ttcactgagg acttctggta tgggtgtagg ctggattcgt 120
cagccttcag ggaagggtct agagtggctg gcacacattt ggtgggatga tgacaagcgc 180
tataatccag ccctgaagag ccgactgaca atctccaagg atacctccag caaccaggta 240
ttcctcaaaa tcgccagtgt ggacactgca gatactgcca catactactg tgctcaaata 300
aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctca 354

<210> 83
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized anti-CD16A heavy chain variable region(Hu3G8VH-5)

<400> 83
caggttaccc tgagagagtc tggccctgcg ctggtgaagc ccacacagac cctcacactg 60
acttgtacct tctctgggtt ttcactgagc acttctggta tgggtgtagg ctggattcgt 120
cagcctcccg ggaaggctct agagtggctg gcacacattt ggtgggatga tgacaagcgc 180
tataatccag ccctgaagag ccgactgaca atctccaagg atacctccaa aaaccaggta 240
gtcctcacaa tgaccaacat ggaccctgtg gatactgcca catactactg tgctcaaata 300
aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctca 354

<210> 84
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<223> VL domain of 3G8 antibody

<400> 84
Asp Thr Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 85
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<223> VL domain of 3G8 antibody

<400> 85
gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120
caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180
gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 86
<211> 333
<212> DNA

<213> Artificial Sequence

<220>
<223> humanized anti-CD16A light chain variable region(Hu3G8VL-1)

<400> 86
gacatcgtga tgacccaatc tccagactct ttggctgtgt ctctagggga gagggccacc 60
atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120
caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180
ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240
agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga ggatccgtac 300
acgttcggac aggggaccaa gcttgagatc aaa 333

<210> 87
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized 2B6 heavy chain variable region

<400> 87
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 Asn Tyr
20 25 30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Val Ile Asp Pro Ser Asp Thr Tyr Pro Asn Tyr Asn Lys Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Val Val Val Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 88
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized 2B6 heavy chain variable region

<400> 88
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta cacctttacc aactactgga tacactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gattggagtg attgatcctt ctgatactta tccaaattac 180
aataaaaagt tcaagggcag agtcaccatg accgtagtcg tatccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaaacggt 300
gattccgatt attactctgg tatggactac tgggggcaag ggaccacggt caccgtctcc 360
tca 363

<210> 89
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized 2B6 light chain variable region

<400> 89
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 90
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized 2B6 light chain variable region

<400> 90
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60
ttcacctgca ggaccagtca gagcattggc acaaacatac actggtacca gcagaaacca 120
gatcagtctc caaagctcct catcaaggag gtttctgagt ctatctctgg agtcccatcg 180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240
gaagatgctg caacgtatta ctgtcaacaa agtaatacct ggccgttcac gttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 91
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> thrombin cleavage recognition site

<400> 91
Leu Val Pro Arg Gly Ser
 1   5

<210> 92
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Factor Xa cleavage recognition site

<220>
<221> VARIANT
<222> 2
<223> Xaa = Glu or Asp

<400> 92
Ile Xaa Gly Arg
 1

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> enterokinase cleavage recognition site

<400> 93
Asp Asp Asp Asp Lys
 1   5

<210> 94
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> furin cleavage recognition site

<220>
<221> VARIANT
<222> 2, 3
<223> Xaa = Any Amino Acid

<400> 94
Arg Xaa Xaa Arg
 1

<210> 95
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> preferred furin cleavage recognition site

<220>
<221> VARIANT
<222> 2
<223> Xaa = Any Amino Acid

<220>
<221> VARIANT
<222> 3
<223> Xaa = Lys or Arg

<400> 95
Arg Xaa Xaa Arg
 1

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AcTEV cleavage recognition site

<400> 96
Glu Asn Leu Tyr Phe Gln Gly
 1   5

<210> 97
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> covalent diabody polyprotein precursor

<400> 97

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Asp Thr Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60
Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
        115                 120                 125
Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
    130                 135                 140
Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145                 150                 155                 160
Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
                165                 170                 175
Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
            180                 185                 190
Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
        195                 200                 205
Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
    210                 215                 220
Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225                 230                 235                 240
Leu Gly Gly Cys Gly Gly Arg Ala Lys Arg Asp Val Gln Met Thr Gln
                245                 250                 255
Ser Pro Ser Asn Leu Ala Ala Ser Pro Gly Glu Ser Val Ser Ile Asn
            260                 265                 270
Cys Lys Ala Ser Glu Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Leu Gln
        275                 280                 285
Lys Pro Gly Lys Ala Asn Lys Leu Leu Met Tyr Asp Gly Ser Thr Leu
    290                 295                 300
Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
305                 310                 315                 320
Phe Thr Leu Thr Ile Arg Ser Leu Glu Pro Glu Asp Phe Gly Leu Tyr
                325                 330                 335
Tyr Cys Gln Gln His Tyr Glu Tyr Pro Ala Thr Phe Gly Ser Gly Thr
            340                 345                 350
Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Thr
        355                 360                 365
Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser
    370                 375                 380
Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Arg Thr Ser Gly Met Gly
385                 390                 395                 400
Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala
                405                 410                 415
His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala Leu Lys Ser
            420                 425                 430
Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val Phe Leu Lys
        435                 440                 445
Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Gln
    450                 455                 460
Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
465                 470                 475                 480
Val Ser Ser Leu Gly Gly Cys
                485
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<210> 98
<211> 1464

<212> DNA
<213> Artificial Sequence

<220>
<223> covalent diabody polyprotein precursor (DNA sequence of SEQ ID NO. 97)

<400> 98
gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180
gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300
acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag 360
gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg 420
tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca 480
acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga 540
gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg 600
caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg 660
ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca 720
ctgggaggct gcggcgggag agctaagagg gatgtccaga tgacccagtc tccatctaat 780
cttgctgcct ctcctggaga aagtgtttcc atcaattgca aggcaagtga gagcattagc 840
aagtatttag cctggtatct acagaaacct gggaaagcaa ataagcttct tatgtacgat 900
gggtcaactt tgcaatctgg aattccatcg aggttcagtg gcagtggatc tggtacagat 960
ttcactctca ccatcagaag cctggagcct gaagattttg gactctatta ctgtcaacag 1020
cattatgaat atccagccac gttcggttct gggaccaagc tggagatcaa aggaggcgga 1080
tccggaggcg gaggccaggt taccctgaaa gagtctggcc ctgggatatt gcagccctcc 1140
cagaccctca gtctgacttg ttctttctct gggttttcac tgaggacttc tggtatgggt 1200
gtaggctgga ttcgtcagcc ttcagggaag ggtctagagt ggctggcaca catttggtgg 1260
gatgatgaca agcgctataa tccagccctg aagagccgac tgacaatctc caaggatacc 1320
tccagcaacc aggtattcct caaaatcgcc agtgtggaca ctgcagatac tgccacatac 1380
tactgtgctc aaataaaccc cgcctggttt gcttactggg gccaagggac tctggtcact 1440
gtgagctcac tgggaggctg ctag 1464

<210> 99
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> covalent diabody polyprotein precursor

<400> 99
Asp Thr Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20   25   30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
                85   90   95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100   105   110
Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
        115   120   125
Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
    130   135   140
Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145   150   155   160
Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
                165   170   175
Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
            180   185   190

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Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
        195                 200                 205
Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
    210                 215                 220
Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225                 230                 235                 240
Leu Gly Gly Cys Gly Gly Arg Ala Lys Arg Ala Pro Val Lys Gln Thr
                245                 250                 255
Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
            260                 265                 270
Gly Pro Asp Val Gln Met Thr Gln Ser Pro Ser Asn Leu Ala Ala Ser
        275                 280                 285
Pro Gly Glu Ser Val Ser Ile Asn Cys Lys Ala Ser Glu Ser Ile Ser
    290                 295                 300
Lys Tyr Leu Ala Trp Tyr Leu Gln Lys Pro Gly Lys Ala Asn Lys Leu
305                 310                 315                 320
Leu Met Tyr Asp Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe
                325                 330                 335
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu
            340                 345                 350
Glu Pro Glu Asp Phe Gly Leu Tyr Tyr Cys Gln Gln His Tyr Glu Tyr
        355                 360                 365
Pro Ala Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
    370                 375                 380
Ser Gly Gly Gly Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile
385                 390                 395                 400
Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe
                405                 410                 415
Ser Leu Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser
            420                 425                 430
Gly Lys Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys
        435                 440                 445
Arg Tyr Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
    450                 455                 460
Ser Ser Asn Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp
465                 470                 475                 480
Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr
                485                 490                 495
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
            500                 505                 510
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<210> 100
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> covalent diabody polyprotein precursor (DNA sequence of SEQ ID NO. 99)

<400> 100

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atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120
caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180
gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300
acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag 360
gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg 420
tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca 480
acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga 540
gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg 600
caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg 660
ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca 720
ctgggaggct gcggcgggag agctaagagg gcccctgtga agcagaccct gaacttcgac 780
ctgctgaagc tggccggaga cgtggagagc aaccccggcc ccgatgtcca gatgacccag 840
tctccatcta atcttgctgc ctctcctgga gaaagtgttt ccatcaattg caaggcaagt 900
gagagcatta gcaagtattt agcctggtat ctacagaaac ctgggaaagc aaataagctt 960
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cttatgtacg atgggtcaac tttgcaatct ggaattccat cgaggttcag tggcagtgga 1020
tctggtacag atttcactct caccatcaga agcctggagc ctgaagattt tggactctat 1080
tactgtcaac agcattatga atatccagcc acgttcggtt ctgggaccaa gctggagatc 1140
aaaggaggcg gatccggagg cggaggccag gttaccctga aagagtctgg ccctgggata 1200
ttgcagccct cccagaccct cagtctgact tgttctttct ctgggttttc actgaggact 1260
tctggtatgg gtgtaggctg gattcgtcag ccttcaggga agggtctaga gtggctggca 1320
cacatttggt gggatgatga caagcgctat aatccagccc tgaagagccg actgacaatc 1380
tccaaggata cctccagcaa ccaggtattc ctcaaaatcg ccagtgtgga cactgcagat 1440
actgccacat actactgtgc tcaaataaac cccgcctggt ttgcttactg gggccaaggg 1500
actctggtca ctgtgagctc actgggaggc tgctag 1536

<210> 101
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody construct

<400> 101
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Phe Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110
Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
115 120 125
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
130 135 140
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145 150 155 160
Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
165 170 175
Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
180 185 190
Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
195 200 205
Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
210 215 220
Gln Gly Thr Leu Val Thr Val Ser Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 102
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> Diabody construct (DNA sequence of SEQ ID NO. 101)

<400> 102
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60
ttcacctgca ggaccagtca gagcattggc acaaacatac actggtacca gcagaaacca 120
gatcagtctc caaagctcct catcaaggag gtttctgagt ctatctctgg agtcccatcg 180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240
gaagatgctg caacgtatta ctgtcaacaa agtaatacct ggccgttcac gttcggcgga 300
gggaccaagg tggagatcaa aggaggcgga tccggaggcg gaggccaggt taccctgaga 360
gagtctggcc ctgcgctggt gaagcccaca cagaccctca cactgacttg taccttctct 420

gggttttcac tgagcacttc tggtatgggt gtaggctgga ttcgtcagcc tcccgggaag 480
gctctagagt ggctggcaca catttggtgg gatgatgaca agcgctataa tccagccctg 540
aagagccgac tgacaatctc caaggatacc tccaaaaacc aggtagtcct cacaatgacc 600
aacatggacc ctgtggatac tgccacatac tactgtgctc aaataaaccc cgcctggttt 660
gcttactggg gccaagggac tctggtcact gtgagctcat tcaacagggg agagtgttag 720

<210> 103
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Diabody construct

<400> 103
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30
Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
115 120 125
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160
Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175
Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190
Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp
195 200 205
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220
Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240
Val Glu Pro Lys Ser Cys
245

<210> 104
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> Diabody construct (DNA sequence of SEQ ID NO. 103)

<400> 104
gacatcgtga tgacccaatc tccagactct ttggctgtgt ctctagggga gagggccacc 60
atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120
caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180
ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240
agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga ggatccgtac 300
acgttcggac aggggaccaa gcttgagatc aaaggaggcg gatccggagg cggaggccag 360
gttcagctgg tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc 420
tgcaaggctt ctggttacac ctttaccaac tactggatac actgggtgcg acaggcccct 480

ggacaagggc ttgagtggat tggagtgatt gatccttctg atacttatcc aaattacaat 540
aaaaagttca agggcagagt caccatgacc gtagtcgtat ccacgagcac agcctacatg 600
gagctgagga gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaacggtgat 660
tccgattatt actctggtat ggactactgg gggcaaggga ccacggtcac cgtctcctca 720
gttgagccca aatcttgtta g 741

<210> 105
<211> 717
<212> DNA
<213> artificial

<220>
<223> H3G8VL-CB3.1VH

<400> 105
gacatcgtga tgacccaatc tccagactct ttggctgtgt ctctagggga gagggccacc 60

atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240

agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggac aggggaccaa gcttgagatc aaaggaggcg gatccggagg cggaggccag 360

gtccaactgc agcagcctgg ggctgagctg gtgaggcctg gggcttcagt gaagctgtcc 420

tgcaaggctt ctggctacac cttcaccagc tactggatga actgggtgaa gcagaggcct 480

ggacaaggcc ttgaatggat tggtatggtt gatccttcag acagtgaaac tcactacaat 540

caaatgttca aggacaaggc cacattgact gttgacaaat cctccagcac agcctacatg 600

cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag agctatgggc 660

tactggggtc aaggaacctc agtcaccgtc tcctcagttg agcccaaatc ttgttag 717

<210> 106
<211> 238
<212> PRT
<213> artificial

<220>
<223> H3G8VL-CB3.1VH

<400> 106

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

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

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser

65 70 75 80

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

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

Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala
115 120 125

Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser
130 135 140

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
145 150 155 160

Gly Gln Gly Leu Glu Trp Ile Gly Met Val Asp Pro Ser Asp Ser Glu
165 170 175

Thr His Tyr Asn Gln Met Phe Lys Asp Lys Ala Thr Leu Thr Val Asp
180 185 190

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
195 200 205

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln
210 215 220

Gly Thr Ser Val Thr Val Ser Ser Val Glu Pro Lys Ser Cys
225 230 235

<210> 107
<211> 735
<212> DNA
<213> artificial

<220>
<223> CB3.1VL-h3G8VH

<400> 107
gatgttgtga tgacccagac tccactcact ttgtcggtta acattggaca accagcctcc 60

atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

caggttaccc tgagagagtc tggccctgcg ctggtgaagc ccacacagac cctcacactg 420

acttgtacct tctctgggtt ttcactgagc acttctggta tgggtgtagg ctggattcgt 480

cagcctcccg ggaaggctct agagtggctg gcacacattt ggtgggatga tgacaagcgc 540

tataatccag ccctgaagag ccgactgaca atctccaagg atacctccaa aaaccaggta 600

gtcctcacaa tgaccaacat ggaccctgtg gatactgcca catactactg tgctcaaata 660

aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctcattcaac 720

aggggagagt gttag 735

<210> 108
<211> 244
<212> PRT
<213> artificial

<220>
<223> CB3.1VL-h3G8VH

<400> 108

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly
115 120 125

Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe
130 135 140

Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp
165 170 175

Asp Asp Lys Arg Tyr Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser
180 185 190

Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met Asp
195 200 205

Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp
210 215 220

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Phe Asn
225 230 235 240

Arg Gly Glu Cys

<210> 109
<211> 704
<212> DNA
<213> artificial

<220>
<223> 8B5-CB3.1-VEPKSC

<400> 109
gacattcaga tgacacagtc tccatcctcc ctacttgcgg cgctgggaga aagagtcagt 60

ctcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggcttca gcagaaacca 120

gatggaacta ttaaacgcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 180

aggttcagtg gcagtgagtc tgggtcagat tattctctca ccatcagcag tcttgagtct 240

gaagattttg cagactatta ctgtctacaa tattttagtt atccgctcac gttcggtgct 300

gggaccaagc tggagctgaa aggaggcgga tccggaggcg gaggccaggt ccaactgcag 360

cagcctgggg ctgagctggt gaggcctggg gcttcagtga agctgtcctg caaggcttct 420

ggctacacct tcaccagcta ctggatgaac tgggtgaagc agaggcctgg acaaggcctt 480

gaatggattg gtatggttga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gaaaggccac attgactgtt gacaaatcct ccagcacagc ctacatgcag ctcagcagcc 600

tgacatctga ggactctgcg gtctattact gtgcaagagc tatgggctac tggggtcaag 660

gaacctcagt caccgtctcc tcagttgagc ccaaatcttg ttag 704

<210> 110
<211> 234
<212> PRT
<213> artificial

<220>
<223> 8B5-CB3.1-VEPKSC

<400> 110

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

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

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

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

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

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

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

Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg
        115                 120                 125

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

Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145                 150                 155                 160

Glu Trp Ile Gly Met Val Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
                165                 170                 175

Gln Met Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
            180                 185                 190

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
        195                 200                 205

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Ser Val
    210                 215                 220

Thr Val Ser Ser Val Glu Pro Lys Ser Cys
225                 230
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<210> 111
<211> 729
<212> DNA
<213> artificial

<220>
<223> CB3.1-8B5-FNRGEC

<400> 111

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gatgttgtga tgacccagac tccactcact ttgtcggtta acattggaca accagcctcc     60

atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg    120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac    180
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tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgtt caacagggga 720

gagtgttag 729

<210> 112
<211> 242
<212> PRT
<213> artificial

<220>
<223> CB3.1-8B5-FNRGEC

<400> 112

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Lys Leu Glu Glu Ser Gly
115 120 125

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

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ser

145 150 155 160

Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

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

Glu Cys

<210> 113
<211> 699
<212> DNA
<213> artificial

<220>
<223> 8B5VL-CB3.1VH-LGGC

<400> 113
gacattcaga tgacacagtc tccatcctcc ctacttgcgg cgctgggaga aagagtcagt 60

ctcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggcttca gcagaaacca 120

gatggaacta ttaaacgcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 180

aggttcagtg gcagtgagtc tgggtcagat tattctctca ccatcagcag tcttgagtct 240

gaagattttg cagactatta ctgtctacaa tattttagtt atccgctcac gttcggtgct 300

gggaccaagc tggagctgaa aggaggcgga tccggaggcg gaggccaggt ccaactgcag 360

cagcctgggg ctgagctggt gaggcctggg gcttcagtga agctgtcctg caaggcttct 420

ggctacacct tcaccagcta ctggatgaac tgggtgaagc agaggcctgg acaaggcctt 480

gaatggattg gtatggttga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacaaggcca cattgactgt tgacaaatcc tccagcacag cctacatgca gctcagcagc 600

ctgacatctg aggactctgc ggtctattac tgtgcaagag ctatgggcta ctggggtcaa 660

ggaacctcag tcaccgtctc ctcactggga ggctgctag 699

<210> 114
<211> 232
<212> PRT
<213> artificial

<220>
<223> 8B5VL-CB3.1VH-LGGC

<400> 114

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

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
            20                  25                  30

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

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

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

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

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

Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg
        115                 120                 125

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

Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145                 150                 155                 160

Glu Trp Ile Gly Met Val Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
                165                 170                 175

Gln Met Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
            180                 185                 190

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
        195                 200                 205

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Ser Val
    210                 215                 220

Thr Val Ser Ser Leu Gly Gly Cys
225                 230
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<210> 115
<211> 723
<212> DNA
<213> artificial

<220>
<223> CB3.1-8B5-LGGC

<400> 115
gatgttgtga tgacccagac tccactcact ttgtcggtta acattggaca accagcctcc 60

atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgct gggaggctgc 720

tag 723

<210> 116
<211> 240
<212> PRT
<213> artificial

<220>
<223> CB3.1-8B5-LGGC

<400> 116

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Lys Leu Glu Glu Ser Gly
115 120 125

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

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ser
145 150 155 160

Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Leu Gly Gly Cys
225 230 235 240

<210> 117
<211> 47
<212> DNA
<213> artificial

<220>
<223> Primer Lgh628F

<400> 117
ggaggcggat ccggaggcgg aggccaggtc caactgcagc agcctgg 47

<210> 118
<211> 49
<212> DNA
<213> artificial

<220>
<223> Primer Lgh629R

<400> 118
tttgaattct aacaagattt gggctcaact gaggagacgg tgactgagg 49

<210> 119
<211> 45
<212> DNA
<213> artificial

<220>
<223> Primer Lgh630R

<400> 119
gcctccgcct ccggatccgc ctcctttcag ctccagcttg gtccc 45

<210> 120
<211> 47
<212> DNA
<213> artificial

<220>
<223> Primer Lgh631F

<400> 120
ggaggcggat ccggaggcgg aggcgaagtg aagcttgagg agtctgg 47

<210> 121
<211> 49
<212> DNA
<213> artificial

<220>
<223> Primer Lgh640R

<400> 121
tttgaattct aacactctcc cctgttgaac gaggagactg tgagagtgg 49

<210> 122
<211> 48
<212> DNA
<213> artificial

<220>
<223> Primer Lgh644R

<400> 122
tttgtcgtca tcatcgtctt tgtagtcgga gtggacacct gtggagag 48

<210> 123
<211> 42
<212> DNA
<213> artificial

<220>
<223> Primer Lgh646R

<400> 123
tttgaattct agcagcctcc cagtgaggag acggtgactg ag 42

<210> 124
<211> 45
<212> DNA
<213> artificial

<220>
<223> Primer Lgh647F

<400> 124
caaagacgat gatgacgaca aagacattca gatgacacag tctcc 45

<210> 125
<211> 43
<212> DNA
<213> artificial

<220>
<223> Primer Lgh648R

<400> 125
tttgaattct agcagcctcc cagcgaggag actgtgagag tgg 43

<210> 126
<211> 1047
<212> DNA
<213> artificial

<220>
<223> 2.4G2-3G8-hKappa

<400> 126
gatgtccaga tgacccagtc tccatctaat cttgctgcct ctcctggaga aagtgtttcc 60

atcaattgca aggcaagtga gagcattagc aagtatttag cctggtatct acagaaacct 120

gggaaagcaa ataagcttct tatgtacgat gggtcaactt tgcaatctgg aattccatcg 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagaag cctggagcct 240

gaagattttg gactctatta ctgtcaacag cattatgaat atccagccac gttcggttct 300

gggaccaagc tggagatcaa aggaggcgga tccggaggcg gaggccaggt taccctgaaa 360

gagtctggcc ctgggatatt gcagccctcc cagaccctca gtctgacttg ttctttctct 420

gggttttcac tgaggacttc tggtatgggt gtaggctgga ttcgtcagcc ttcagggaag 480

ggtctagagt ggctggcaca catttggtgg gatgatgaca agcgctataa tccagccctg 540

aagagccgac tgacaatctc caaggatacc tccagcaacc aggtattcct caaaatcgcc 600

agtgtggaca ctgcagatac tgccacatac tactgtgctc aaataaaccc cgcctggttt 660

gcttactggg gccaagggac tctggtcact gtgagctcac tgggaggctg cggcggaggg 720

agccgtacgg tggctgcacc atcggtcttc atcttcccgc catctgatga gcagttgaaa 780

tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta 840

cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 900

gacagcaagg acagcaccta cagcctcagc agcaccctga cgctgagcaa agcagactac 960

gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca 1020

aagagcttca acaggggaga gtgttag 1047

<210> 127
<211> 348
<212> PRT
<213> artificial

<220>
<223> 2.4G2-3G8-hKappa

<400> 127

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

Glu Ser Val Ser Ile Asn Cys Lys Ala Ser Glu Ser Ile Ser Lys Tyr
20 25 30

```
Leu Ala Trp Tyr Leu Gln Lys Pro Gly Lys Ala Asn Lys Leu Leu Met
        35                  40                  45

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

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

Glu Asp Phe Gly Leu Tyr Tyr Cys Gln Gln His Tyr Glu Tyr Pro Ala
                85                  90                  95

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

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    130                 135                 140

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
145                 150                 155                 160

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
            180                 185                 190

Asn Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Gly Gly Gly
225                 230                 235                 240

Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                245                 250                 255

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
        275                 280                 285

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
    290                 295                 300
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Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
305 310 315 320

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
325 330 335

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
340 345

<210> 128
<211> 1737
<212> DNA
<213> artificial

<220>
<223> 3G8-2.4G2-hG1

<400> 128
gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag 360

gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg 420

tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca 480

acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga 540

gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg 600

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg 660

ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca 720

ctgggaggct gcggcggagg gagcgcctcc accaagggcc catcggtctt ccccctggca 780

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 840

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 900

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 960

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 1020

aaggtggaca agagagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 1080

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1140

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1200

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1260

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1320

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1380

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1440

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1500

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1560

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1620

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1680

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga 1737

<210> 129
<211> 578
<212> PRT
<213> artificial

<220>
<223> 3G8-2.4G2-hG1

<400> 129

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

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

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
115 120 125

Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
130 135 140

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145 150 155 160

Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
165 170 175

Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

180 185 190

Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
195 200 205

Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
210 215 220

Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225 230 235 240

Leu Gly Gly Cys Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
260 265 270

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
290 295 300

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
305 310 315 320

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
325 330 335

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
340 345 350

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
355 360 365

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
370 375 380

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
385 390 395 400

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
405 410 415

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
420 425 430

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
435 440 445

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

450 455 460

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
465 470 475 480

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
485 490 495

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
500 505 510

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
515 520 525

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
530 535 540

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
545 550 555 560

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
565 570 575

Gly Lys

<210> 130
<211> 723
<212> DNA
<213> artificial

<220>
<223> CD79VL-CD32BVH

<400> 130
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atctcctgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

tttcagcaga ggccaggcca atctccaaac cgcctaattt atctggtgtc taaactggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgct ggcaaggtac acattttccg 300

ctcacgttcg gcggagggac caagcttgag atcaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgct gggaggctgc 720

<210> 131
<211> 240
<212> PRT
<213> artificial

<220>
<223> CD79-CD32BVH

<400> 131

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly
        115                 120                 125

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
    130                 135                 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ala
145                 150                 155                 160

Pro Gly Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
                165                 170                 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
            180                 185                 190

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
        195                 200                 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
    210                 215                 220
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Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225 230 235 240

<210> 132
<211> 699
<212> DNA
<213> artificial

<220>
<223> CD32BVL-CD79VH-1

<400> 132
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc 60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgctga 699

<210> 133
<211> 232
<212> PRT
<213> artificial

<220>
<223> CD32BVL-CD79VH-1

<400> 133

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

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

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

Gln Met Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
210 215 220

Thr Val Ser Ser Leu Gly Gly Cys
225 230

<210> 134
<211> 703
<212> DNA
<213> artificial

<220>
<223> CD32BVL-CD79VH-2

<400> 134
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc 60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aaagttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgctgaa ttc 703

<210> 135
<211> 232
<212> PRT
<213> artificial

<220>
<223> CD32BVL-CD79VH-2

<400> 135

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

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

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
195 200 205

```
Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
    210                 215                 220

Thr Val Ser Ser Leu Gly Gly Cys
225                 230
```