

<110> LG CHEM, LTD.  
 <120> GUCY2C BINDING POLYPEPTIDE AND USES THEREOF  
 <130> OPP20221098KR  
 <150> KR 10-2021-0045510  
 <151> 2021-04-07  
 <160> 115  
 <170> koPatentIn 3.0  
 <210> 1  
 <211> 246  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic\_GUCY2C-binding scFv  
  
 <400> 1  
 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 Ser Tyr  
 20 25 30  
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Glu Phe  
 50 55 60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Gly Gln Trp Leu Gln Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 115 120 125  
 Gly Gly Gly Ala Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu  
 130 135 140

Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 145 150 155 160  
 Ser Leu Leu Lys Lys Ser Asp Gly Asn Thr Tyr Leu Ser Trp Tyr His  
 165 170 175  
 Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn  
 180 185 190  
 Arg Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Asp Thr  
 195 200 205  
 Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly Ile  
 210 215 220  
 Tyr Tyr Cys Met Gln Gly Ser His Trp Pro Pro Thr Phe Gly Gln Gly  
 225 230 235 240  
 Thr Lys Val Glu Ile Lys  
 245

<210> 2  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 2  
 Glu Val Gln Leu Val Gln Pro Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Leu Ser Ser Tyr  
 20 25 30  
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
 85 90 95

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

<210> 3  
 <211> 245  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 3  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
 20 25 30  
 Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Glu Leu Glu Trp Met  
 35 40 45

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

<210> 4  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic\_GUCY2C-binding scFv  
  
 <400> 4

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

<210> 5

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

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

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

Cys Ser Ser Tyr Ala Gly Ser Asn Asn Phe Val Phe Gly Thr Gly Thr  
 225 230 235 240

Lys Val Thr Val Leu  
 245

<210> 6  
 <211> 245  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 6  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe  
 50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 115 120 125

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

Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr  
 145 150 155 160

Ser Ser Asp Val Gly Ala Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His  
 165 170 175

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

Ser Gly Val Pro Asp Arg Phe Ser Ala Ser Lys Ser Gly Asn Thr Ala  
195 200 205

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

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

Lys Leu Thr Val Leu  
245

<210> 7  
<211> 244  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_GUCY2C-binding scFv

<400> 7  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

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

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

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

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

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

Arg Asp Val Trp Gly Ser Gly Gln Ser Phe Asp Ser Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
115 120 125

Ser Gly Gly Gly Ala Ser Asn Phe Met Leu Thr Gln Pro His Ser Val  
 130 135 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Thr Arg Ser Ser  
 145 150 155 160

Gly Ser Ile Ala Ser Asn Tyr Val Gln Trp Tyr Gln Gln Arg Leu Gly  
 165 170 175

Ser Ser Pro Thr Thr Val Ile Tyr Glu His Ser Arg Arg Pro Ser Gly  
 180 185 190

Val Pro Asp Arg Phe Ser Ala Ser Ile Asp Ser Ser Ser Asn Ser Ala  
 195 200 205

Ser Leu Thr Ile Ser Gly Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr  
 210 215 220

Cys Gln Ser Tyr Asp Val Ser Asn Arg Val Phe Gly Gly Gly Thr Lys  
 225 230 235 240

Leu Thr Val Leu

<210> 8  
 <211> 246  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 8  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

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

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val  
 50 55 60

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



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

<210> 10  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic\_GUCY2C-binding scFv

<400> 10

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

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

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

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

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

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

Ala Arg Asp Gln Arg Pro Ala Ser Met Asp Val Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser  
145 150 155 160

Asp Val Gly Gly Tyr Ile Tyr Val Ser Trp Tyr Gln Gln His Pro Gly  
165 170 175

Lys Val Pro Lys Leu Met Ile His Asp Val Ser His Arg Pro Ser Gly  
180 185 190

Val Ser Asn Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Ser Leu  
195 200 205

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Phe Cys Ser  
210 215 220

Ser Tyr Thr Ser Ser Asn Asn Tyr Val Phe Gly Thr Gly Thr Lys Val  
225 230 235 240

Thr Val Leu

<210> 11  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

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

195                      200                      205  
 Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser  
 210                      215                      220  
 Thr Val Thr Ser Leu Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Leu  
 225                      230                      235                      240  
 Thr Val Leu

<210>      12  
 <211>      247  
 <212>      PRT  
 <213>      Artificial Sequence

<220>  
 <223>      Synthetic\_GUCY2C-binding scFv

<400>      12  
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ser  
 1                      5                      10                      15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20                      25                      30  
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35                      40                      45  
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
 50                      55                      60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
 65                      70                      75                      80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85                      90                      95  
 Ala Ala Gly Thr Tyr Ser Ser Gly Trp Thr Ile Asp Tyr Trp Gly Gln  
 100                      105                      110  
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 115                      120                      125  
 Gly Ser Gly Gly Gly Ala Ser Asp Ile Val Met Thr Gln Ser Pro Leu  
 130                      135                      140  
 Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser



|         |                                                         |     |     |     |         |
|---------|---------------------------------------------------------|-----|-----|-----|---------|
|         | 100                                                     |     | 105 |     | 110     |
| Val Thr | Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly |     |     |     |         |
|         | 115                                                     |     | 120 |     | 125     |
| Gly Gly | Ala Ser Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser |     |     |     |         |
|         | 130                                                     |     | 135 |     | 140     |
| Val Ser | Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser |     |     |     |         |
|         | 145                                                     |     | 150 |     | 155 160 |
| Val Ser | Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro |     |     |     |         |
|         |                                                         | 165 |     | 170 | 175     |
| Arg Leu | Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala |     |     |     |         |
|         |                                                         | 180 |     | 185 | 190     |
| Arg Phe | Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser |     |     |     |         |
|         |                                                         | 195 |     | 200 | 205     |
| Ser Leu | Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn |     |     |     |         |
|         |                                                         | 210 |     | 215 | 220     |
| Asn Trp | Pro Ser Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys         |     |     |     |         |
|         |                                                         | 225 |     | 230 | 235     |

<210> 14  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic\_GUCY2C-binding scFv

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| <400>                                                           | 14       |
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser |          |
| 1                                                               | 5 10 15  |
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr |          |
|                                                                 | 20 25 30 |
| Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met |          |
|                                                                 | 35 40 45 |
| Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe |          |
|                                                                 | 50 55 60 |
| Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr |          |

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

<210> 15  
 <211> 247  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> | 15  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln   | Val | Gln | Leu | Val | Glu | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ser |
| 1     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser   | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly | Thr | Phe | Ser | Ser | Tyr |
|       |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala   | Ile | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |

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

<210> 16  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic\_GUCY2C-binding scFv

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

<210> 17  
 <211> 247  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 17  
 Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Val Arg Gly Tyr Ser Ser Ile Tyr Tyr Tyr Gly Met Asp Val Trp  
 100 105 110  
 Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
 115 120 125  
 Gly Gly Gly Ser Gly Gly Gly Ala Ser Gln Ser Gly Leu Thr Gln Pro  
 130 135 140  
 Arg Ser Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr  
 145 150 155 160  
 Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln  
 165 170 175  
 Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Lys  
 180 185 190  
 Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn  
 195 200 205

Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp  
 210 215 220

Tyr Tyr Cys Gly Ser Tyr Thr Ser Asp Gly Thr Leu Val Phe Gly Gly  
 225 230 235 240

Gly Thr Lys Leu Thr Val Leu  
 245

<210> 18  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 18  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe  
 50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ile Ser  
 145 150 155 160

Asp Val Gly Asp Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly  
 165 170 175  
 Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Asn Asn Arg Pro Ser Gly  
 180 185 190  
 Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu  
 195 200 205  
 Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser  
 210 215 220  
 Ser Tyr Thr Ser Ser Ser Thr Leu Val Phe Gly Gly Gly Thr Lys Leu  
 225 230 235 240  
 Thr Val Leu

<210> 19  
 <211> 250  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv

<400> 19  
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Gly Ser Leu Gln Ser  
 65 70 75 80  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Lys Thr Trp Pro Arg  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Asn Val Glu Ile Lys Ala Ser Gly Gly Gly  
 100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 115 120 125  
 Ser Glu Leu Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys  
 130 135 140  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Phe Gly Gly Ser Phe  
 145 150 155 160  
 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 165 170 175  
 Glu Trp Ile Gly Glu Ile Asn His Arg Gly Asn Thr Asn Asp Asn Pro  
 180 185 190  
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln  
 195 200 205  
 Phe Ala Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 210 215 220  
 Tyr Cys Ala Arg Glu Arg Gly Tyr Thr Tyr Gly Asn Phe Asp His Trp  
 225 230 235 240  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 245 250

<210> 20  
 <211> 738  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 20  
 caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60  
 tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120  
 cctggacaag ggcttgagt gatgggaata atcaacccta gtggtggttag cacaagctac 180  
 gcacaggagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240  
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatggg 300  
 cagtggttc aatttgacta ctggggccaa ggaaccctgg tcaccgtctc gagggtgga 360

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ggcggttcag gcgaggtgg ctctggcggg ggcgctagcg atattgtgat gacacagtct   | 420 |
| ccactctccc tgcccgtcac cttgggcag ccggcctcca tctcctgcag gtctagtcaa   | 480 |
| agcctcctaa aaaagagtga tgggaacacc tacttgagtt ggtatcacca gaggccaggc  | 540 |
| caatctccac gggcctaatt ttataaggtt tctaatacggg actctggggg cccagacaga | 600 |
| ttcagcggca gtgggtcaga cactgatttc actctgaaaa tcagcagagt ggagactgag  | 660 |
| gatgttgga tttattactg catgcaaggt tcacactggc ctccgacgtt cggccaaggg   | 720 |
| accaaggtgg aaatcaaa                                                | 738 |

<210> 21  
 <211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 21                                                           |     |
| gaggtgcagc tgggtgcagcc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccctcagc agctatgcta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagt gatgggaagg atcatcccta tccttggtat aacaaactac   | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt atttctgtgc gagagatcag  | 300 |
| cggccggcga gcatggacgt ctggggccag ggcaccctgg tcaccgtctc gagtgggtgga | 360 |
| ggcggttcag gcgaggtgg ctctggcggg ggcgctagcc agtctgagct gactcagcct   | 420 |
| gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt  | 480 |
| gacgttggtg gttatatcta tgtctcctgg taccaacagc acccaggcaa agtccccaaa  | 540 |
| ctcatgattc atgatgtcag tcacggccc tcaggggttt ctaatcgctt ctctggctcc   | 600 |
| aggctctggca acacggcctc cctgaccatc tctgggctcc aggctgagga cgaggctgac | 660 |
| tatttctgca gtcatatgc aggcagcaac aattatgtct tcggaactgg gaccaaggtc   | 720 |
| accgtccta                                                          | 729 |

<210> 22  
 <211> 735  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 22  
 cagggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60  
 tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc 120  
 cctggacaag agcttgagt gatgggaagg atcatcccta tccttggtat agcaaactac 180  
 gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240  
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagattat 300  
 agcagcagct ggaactctat ggacgtctgg ggccagggaa ccctggtcac cgtctcgagt 360  
 ggtggaggcg gttcaggcgg aggtggctct ggcgggtggcg ctagccagtc tgggctgact 420  
 cagcctccct ccgcgtccgg gtctcctgga cagtcagtca ccatctcctg cactggaacc 480  
 agcagtgaca ttggttatta tcactatgtc tcctggtacc aacaacaccc gggcaaagcc 540  
 cccaaactca tgatttatga ggacagtaag aggccctcag ggatttctaa tcgtttctct 600  
 ggctccaagt ctggcaccac ggcctccctg accgtctctg ggctccaggc tgaggacgag 660  
 gctcattatt actgcagttc ttttacaagt agaagtactt gggtgttcgg cggagggacc 720  
 cagctcaccg tccta 735

<210> 23  
 <211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 23  
 gaggtgcagc tgggtgcagc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| tcctgcaagg cttctggagg caccctcagc agctatgcta tcagctgggt gcgacaggcc | 120 |
| cctggacaag ggcttgagt gatgggaagg atcatcccta tccttggtat aacaaactac  | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt atttctgtgc gagagatcag | 300 |
| cggccggcga gcatggacgt ctggggccag ggcaccctgg tcaccgtctc gagggtgga  | 360 |
| ggcggttcag gcggaggtgg ctctggcggg ggcgctagcc agtctgagct gactcagcct | 420 |
| gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt | 480 |
| gacgttggtg gttatatcta tgtctcctgg taccaacagc acccaggcaa agtccccaaa | 540 |
| ctcatgattc atgatgtcag tcatcgcccc tcaggggttt ctaatcgctt ctctggctcc | 600 |
| aggtctggca acacggcctc cctgaccatc tctgggctcc aggctgagga cgaggctgac | 660 |
| tatttctgca gtcataatac aagcagcaac aattattact tcggaactgg gaccaaggtc | 720 |
| accgtccta                                                         | 729 |

<210> 24  
 <211> 735  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 24                                                           |     |
| caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcagc agctatacta tcacctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagt gatgggaagg atcatccctg tccttggtat agcaaactac   | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagattat  | 300 |
| agcagcagct ggaactctat ggacgtctgg ggccaggga ccctgggtcac cgtctcgagt  | 360 |
| ggtggaggcg gttcaggcgg aggtggctct ggcggtggcg ctagccagtc tgggctgact  | 420 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| cagcctcgct cagtgtccgg gtctcctgga cagtcagtca ccattctctg cactggaacc | 480 |
| agcagtgatg ttggtgggta taactatgtc tcctgggtacc aacagcacc aggcaaagcc | 540 |
| cccaaactca tgatttatga tgtcagtaag cggccctcag gggtccctga tcgcttctcc | 600 |
| ggctccaagt ctgggaacac ggctccctg accgtctctg ggctccacgc tgaggatgag  | 660 |
| gctgattatt actgcagctc atatgcaggc agcaacaatt ttgtcttcgg aactgggacc | 720 |
| aaggtcaccg tccta                                                  | 735 |

<210> 25  
 <211> 735  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 25                                                           |     |
| caggtgcagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcggc agctatacta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac  | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagattat  | 300 |
| agcagcagct ggaactctat ggacgtctgg ggccaaggaa ccctgggtcac cgtctcgagt | 360 |
| gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg ctagccagtc tgggctgact | 420 |
| cagcctcgct cagtgtccgg gtctcctgga cagtcagtca ccattctctg cactggaacc  | 480 |
| agcagtgatg ttggtgctta taactatgtc tcctgggtacc aacagcacc aggcaaagcc  | 540 |
| cccaaactca tgatttatga ggtcagtaag cggccctcag gggtccctga tcgcttctct  | 600 |
| gcctccaagt ctggcaacac ggctccctg accgtctctg ggctccaggc tgaggatgag   | 660 |
| gctgattatt actgcagctc atatgcaggc agcaacaatt gggtgttcgg cggagggacc  | 720 |
| aagctgaccg tccta                                                   | 735 |

<210> 26  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 26  
 caggtgcagc tgcaggagtc gggcccaggg cttgtgaagc cttcggagac cctgtccctc 60  
 acttgcaactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120  
 ccagggaagg gactggagtg gattgggtct atctattaca gtgggagcac caactacaac 180  
 ccctccctca agagtcgagt caccatctca agagacaagt cgaagaacca gttgtttctg 240  
 aagttgaatt ctatgaccgc cgcggacacg gccgtctatt attgtgcgag agatgtttgg 300  
 ggcagtggcc agtcatttga cagttggggc cagggcaccc tggtcaccgt ctcgagtggg 360  
 ggaggcgggt caggcggagg tggctctggc ggtggcgcta gcaattttat gctgactcag 420  
 ccccaactctg tgtcggagtc tccggggaag acggtaacca tctcctgcac ccgcagcagt 480  
 ggcagcattg ccagcaacta tgtgcagtgg taccagcagc gcttgggcag ttccccacc 540  
 actgtgatct atgaacatag ccgaagaccc tctgggggtcc ctgatcggtt ctctgcctcc 600  
 atcgacagct cctccaactc tgcctccctc accatctctg gactgaagac tgaggacgag 660  
 gctgactact actgtcagtc ttatgatgtc agcaatcgag tgttcggcgg agggaccaag 720  
 ctgaccgtcc ta 732

<210> 27  
 <211> 738  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 27  
 gaggtgcagc tgttggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ccaggggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat | 180 |
| gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcgctgtat  | 240 |
| ctgcaaatga acagcctgag agctgaggac acggctgtgt attattgtgc gaaagccccg  | 300 |
| tggtatagca gctcgccgac accctacggt atggacgtct ggggccaggg caccctggtc  | 360 |
| accgtctcga gtgggtggagg cggttcaggc ggaggtggct ctggcggtgg cgctagcgac | 420 |
| atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc  | 480 |
| acttgccagg cgagtcagga cattagcaac tatttaaatt ggtatcagca gaaaccaggg  | 540 |
| aaagccccta ggcgctgat ctatggtgca tccactttga tgagtggggt cccatcaagg   | 600 |
| ttcagcggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa  | 660 |
| gattttgcaa ctactactg tcaacagagt tacagtacac ctctcacttt cggcggaggg   | 720 |
| accaaggtgg aaatcaaa                                                | 738 |

<210> 28  
 <211> 738  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| <400> 28                                                            |     |
| gagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc   | 120 |
| cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac   | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac   | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaacacgt   | 300 |
| tacatttggg ggagttatcg ggcatacggg atggacgtct ggggccaaagg gacaatggtc  | 360 |
| accgtctcga gtgggtggagg cggttcaggc ggaggtggct ctggcggtgg cgctagcgac  | 420 |
| atccagatga cccagtctcc atcctccatg tctgcatctg taggagacag agtcaccatc   | 480 |

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acttgccgcg cgagtcagag cattagcagt catttaaatt ggtatcagca gctgccaggc   | 540 |
| aatgccccta ctctcctgat ctattatgct tccaatttac aaagtgggggt cccatctagg  | 600 |
| ttcagtgaggca gtggatctgg gacagatttc actctcacca tcagcagtct gcagcctgat | 660 |
| gatttttgcaa cttactactg tcaacagagt atcagtctcc cgtacacttt tggccagggg  | 720 |
| accaaggtgg agatcaaa                                                 | 738 |

<210> 29  
 <211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 29                                                           |     |
| gaggtgcagc tgggtgcagcc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccctcagc agctatgcta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat aacaaactac  | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt atttctgtgc gagagatcag  | 300 |
| cggccggcga gcatggacgt ctggggccag ggcaccctgg tcaccgtctc gagggtgga   | 360 |
| ggcggttcag gcggagggtgg ctctggcggg ggcgctagcc agtctgagct gactcagcct | 420 |
| gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt  | 480 |
| gacgttggtg gttatatcta tgtctcctgg taccaacagc acccaggcaa agtccccaaa  | 540 |
| ctcatgattc atgatgtcag tcacggccc tcaggggttt ctaatcgctt ctctggctcc   | 600 |
| aggctctggca acacggcctc cctgaccatc tctgggctcc aggctgagga cgaggctgac | 660 |
| tatttctgca gtcataatac aagcagcaac aattatgtct tcggaactgg gaccaaggtc  | 720 |
| accgtccta                                                          | 729 |

<210> 30  
 <211> 729

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 30  
gaggtgcagc tgggtgcagcc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60  
tcctgcaagg cttctggagg caccctcagc agctatgcta tcagctgggt gcgacaggcc 120  
cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat aacaaactac 180  
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240  
atggagctga gcagcctgag atctgaggac acggccgtgt atttctgtgc gagagatcag 300  
cggccggcga gcatggacgt ctggggccag ggcaccctgg tcaccgtctc gagtgggtgga 360  
ggcggttcag gcggaggtgg ctctggcggg ggcgctagcc agtctgggct gactcagcct 420  
gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480  
gatgttggtg gttataacta tgtctcctgg taccaacagc acccaggcaa agccccaaa 540  
ctcatgattt atgaggtcag taatcgggcc tcaggggttt ctaatcgctt ctctggctcc 600  
aagtctggca acacggcctc cctgaccatc tctgggctcc aggctgagga cgaggctgat 660  
tactactgca gcacagttac aagcctcagc acttatgtct tcggaactgg gaccaagctg 720  
accgtccta 729

<210> 31  
<211> 741  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 31  
gaggtgcagc tgggtgcagtc tggggctgag gtgaagaggc ctgggtcctc ggtgaaggtc 60  
tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120  
cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc ggcaggaacg | 300 |
| tatagcagtg gctggacgat tgactactgg gggcaaggga ccacggtcac cgtctcgagt | 360 |
| ggtggaggcg gttcaggcgg aggtggctct ggcggtggcg ctagcgatat tgtgatgacg | 420 |
| cagtctccac tctccctgcc cgtcacctt ggacagccgg cctccatctc ctgcaggtct  | 480 |
| agtcaaagcc tcgtatacac tgatggaaac acctacttga attggtttca gcagaggcca | 540 |
| ggccaatctc caaggcgcct aatttataag gtttctaacc gggactctgg ggtcccagac | 600 |
| agattcagcg gcagtgggtc aggcactgat ttcacactga aaatcagcag ggtggaggct | 660 |
| gaggatgttg ggatttatta ctgcatgcat agtaaacagt ggcctccac tttcggcgga  | 720 |
| gggaccaagg tggaaatcaa a                                           | 741 |

<210> 32  
 <211> 714  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 32                                                           |     |
| gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagt gatgggagg atcatcccta tctttggtac agcaaactac    | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggacac  | 300 |
| tactactaca tggacgtctg ggggcaagg accacgtca ccgtctcgag tgggtggaggc   | 360 |
| ggttcaggcg gaggtggctc tggcggtggc gctagcgata ttgtgatgac tcagtctcca  | 420 |
| gccaccctgt ctgtgtctcc aggggaagga gccaccctct cctgcagggc cagtcagagt  | 480 |
| gtagcagca acttagcctg gtatcagcag aaacctggcc gggctcccag gctcctcatc   | 540 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| tatggtgcat ccaccagggc cactggtatc ccagccaggt tcagtggcag tgggtctggg | 600 |
| acagagttca ctctcaccat cagcagcctg cagtctgaag attttgcagt ttattactgt | 660 |
| cagcagtata ataactggcc cagtttcggc ggagggacca agctggagat caaa       | 714 |

<210> 33  
 <211> 714  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 33                                                           |     |
| gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagt gatgggaggg atcatcccta tctttggtac agcaaactac   | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggacac  | 300 |
| tactactaca tggacgtctg ggggcaaggg accacggtca ccgtctcgag tgggtgaggc  | 360 |
| ggttcaggcg gaggtggctc tggcggtggc gctagcgata ttgtgatgac tcagtctcca  | 420 |
| gccaccctgt ctgtgtctcc aggggaagga gccaccctct cctgcagggc cagtcagagt  | 480 |
| gtagcagca acttagcctg gtatcagcag aaacctggcc gggctcccag gctcctcatc   | 540 |
| tatggtgcat ccaccagggc cactggtatc ccagccaggt tcagtggcag tgggtctggg  | 600 |
| acagagttca ctctcaccat cagcagcctg cagtctgaag attttgcagt ttattactgt  | 660 |
| cagcagtata ataactggcc cactttcggc ggagggacca agctggagat caaa        | 714 |

<210> 34  
 <211> 741  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 34  
caggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60  
tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120  
cctggacaag gacttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180  
gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240  
atggagctga gcggcctgag atctgaggac acggccgtgt attactgtgc gagaggtata 300  
cagcctcttc gctactacgg tatggacgtc tggggccaag gaacctggt caccgtctcg 360  
agtgggtggag gcggttcagg cggaggtggc tctggcggtg gcgctagcca gtctgcgctg 420  
actcagccac cctcagcgtc tgggaccccc gggcagaggg tcaccatctc ttgttctgga 480  
agcagctcca acatcggaag taattatgta tactgggtacc agcagctccc aggaacggcc 540  
cccaaactcc tcatttatag gaataatcag cggccctcag gggtccctga ccgattctct 600  
ggctccaagt ctggcacctc agcctccctg gccatcagtg ggctccggtc cgaggatgag 660  
gctgattatt actgtgcagc atgggatgac agcctgagtg gtcggggagt gttcggcgga 720  
gggacccagc tcaccgtcct a 741

<210> 35  
<211> 729  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 35  
caggtgcagc tgggtggagtc tgggggagggc ctgggtcaagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac acactacgca 180  
gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240  
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag gggggctggt 300  
accttaaatg cttttgatat ctgggggcaa gggaccacgg tcaccgtctc gagtgggtgga 360

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ggcggttcag gcggaggtgg ctctggcggt ggcgctagcc agtctgggct gactcagcct | 420 |
| ccctccacgt ccgggtctcc tggacagtca gtcaccatct cctgcactgg aaccagcagt | 480 |
| gacgttggtg cttatagcta tgtctcctgg tatcaacaac acccaggcaa agcccccaaa | 540 |
| cttctcattt atgcggtcac taagaggccc tcgggggtcc ctgatacgtt ctctggctcc | 600 |
| aagtctggca acacggcctc cctgaccgtc tctggactcc aggatgagga tgaggctgat | 660 |
| tattactgca gctcttttgc aggcggcagc actctggtgt tcggcggagg gaccaagctg | 720 |
| accgtccta                                                         | 729 |

<210> 36  
 <211> 741  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_GUCY2C-binding scFv coding sequence

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 36                                                           |     |
| caaatgcagc tggatgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc | 60  |
| tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc  | 120 |
| cctggacaag ggcttgagt gatgggaggg atcatcccta tctttggtac agcaaactat   | 180 |
| gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac  | 240 |
| atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgt gagaggatac  | 300 |
| agttcaatat actactacta cggtatggac gtctggggcc aagggacaat ggtcaccgtc  | 360 |
| tcgagtgggtg gaggcggttc aggcggaggt ggctctggcg gtggcgctag ccagtctggg | 420 |
| ctgactcagc ctcgctcagt gtccgggtct cctggacagt cagtcaccat ctcctgcact  | 480 |
| ggaaccagca gtgatgttgg tggttataac tatgtctcct ggtaccaaca gcaccaggc   | 540 |
| aaagccccca aactcatgat ttatgatgtc agtaagcggc cctcaggggt ttctgatcgc  | 600 |
| ttctctgggt ccaagtctgg caacacggcc tccctgacca tctctgggct ccaggctgag  | 660 |
| gacgaggctg attattactg cggctcatat acaagcgacg ggactctagt attcggcgga  | 720 |

gggaccaagc tgaccgtcct a

741

<210> 37  
<211> 729  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic\_GUCY2C-binding scFv coding sequence

<400> 37  
caggtgcagc tggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60  
tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc 120  
cctggacaag ggcttgagt gatgggaagg atcatcccta tccttggtat agcaaactac 180  
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240  
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatagg 300  
tcttacaact ggctcgacc ctggggccgt ggcaccctgg tcaccgtctc gagtgggtgga 360  
ggcggttcag gcggaggtgg ctctggcggt ggcgctagcc agtctgcgct gactcagcct 420  
gtctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccatcagt 480  
gacgttggtg attataacta tgtctcctgg taccaacagc acccaggcaa agccccaaa 540  
ctcatgattt atgacgtcaa taatcgccc tcaggggttt ctaatcgctt ctctggctcc 600  
aagtctggca acacggcctc cctgaccatc tctgggctcc aggctgagga cgaggctgat 660  
tattactgca gctcatatac aagcagcagc actctggtat tcggcggagg gaccaagctg 720  
accgtccta 729

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

<220>  
<223> Synthetic\_CDR-H1

<400> 38

Gly Tyr Thr Phe Thr Ser Tyr Tyr  
1 5

<210> 39  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H1

<400> 39  
Gly Gly Thr Leu Ser Ser Tyr Ala  
1 5

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H1

<400> 40  
Gly Gly Thr Phe Ser Ser Tyr Thr  
1 5

<210> 41  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H1

<400> 41  
Gly Gly Thr Phe Gly Ser Tyr Thr  
1 5

<210> 42  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H1

<400> 42

Gly Gly Ser Ile Ser Ser Tyr Tyr  
1 5

<210> 43

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H1

<400> 43

Gly Phe Thr Phe Ser Ser Tyr Trp  
1 5

<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H1

<400> 44

Gly Gly Thr Phe Ser Ser Tyr Ala  
1 5

<210> 45

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H1

<400> 45

Gly Phe Thr Phe Ser Ser Tyr Ser  
1 5

<210> 46  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H2

<400> 46  
Ile Asn Pro Ser Gly Gly Ser Thr  
1 5

<210> 47  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H2

<400> 47  
Ile Ile Pro Ile Leu Gly Ile Thr  
1 5

<210> 48  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H2

<400> 48  
Ile Ile Pro Ile Leu Gly Ile Ala  
1 5

<210> 49  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H2

<400> 49

Ile Ile Pro Val Leu Gly Ile Ala  
1 5

<210> 50

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H2

<400> 50

Ile Tyr Tyr Ser Gly Ser Thr  
1 5

<210> 51

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H2

<400> 51

Ile Lys Gln Asp Gly Ser Glu Lys  
1 5

<210> 52

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-H2

<400> 52

Ile Ile Pro Ile Phe Gly Thr Ala  
1 5

<210> 53  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H2

<400> 53  
Ile Tyr Ser Gly Gly Ser Thr  
1 5

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

<220>  
<223> Synthetic\_CDR-H3

<400> 54  
Asp Gly Gln Trp Leu Gln Phe Asp Tyr  
1 5

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

<220>  
<223> Synthetic\_CDR-H3

<400> 55  
Asp Gln Arg Pro Ala Ser Met Asp Val  
1 5

<210> 56  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 56  
Asp Tyr Ser Ser Ser Trp Asn Ser Met Asp Val  
1 5 10

<210> 57  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 57  
Asp Val Trp Gly Ser Gly Gln Ser Phe Asp Ser  
1 5 10

<210> 58  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 58  
Ala Pro Trp Tyr Ser Ser Ser Pro Thr Pro Tyr Gly Met Asp Val  
1 5 10 15

<210> 59  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 59  
Thr Arg Tyr Ile Trp Gly Ser Tyr Arg Ala Tyr Gly Met Asp Val  
1 5 10 15

<210> 60  
<211> 11

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 60  
Gly Thr Tyr Ser Ser Gly Trp Thr Ile Asp Tyr  
1 5 10

<210> 61  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 61  
Gly His Tyr Tyr Tyr Met Asp Val  
1 5

<210> 62  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 62  
Gly Ile Gln Pro Leu Arg Tyr Tyr Gly Met Asp Val  
1 5 10

<210> 63  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 63

Gly Ala Gly Thr Leu Asn Ala Phe Asp Ile  
1 5 10

<210> 64  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 64  
Gly Tyr Ser Ser Ile Tyr Tyr Tyr Tyr Gly Met Asp Val  
1 5 10

<210> 65  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-H3

<400> 65  
Asp Arg Ser Tyr Asn Trp Leu Asp Pro  
1 5

<210> 66  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L1

<400> 66  
Gln Ser Leu Leu Lys Lys Ser Asp Gly Asn Thr Tyr  
1 5 10

<210> 67  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 67

Ser Ser Asp Val Gly Gly Tyr Ile Tyr  
1 5

<210> 68

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 68

Ser Ser Asp Ile Gly Tyr Tyr His Tyr  
1 5

<210> 69

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 69

Ser Ser Asp Val Gly Gly Tyr Asn Tyr  
1 5

<210> 70

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 70

Ser Ser Asp Val Gly Ala Tyr Asn Tyr  
1 5

<210> 71  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L1

<400> 71  
Ser Gly Ser Ile Ala Ser Asn Tyr  
1 5

<210> 72  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L1

<400> 72  
Gln Asp Ile Ser Asn Tyr  
1 5

<210> 73  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L1

<400> 73  
Gln Ser Ile Ser Ser His  
1 5

<210> 74  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 74

Gln Ser Leu Val Tyr Thr Asp Gly Asn Thr Tyr  
1 5 10

<210> 75

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 75

Gln Ser Val Ser Ser Asn  
1 5

<210> 76

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 76

Ser Ser Asn Ile Gly Ser Asn Tyr  
1 5

<210> 77

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L1

<400> 77

Ser Ser Asp Val Gly Ala Tyr Ser Tyr  
1 5

<210> 78  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L1

<400> 78  
Ile Ser Asp Val Gly Asp Tyr Asn Tyr  
1 5

<210> 79  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 79  
Lys Val Ser  
1

<210> 80  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 80  
Asp Val Ser  
1

<210> 81  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 81  
Glu Asp Ser  
1

<210> 82  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 82  
Glu Val Ser  
1

<210> 83  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 83  
Glu His Ser  
1

<210> 84  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 84  
Gly Ala Ser  
1

<210> 85  
<211> 3

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 85  
Tyr Ala Ser  
1

<210> 86  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 86  
Arg Asn Asn  
1

<210> 87  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic\_CDR-L2

<400> 87  
Ala Val Thr  
1

<210> 88  
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<220>  
<223> Synthetic\_CDR-L2

<400> 88

Asp Val Asn  
1

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<223> Synthetic\_CDR-L3

<400> 89  
Met Gln Gly Ser His Trp Pro Pro Thr  
1 5

<210> 90  
<211> 10  
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<223> Synthetic\_CDR-L3

<400> 90  
Ser Ser Tyr Ala Gly Ser Asn Asn Tyr Val  
1 5 10

<210> 91  
<211> 10  
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<220>  
<223> Synthetic\_CDR-L3

<400> 91  
Ser Ser Phe Thr Ser Arg Ser Thr Trp Val  
1 5 10

<210> 92  
<211> 10  
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<223> Synthetic\_CDR-L3

<400> 92

Ser Ser Tyr Thr Ser Ser Asn Asn Tyr Tyr  
1 5 10

<210> 93

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L3

<400> 93

Ser Ser Tyr Ala Gly Ser Asn Asn Phe Val  
1 5 10

<210> 94

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Synthetic\_CDR-L3

<400> 94

Ser Ser Tyr Ala Gly Ser Asn Asn Trp Val  
1 5 10

<210> 95

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic\_CDR-L3

<400> 95

Gln Ser Tyr Asp Val Ser Asn Arg Val  
1 5

<210> 96  
<211> 9  
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<220>  
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<400> 96  
Gln Gln Ser Tyr Ser Thr Pro Leu Thr  
1 5

<210> 97  
<211> 9  
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<220>  
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<400> 97  
Gln Gln Ser Ile Ser Leu Pro Tyr Thr  
1 5

<210> 98  
<211> 10  
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<220>  
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<400> 98  
Ser Ser Tyr Thr Ser Ser Asn Asn Tyr Val  
1 5 10

<210> 99  
<211> 10  
<212> PRT  
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<223> Synthetic\_CDR-L3

<400> 99

Ser Thr Val Thr Ser Leu Ser Thr Tyr Val  
1 5 10

<210> 100

<211> 9

<212> PRT

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<223> Synthetic\_CDR-L3

<400> 100

Met His Ser Lys Gln Trp Pro Pro Thr  
1 5

<210> 101

<211> 8

<212> PRT

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<223> Synthetic\_CDR-L3

<400> 101

Gln Gln Tyr Asn Asn Trp Pro Ser  
1 5

<210> 102

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Synthetic\_CDR-L3

<400> 102

Gln Gln Tyr Asn Asn Trp Pro Thr  
1 5

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<211> 12  
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<400> 103  
Ala Ala Trp Asp Asp Ser Leu Ser Gly Arg Gly Val  
1 5 10

<210> 104  
<211> 10  
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<400> 104  
Ser Ser Phe Ala Gly Gly Ser Thr Leu Val  
1 5 10

<210> 105  
<211> 10  
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<220>  
<223> Synthetic\_CDR-L3

<400> 105  
Gly Ser Tyr Thr Ser Asp Gly Thr Leu Val  
1 5 10

<210> 106  
<211> 10  
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<220>  
<223> Synthetic\_CDR-L3

<400> 106  
Ser Ser Tyr Thr Ser Ser Ser Thr Leu Val  
1 5 10

<210> 107  
<211> 8  
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<400> 107  
Gly Gly Ser Phe Ser Gly Tyr Tyr  
1 5

<210> 108  
<211> 7  
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<220>  
<223> Synthetic\_CDR-H2

<400> 108  
Ile Asn His Arg Gly Asn Thr  
1 5

<210> 109  
<211> 11  
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<220>  
<223> Synthetic\_CDR-H3

<400> 109  
Glu Arg Gly Tyr Thr Tyr Gly Asn Phe Asp His  
1 5 10

<210> 110  
<211> 6

<212> PRT  
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<220>  
<223> Synthetic\_CDR-L1

<400> 110  
Gln Ser Val Ser Arg Asn  
1 5

<210> 111  
<211> 9  
<212> PRT  
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<220>  
<223> Synthetic\_CDR-L3

<400> 111  
Gln Gln Tyr Lys Thr Trp Pro Arg Thr  
1 5

<210> 112  
<211> 430  
<212> PRT  
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<220>  
<223> Synthetic\_Hu-GUCY2C

<400> 112  
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln  
1 5 10 15

Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn  
20 25 30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala  
35 40 45

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile  
50 55 60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala  
65 70 75 80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg  
 85 90 95  
 Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala  
 100 105 110  
 Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr  
 115 120 125  
 Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala  
 130 135 140  
 Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu  
 145 150 155 160  
 Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys  
 165 170 175  
 Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val  
 180 185 190  
 Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala  
 195 200 205  
 Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val  
 210 215 220  
 Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn  
 225 230 235 240  
 Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr  
 245 250 255  
 Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu  
 260 265 270  
 Val Asp Leu Phe Asn Asp Gln Tyr Phe Glu Asp Asn Val Thr Ala Pro  
 275 280 285  
 Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser  
 290 295 300  
 Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp  
 305 310 315 320  
 Phe Ala Leu Ala Tyr Leu Asn Gly Ile Leu Leu Phe Gly His Met Leu  
 325 330 335  
 Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala

340                      345                      350  
 His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr  
           355                      360                      365  
 Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr  
           370                      375                      380  
 Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His  
 385                      390                      395                      400  
 Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys  
                           405                      410                      415  
 Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln  
                           420                      425                      430

<210>      113  
 <211>      430  
 <212>      PRT  
 <213>      Artificial Sequence

<220>  
 <223>      Synthetic\_Mu-GUCY2C

<400>      113  
 Met Thr Ser Leu Leu Gly Leu Ala Val Arg Leu Leu Leu Phe Gln Pro  
   1                      5                      10                      15  
 Ala Leu Met Val Phe Trp Ala Ser Gln Val Arg Gln Asn Cys Arg Asn  
           20                      25                      30  
 Gly Ser Tyr Glu Ile Ser Val Leu Met Met Asp Asn Ser Ala Tyr Lys  
           35                      40                      45  
 Glu Pro Met Gln Asn Leu Arg Glu Ala Val Glu Glu Gly Leu Asp Ile  
           50                      55                      60  
 Val Arg Lys Arg Leu Arg Glu Ala Asp Leu Asn Val Thr Val Asn Ala  
   65                      70                      75                      80  
 Thr Phe Ile Tyr Ser Asp Gly Leu Ile His Lys Ser Gly Asp Cys Arg  
           85                      90                      95  
 Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Glu Ile Thr Arg Asp  
           100                      105                      110  
 His Lys Met Gly Cys Ala Leu Met Gly Pro Ser Cys Thr Tyr Ser Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Phe Gln Met Tyr Leu Asp Thr Glu Leu Asn Tyr Pro Met Ile Ser Ala |     |     |
| 130                                                             | 135 | 140 |
| Gly Ser Tyr Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Ile |     |     |
| 145                                                             | 150 | 155 |
| Leu Pro Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asp Phe Trp Lys |     |     |
| 165                                                             | 170 | 175 |
| Val Asn Asn Ala Ser Phe Lys Pro Phe Ser Trp Asn Ser Ser Tyr Val |     |     |
| 180                                                             | 185 | 190 |
| Tyr Lys Asn Gly Ser Glu Pro Glu Asp Cys Phe Trp Tyr Leu Asn Ala |     |     |
| 195                                                             | 200 | 205 |
| Leu Glu Ala Gly Val Ser Tyr Phe Ser Glu Val Leu Asn Phe Lys Asp |     |     |
| 210                                                             | 215 | 220 |
| Val Leu Arg Arg Ser Glu Gln Phe Gln Glu Ile Leu Thr Gly His Asn |     |     |
| 225                                                             | 230 | 235 |
| Arg Lys Ser Asn Val Ile Val Met Cys Gly Thr Pro Glu Ser Phe Tyr |     |     |
| 245                                                             | 250 | 255 |
| Asp Val Lys Gly Asp Leu Gln Val Ala Glu Asp Thr Val Val Ile Leu |     |     |
| 260                                                             | 265 | 270 |
| Val Asp Leu Phe Ser Asn His Tyr Phe Glu Glu Asn Thr Thr Ala Pro |     |     |
| 275                                                             | 280 | 285 |
| Glu Tyr Met Asp Asn Val Leu Val Leu Thr Leu Pro Ser Glu Gln Ser |     |     |
| 290                                                             | 295 | 300 |
| Thr Ser Asn Thr Ser Val Ala Glu Arg Phe Ser Ser Gly Arg Ser Asp |     |     |
| 305                                                             | 310 | 315 |
| Phe Ser Leu Ala Tyr Leu Glu Gly Thr Leu Leu Phe Gly His Met Leu |     |     |
| 325                                                             | 330 | 335 |
| Gln Thr Phe Leu Glu Asn Gly Glu Asn Val Thr Gly Pro Lys Phe Ala |     |     |
| 340                                                             | 345 | 350 |
| Arg Ala Phe Arg Asn Leu Thr Phe Gln Gly Phe Ala Gly Pro Val Thr |     |     |
| 355                                                             | 360 | 365 |
| Leu Asp Asp Ser Gly Asp Ile Asp Asn Ile Met Ser Leu Leu Tyr Val |     |     |
| 370                                                             | 375 | 380 |

Ser Leu Asp Thr Arg Lys Tyr Lys Val Leu Met Lys Tyr Asp Thr His  
 385 390 395 400

Lys Asn Lys Thr Ile Pro Val Ala Glu Asn Pro Asn Phe Ile Trp Lys  
 405 410 415

Asn His Lys Leu Pro Asn Asp Val Pro Gly Leu Gly Pro Gln  
 420 425 430

<210> 114  
 <211> 430  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_Cy-GUCY2C

<400> 114  
 Met Lys Thr Leu Leu Leu Asp Leu Val Leu Trp Ser Leu Leu Phe Gln  
 1 5 10 15

Pro Glu Trp Leu Tyr Leu Thr Ser Gln Val Ser Gln Asn Cys His Asn  
 20 25 30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Asp Asn Ser Ala Phe Ala  
 35 40 45

Glu Pro Leu Glu Asn Val Glu Asp Ala Val Asn Glu Gly Leu Glu Ile  
 50 55 60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala  
 65 70 75 80

Ser Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg  
 85 90 95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala  
 100 105 110

Lys Arg Met Gly Cys Val Leu Met Gly Pro Ser Cys Thr Tyr Ser Thr  
 115 120 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala  
 130 135 140

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

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

<210> 115  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic\_rCD4

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