

pctgb2015050649-seq1
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<150> 1403972.1

<151> 2014-03-06

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<170> PatentIn version 3.5

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<223> Heavy chain variable region CDR1

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Ser Tyr Asn Ile His
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Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser
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Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr

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25

30

Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu

35

40

45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met

50

55

60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu

65

70

75

80

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

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Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr

100

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

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

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

Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly
165 170 175

Ala Ser Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Gly Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
195 200 205

Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
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Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Ala Gly Thr Lys Val Glu
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Val Lys Arg

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Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr
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Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

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90

95

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

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<223> Murine KM666 VH (heavy chain variable region) sequence

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20 25 30
Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

Gln Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
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Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ala
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Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr
20 25 30

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

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

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

Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ser
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Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
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Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Val Trp
35 40 45

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

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

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro
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Ile Thr Phe Gly Ala Gly Thr Lys Val Glu Val Lys
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<223> Humanised KM666 VL sequence

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

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

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

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

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

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

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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 <223> Transmembrane domain

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Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
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Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
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Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
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Pro Arg Asp Phe Ala Ala Tyr
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 <223> CD40 endodomain

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Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
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Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
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Ser Thr Leu Ala Lys Ile
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 <223> CD3 zeta endodomain

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Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
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Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
20 25 30

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
35 40 45

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
50 55 60

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
65 70 75 80

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
85 90 95

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
100 105 110

Pro Arg

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<223> CD28Z

<400> 17

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
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Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
35 40 45

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
50 55 60

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
65 70 75 80

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
85 90 95

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Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
100 105 110

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
115 120 125

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
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Leu His Met Gln Ala Leu Pro Pro Arg
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<223> CD280XZ

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Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro
35 40 45

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

Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys
65 70 75 80

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
85 90 95

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
100 105 110

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
115 120 125

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
130 135 140

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
145 150 155 160

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp

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165

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175

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<223> Signal peptide

<400> 19

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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Gly Ser Thr Gly
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<223> Hinge-CH2CH3 of human IgG1 spacer

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

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

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

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

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
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130

135

140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp
225 230

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<211> 46

<212> PRT

<213> Artificial Sequence

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<223> Human CD8 stalk spacer

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

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
35 40 45

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<223> Human IgG1 hinge spacer

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Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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Lys Asp Pro Lys
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<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 Hinge-Fc spacer

<400> 23

Ala Glu Pro Lys Ser Pro 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 Lys Asp Pro Lys
225 230 235

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<210> 24
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 <213> Artificial Sequence

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

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gcacagtgc	tacatgaaca	tgactccccg	ccgccccggg	cccacccgca	agcattacca	4080
gccctatgcc	ccaccacgcg	acttcgcagc	ctatcgctcc	cgggtgaagt	tctctcgctc	4140
tgccgatgcc	ccagcctatc	agcagggcca	gaatcagctg	tacaatgaac	tgaacctggg	4200
caggcgggag	gagtacgacg	tgctggataa	gcggagaggc	agagaccccc	agatgggcgg	4260
caaaccacgg	cgcaaaaatc	cccaggaggg	actctataac	gagctgcaga	aggacaaaat	4320
ggccgaggcc	tattccgaga	tcggcatgaa	gggagagaga	agacgcggaa	agggccacga	4380
cggcctgtat	cagggattgt	ccaccgctac	aaaagataca	tatgatgccc	tgacatgca	4440
ggccctgcc	cccagatgac	gcgtatcgat	actgttctca	tcacatcata	tcaaggttat	4500
ataccatcaa	tattgccaca	gatgttactt	agccttttaa	tatttctcta	atttagtgta	4560
tatgcaatga	tagttctctg	atttctgaga	ttgagtttct	catgtgtaat	gattatttag	4620
agtttctctt	tcacatgctc	aaatttttgt	ctagttttat	tttttactga	tttgtaagac	4680
ttctttttat	aatctgcata	ttacaattct	ctttactggg	gtgttgcaaa	tattttctgt	4740
cattctatgg	cctgactttt	cttaatgggt	ttttaatttt	aaaaataagt	cttaatatct	4800
atgcaatcta	attaacaatc	ttttctttgt	ggttaggact	ttgagtcata	agaaattttt	4860
ctctacactg	aagtcatgat	ggcatgcttc	tatattattt	tctaaaagat	ttaaagtttt	4920
gccttctcca	tttagactta	taattcactg	gaattttttt	gtgtgtatgg	tatgacatat	4980
gggttccctt	ttatttttta	catataaata	tatttccctg	tttttctaaa	aaagaaaaag	5040
atcatcattt	tccatttgta	aaatgccata	tttttttcat	aggtcactta	catatatcaa	5100
tgggtctgtt	tctgagctct	actctatttt	atcagcctca	ctgtctatcc	ccacacatct	5160
catgctttgc	tctaaatctt	gatatttagt	ggaacattct	ttcccatttt	gttctacaag	5220
aatatttttg	ttattgtctt	tgggctttct	atatacattt	tgaaatgagg	ttgacaagtt	5280
cggattagtc	caatttggtt	aagacaggat	atcagtgggc	caggctctag	ttttgactca	5340
acaatatcac	cagctgaagc	ctatagagta	cgagccatag	ataaaataaa	agattttatt	5400
tagtctccag	aaaaaggggg	gaatgaaaga	ccccacctgt	aggtttgga	agctagctta	5460
agtaacgcca	ttttgcaagg	catggaaaaa	tacataactg	agaatagaga	agttcagatc	5520
aaggtcagga	acagatggaa	cagctgaata	tgggccaac	aggatatctg	tggttaagcag	5580
ttcctgcccc	ggctcagggc	caagaacaga	tggaaacagc	gaatatgggc	caaacaggat	5640
atctgtggta	agcagttcct	gccccggctc	aggccaaga	acagatgggc	cccagatgcg	5700
gtccagccct	cagcagtttc	tagagaacca	tcagatgttt	ccagggtgcc	ccaaggacct	5760

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gaaatgaccc tgtgccttat ttgaactaac caatcagttc gcttctcgct tctgttcgcg	5820
cgcttctgct ccccgagctc aataaaagag cccacaaccc ctactcggg gcgccagtcc	5880
tccgattgac tgagtcgccc gggtagccgt gtatccaata aaccctcttg cagttgcatc	5940
cgacttgtagg tctcgctggt ccttgggagg gtctcctctg agtgattgac taccggtcag	6000
cggggggtctt tcac	6014

<210> 26
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-GD2 CAR, muKM666-HCH2CH3-CD28OXZ

<400> 26

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

Gly Ser Thr Gly Gln Val Gln Leu Lys Glu Ser Gly Pro Val Leu Val
 20 25 30

Ala Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
 65 70 75 80

Ser Ala Leu Met Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser
 85 90 95

Gln Val Phe Leu Gln Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln
 145 150 155 160

Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr
 165 170 175

Cys Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln
 180 185 190

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Gln Lys Ser Gly Ala Ser Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn
195 200 205

Leu Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser Gly Thr
210 215 220

Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Ala Gly
245 250 255

Thr Lys Val Glu Val Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro
260 265 270

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460

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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495
 Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
 500 505 510
 Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 515 520 525
 Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 530 535 540
 Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 545 550 555 560
 Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu
 565 570 575
 Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
 580 585 590
 Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
 595 600 605
 Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 610 615 620
 Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
 625 630 635 640
 Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
 645 650 655
 Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 660 665 670
 Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 675 680 685
 Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
 690 695 700
 Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 705 710 715

<210> 27
 <211> 718

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<212> PRT

<213> Artificial Sequence

<220>

<223> anti-GD2 CAR, huKM666-HCH2CH3-CD28OXZ

<400> 27

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

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Tyr Cys Gln Gln Tyr 245 Ser Gly Tyr Pro Ile 250 Thr Phe Gly Gln Gly 255 Thr
 Lys Val Glu Ile 260 Lys Arg Ser Asp Pro 265 Ala Glu Pro Lys Ser 270 Pro Asp
 Lys Thr His 275 Thr Cys Pro Pro Cys 280 Pro Ala Pro Glu Leu 285 Leu Gly Gly
 Pro Ser 290 Val Phe Leu Phe Pro 295 Pro Lys Pro Lys Asp 300 Thr Leu Met Ile
 Ser 305 Arg Thr Pro Glu Val 310 Thr Cys Val Val Val 315 Asp Val Ser His Glu 320
 Asp Pro Glu Val Lys 325 Phe Asn Trp Tyr Val 330 Asp Gly Val Glu Val 335 His
 Asn Ala Lys Thr 340 Lys Pro Arg Glu Glu 345 Gln Tyr Asn Ser Thr 350 Tyr Arg
 Val Val Ser 355 Val Leu Thr Val Leu 360 His Gln Asp Trp Leu 365 Asn Gly Lys
 Glu Tyr 370 Lys Cys Lys Val Ser 375 Asn Lys Ala Leu Pro 380 Ala Pro Ile Glu
 Lys Thr Ile Ser Lys Ala 390 Lys Gly Gln Pro Arg 395 Glu Pro Gln Val Tyr 400
 Thr Leu Pro Pro Ser 405 Arg Asp Glu Leu Thr 410 Lys Asn Gln Val Ser 415 Leu
 Thr Cys Leu Val 420 Lys Gly Phe Tyr Pro 425 Ser Asp Ile Ala Val 430 Glu Trp
 Glu Ser Asn 435 Gly Gln Pro Glu Asn 440 Asn Tyr Lys Thr Thr 445 Pro Pro Val
 Leu Asp 450 Ser Asp Gly Ser Phe 455 Phe Leu Tyr Ser Lys 460 Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln 470 Gly Asn Val Phe Ser 475 Cys Ser Val Met His 480
 Glu Ala Leu His Asn 485 His Tyr Thr Gln Lys 490 Ser Leu Ser Leu Ser 495 Pro
 Gly Lys Lys Asp 500 Pro Lys Phe Trp Val 505 Leu Val Val Val Gly 510 Gly Val

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Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
515 520 525

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
530 535 540

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
545 550 555 560

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro
565 570 575

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

Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val
595 600 605

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
610 615 620

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
625 630 635 640

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
645 650 655

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
660 665 670

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
675 680 685

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
690 695 700

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705 710 715

<210> 28

<211> 717

<212> PRT

<213> Artificial sequence

<220>

<223> anti-GD2 CAR, huKM666-HCH2CH3pvaa-CD280XZ

<400> 28

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

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

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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495
 Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
 500 505 510
 Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 515 520 525
 Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 530 535 540
 Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 545 550 555 560
 Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro
 565 570 575

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Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln
580 585 590

Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys
595 600 605

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
610 615 620

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
625 630 635 640

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
645 650 655

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
660 665 670

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
675 680 685

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
690 695 700

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705 710 715

<210> 29
<211> 527
<212> PRT
<213> Artificial sequence

<220>
<223> anti-GD2 CAR, huKM666-HSTK-CD28OXZ

<400> 29

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

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Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
245 250 255

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

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Phe Trp Val Leu Val Val Val Gly Gly
305 310 315 320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
325 330 335

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
340 345 350

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Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
355 360 365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu
370 375 380

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
385 390 395 400

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
405 410 415

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
420 425 430

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
435 440 445

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
450 455 460

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
465 470 475 480

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
485 490 495

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
500 505 510

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520 525

<210> 30

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-GD2 CAR, huKM666-STK-CD28XOXZ

<400> 30

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

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Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
 65 70 75 80
 Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
 85 90 95
 Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
 115 120 125
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
 145 150 155 160
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 165 170 175
 Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln
 180 185 190
 Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
 195 200 205
 Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220
 Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 225 230 235 240
 Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
 245 250 255
 Lys Val Glu Ile Lys Arg Ser Asp Pro Thr Thr Thr Pro Ala Pro Arg
 260 265 270
 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 275 280 285
 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 290 295 300
 Leu Asp Phe Ala Cys Asp Ile Phe Trp Val Leu Val Val Val Gly Gly
 305 310 315 320
 Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 325 330 335

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Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
340 345 350

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
355 360 365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu
370 375 380

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
385 390 395 400

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
405 410 415

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
420 425 430

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
435 440 445

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
450 455 460

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
465 470 475 480

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
485 490 495

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
500 505 510

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520 525

<210> 31
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GD2 CAR, huKM666-HNG-CD28OXZ

<400> 31

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

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Lys Pro Ser₃₅ Gln Thr Leu Ser Ile₄₀ Thr Cys Thr Val Ser₄₅ Gly Phe Ser
 Leu Ala Ser Tyr Asn Ile His₅₅ Trp Val Arg Gln Pro₆₀ Pro Gly Lys Gly
 Leu Glu Trp Leu Gly Val₇₀ Ile Trp Ala Gly Gly₇₅ Ser Thr Asn Tyr Asn₈₀
 Ser Ala Leu Met Ser₈₅ Arg Leu Thr Ile Ser₉₀ Lys Asp Asn Ser Lys₉₅ Asn
 Gln Val Phe Leu₁₀₀ Lys Met Ser Ser Leu₁₀₅ Thr Ala Ala Asp Thr₁₁₀ Ala Val
 Tyr Tyr Cys₁₁₅ Ala Lys Arg Ser Asp₁₂₀ Asp Tyr Ser Trp Phe₁₂₅ Ala Tyr Trp
 Gly Gln Gly Thr Leu Val Thr₁₃₅ Val Ser Ser Gly Gly₁₄₀ Gly Gly Ser Gly
 Gly Gly Gly Ser Gly Gly₁₅₀ Gly Gly Ser Glu Asn₁₅₅ Gln Met Thr Gln Ser₁₆₀
 Pro Ser Ser Leu Ser₁₆₅ Ala Ser Val Gly Asp₁₇₀ Arg Val Thr Met Thr₁₇₅ Cys
 Arg Ala Ser Ser₁₈₀ Ser Val Ser Ser Ser₁₈₅ Tyr Leu His Trp Tyr₁₉₀ Gln Gln
 Lys Ser Gly₁₉₅ Lys Ala Pro Lys Val₂₀₀ Trp Ile Tyr Ser Thr₂₀₅ Ser Asn Leu
 Ala Ser Gly Val Pro Ser Arg₂₁₅ Phe Ser Gly Ser Gly₂₂₀ Ser Gly Thr Asp
 Tyr Thr Leu Thr Ile Ser₂₃₀ Ser Leu Gln Pro Glu₂₃₅ Asp Phe Ala Thr Tyr₂₄₀
 Tyr Cys Gln Gln Tyr₂₄₅ Ser Gly Tyr Pro Ile₂₅₀ Thr Phe Gly Gln Gly₂₅₅ Thr
 Lys Val Glu Ile₂₆₀ Lys Arg Ser Asp Pro₂₆₅ Ala Glu Pro Lys Ser₂₇₀ Pro Asp
 Lys Thr His₂₇₅ Thr Cys Pro Pro Cys₂₈₀ Pro Lys Asp Pro Lys₂₈₅ Phe Trp Val
 Leu Val₂₉₀ Val Val Gly Gly Val₂₉₅ Leu Ala Cys Tyr Ser₃₀₀ Leu Leu Val Thr

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Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
305 310 315 320

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
325 330 335

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
340 345 350

Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
355 360 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
370 375 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385 390 395 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
405 410 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
420 425 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
435 440 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
485 490 495

Ala Leu Pro Pro Arg
500

<210> 32
<211> 642
<212> PRT
<213> Artificial sequence

<220>
<223> anti-GD2 CAR, huKM666-HCH2CH3pvaa-CD28tmZ

<400> 32

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

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

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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495
 Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
 500 505 510
 Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 515 520 525
 Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 530 535 540
 Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 545 550 555 560
 Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
 565 570 575

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Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
580 585 590

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
595 600 605

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
610 615 620

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
625 630 635 640

Pro Arg

<210> 33
<211> 681
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GD2 CAR, huMK666-HCH2CH3pvaa-CD28Z

<400> 33

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

Gly Ser Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
20 25 30

Lys Pro Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Ala Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn
65 70 75 80

Ser Ala Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn
85 90 95

Gln Val Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly ser Gly
130 135 140

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
165 170 175

Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu
195 200 205

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr
245 250 255

Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp
260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala
290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
325 330 335

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
405 410 415

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Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
500 505 510

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
515 520 525

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
530 535 540

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
545 550 555 560

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
565 570 575

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
580 585 590

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
595 600 605

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
610 615 620

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
625 630 635 640

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
645 650 655

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
660 665 670

Leu His Met Gln Ala Leu Pro Pro Arg
675 680

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<210> 34

<211> 1103

<212> PRT

<213> Artificial sequence

<220>

<223> anti-GD2 CAR co-expressed with iCasp9 suicide gene

<400> 34

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

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
20 25 30

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
35 40 45

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
50 55 60

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

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
85 90 95

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
100 105 110

Gly Gly Ser Gly Val Asp Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
115 120 125

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
130 135 140

Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
145 150 155 160

Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
165 170 175

Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
180 185 190

Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
195 200 205

Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
210 215 220

Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
225 230 235 240

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Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
245 250 255

Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
260 265 270

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
355 360 365

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
370 375 380

Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395 400

Ala Ser Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
405 410 415

Glu Glu Asn Pro Gly Pro Met Glu Thr Asp Thr Leu Leu Leu Trp Val
420 425 430

Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Gln Val Gln Leu Gln Glu
435 440 445

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

Thr Val Ser Gly Phe Ser Leu Ala Ser Tyr Asn Ile His Trp Val Arg
465 470 475 480

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ala Gly
485 490 495

Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu Thr Ile Ser
500 505 510

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Lys Asp Asn Ser Lys Asn Gln Val Phe Leu Lys Met Ser Ser Leu Thr
 515 520 525
 Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys Arg Ser Asp Asp Tyr
 530 535 540
 Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 545 550 555 560
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 565 570 575
 Asn Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 580 585 590
 Arg Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser Tyr
 595 600 605
 Leu His Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Lys Val Trp Ile
 610 615 620
 Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 625 630 635 640
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 645 650 655
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro Ile
 660 665 670
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ser Asp Pro Ala
 675 680 685
 Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 690 695 700
 Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 705 710 715 720
 Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val
 725 730 735
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 740 745 750
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 755 760 765
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 770 775 780

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Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 785 790 795 800
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 805 810 815
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 820 825 830
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 835 840 845
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 850 855 860
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 865 870 875 880
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 885 890 895
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 900 905 910
 Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val
 915 920 925
 Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
 930 935 940
 Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
 945 950 955 960
 Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
 965 970 975
 Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
 980 985 990
 Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 995 1000 1005
 Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 1010 1015 1020
 Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 1025 1030 1035
 Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 1040 1045 1050

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Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
1055 1060 1065

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
1070 1075 1080

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
1085 1090 1095

Ala Leu Pro Pro Arg
1100

<210> 35
<211> 858
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GD2 CAR co-expressed with RQR8 suicide gene

<400> 35

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser Gly
20 25 30

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

Thr Asn Val Ser Pro Ala Lys Pro Thr Thr Thr Ala Cys Pro Tyr Ser
50 55 60

Asn Pro Ser Leu Cys Ser Gly Gly Gly Gly Ser Pro Ala Pro Arg Pro
65 70 75 80

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
85 90 95

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

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
115 120 125

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg
130 135 140

Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Arg Ala Glu
145 150 155 160

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Gly Arg Gly Ser Leu₁₆₅ Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly₁₇₅

Pro Met Glu Thr₁₈₀ Asp Thr Leu Leu Leu₁₈₅ Trp Val Leu Leu Leu₁₉₀ Trp Val

Pro Gly Ser₁₉₅ Thr Gly Gln Val Gln₂₀₀ Leu Gln Glu Ser Gly₂₀₅ Pro Gly Leu

Val Lys₂₁₀ Pro Ser Gln Thr Leu₂₁₅ Ser Ile Thr Cys Thr₂₂₀ Val Ser Gly Phe

Ser₂₂₅ Leu Ala Ser Tyr Asn₂₃₀ Ile His Trp Val Arg₂₃₅ Gln Pro Pro Gly Lys₂₄₀

Gly Leu Glu Trp Leu₂₄₅ Gly Val Ile Trp Ala₂₅₀ Gly Gly Ser Thr Asn₂₅₅ Tyr

Asn Ser Ala Leu₂₆₀ Met Ser Arg Leu Thr₂₆₅ Ile Ser Lys Asp Asn₂₇₀ Ser Lys

Asn Gln Val₂₇₅ Phe Leu Lys Met Ser₂₈₀ Ser Leu Thr Ala Ala₂₈₅ Asp Thr Ala

Val Tyr₂₉₀ Tyr Cys Ala Lys Arg₂₉₅ Ser Asp Asp Tyr Ser₃₀₀ Trp Phe Ala Tyr

Trp₃₀₅ Gly Gln Gly Thr Leu₃₁₀ Val Thr Val Ser Ser₃₁₅ Gly Gly Gly Gly Ser₃₂₀

Gly Gly Gly Gly Ser₃₂₅ Gly Gly Gly Gly Ser₃₃₀ Glu Asn Gln Met Thr₃₃₅ Gln

Ser Pro Ser Ser₃₄₀ Leu Ser Ala Ser Val₃₄₅ Gly Asp Arg Val Thr₃₅₀ Met Thr

Cys Arg Ala₃₅₅ Ser Ser Ser Val Ser₃₆₀ Ser Ser Tyr Leu His₃₆₅ Trp Tyr Gln

Gln Lys₃₇₀ Ser Gly Lys Ala Pro₃₇₅ Lys Val Trp Ile Tyr₃₈₀ Ser Thr Ser Asn

Leu₃₈₅ Ala Ser Gly Val Pro₃₉₀ Ser Arg Phe Ser Gly₃₉₅ Ser Gly Ser Gly Thr₄₀₀

Asp Tyr Thr Leu Thr₄₀₅ Ile Ser Ser Leu Gln₄₁₀ Pro Glu Asp Phe Ala₄₁₅ Thr

Tyr Tyr Cys Gln₄₂₀ Gln Tyr Ser Gly Tyr₄₂₅ Pro Ile Thr Phe Gly₄₃₀ Gln Gly

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Thr Lys Val Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro
435 445

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
450 455 460

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
465 470 475 480

Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
485 490 495

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
500 505 510

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
515 520 525

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
530 535 540

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
545 550 555 560

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
565 570 575

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
580 585 590

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
595 600 605

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
610 615 620

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
625 630 635 640

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
645 650 655

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
660 665 670

Gly Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val
675 680 685

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
690 695 700

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Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
705 710 715 720

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
725 730 735

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
740 745 750

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
755 760 765

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
770 775 780

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
785 790 795 800

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
805 810 815

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
820 825 830

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
835 840 845

Ala Leu His Met Gln Ala Leu Pro Pro Arg
850 855

<210> 36
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> Inducible Caspase 9 (iCasp9) sequence

<400> 36

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

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
20 25 30

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
35 40 45

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
50 55 60

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

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Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
85 90 95

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
100 105 110

Gly Gly Ser Gly Val Asp Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
115 120 125

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
130 135 140

Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
145 150 155 160

Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
165 170 175

Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
180 185 190

Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
195 200 205

Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
210 215 220

Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
225 230 235 240

Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
245 250 255

Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
260 265 270

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350

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Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 355 360 365
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 370 375 380
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 385 390 395 400

Ala Ser

<210> 37
 <211> 157
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Novel marker/suicide gene RQR8 sequence
 <400> 37

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