SEQUENCE LISTING

<110> PALLEON PHARMACEUTICALS INC.

<120> ANTI-INFLAMMATORY SIGLEC PROTEINS AND METHODS OF MAKING AND USING SAME

<130> PAL-026WO

<140> PCT/US2022/025087
<141> 2022-04-15

<150> US 63/175,826
<151> 2021-04-16

<160> 161

<170> PatentIn version 3.5

<210> 1
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(227)
<223> hIgG1 Fc - Shorter (No N-terminal EPKSC)

<400> 1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
225

<210> 2
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - Hole (Y407T) - Shorter

<400> 2

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
225

<210> 3
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - Knob (T366Y) - Shorter

<400> 3

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
225

<210> 4
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - N297G - Shorter

<400> 4

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
225

<210> 5
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(232)
<223> hIgG1 Fc - Longer (N-terminal EPKSC)

<400> 5

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

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

Lys Asp Thr Leu Met Ile Ser 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 Glu Glu Met Thr
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
225 230

<210> 6
<211> 232
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - Knob (T366Y) - Longer

<400> 6

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

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

Lys Asp Thr Leu Met Ile Ser 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 Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Tyr 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
225 230

<210> 7
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - Hole (Y407T) - Longer

<400> 7

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

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

Lys Asp Thr Leu Met Ile Ser 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 Glu Glu Met Thr
    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 Thr
            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
225 230

<210> 8
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc - N297G - Longer

<400> 8

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

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

Lys Asp Thr Leu Met Ile Ser 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 Gly 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 Glu Glu Met Thr
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
225 230

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

<220>
<223> Synthetic: linker

<400> 9

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

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<400> 10

Gly Gly Gly Gly Ser
1 5

<210> 11
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<400> 11

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

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<400> 12

Glu Pro Lys Ser Ser
1 5

<210> 13
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<220>
<221> REPEAT
<222> (1)..(15)
<223> "Gly Gly Pro" is present at least once and may repeat up to five times

<400> 13

Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
1 5 10 15

<210> 14
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<220>
<221> REPEAT
<222> (1)..(25)
<223> "Gly Gly Gly Gly Ser" is present at least once and may repeat up to five times

<400> 14

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 15
<211> 1709
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1709)
<223> Siglec 1 FL

<400> 15

Met Gly Phe Leu Pro Lys Leu Leu Leu Leu Ala Ser Phe Phe Pro Ala
1 5 10 15

Gly Gln Ala Ser Trp Gly Val Ser Ser Pro Gln Asp Val Gln Gly Val
20 25 30

Lys Gly Ser Cys Leu Leu Ile Pro Cys Ile Phe Ser Phe Pro Ala Asp
35 40 45

Val Glu Val Pro Asp Gly Ile Thr Ala Ile Trp Tyr Tyr Asp Tyr Ser
50 55 60

Gly Gln Arg Gln Val Val Ser His Ser Ala Asp Pro Lys Leu Val Glu
65 70 75 80

Ala Arg Phe Arg Gly Arg Thr Glu Phe Met Gly Asn Pro Glu His Arg
85 90 95

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

Tyr Asn Phe Arg Phe Glu Ile Ser Glu Val Asn Arg Trp Ser Asp Val
115 120 125

Lys Gly Thr Leu Val Thr Val Thr Glu Glu Pro Arg Val Pro Thr Ile
130 135 140

Ala Ser Pro Val Glu Leu Leu Glu Gly Thr Glu Val Asp Phe Asn Cys
145 150 155 160

Ser Thr Pro Tyr Val Cys Leu Gln Glu Gln Val Arg Leu Gln Trp Gln
165 170 175

Gly Gln Asp Pro Ala Arg Ser Val Thr Phe Asn Ser Gln Lys Phe Glu
180 185 190

Pro Thr Gly Val Gly His Leu Glu Thr Leu His Met Ala Met Ser Trp
195 200 205

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

Arg Ala Gln Ser Glu Ile His Leu Gln Val Lys Tyr Ala Pro Lys Gly
225 230 235 240

Val Lys Ile Leu Leu Ser Pro Ser Gly Arg Asn Ile Leu Pro Gly Glu
245 250 255

Leu Val Thr Leu Thr Cys Gln Val Asn Ser Ser Tyr Pro Ala Val Ser
260 265 270

Ser Ile Lys Trp Leu Lys Asp Gly Val Arg Leu Gln Thr Lys Thr Gly
275 280 285

Val Leu His Leu Pro Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr
290 295 300

Cys Gln Ala Glu Asn Gly Val Gly Ser Leu Val Ser Pro Pro Ile Ser
305 310 315 320

Leu His Ile Phe Met Ala Glu Val Gln Val Ser Pro Ala Gly Pro Ile
325 330 335

Leu Glu Asn Gln Thr Val Thr Leu Val Cys Asn Thr Pro Asn Glu Ala
340 345 350

Pro Ser Asp Leu Arg Tyr Ser Trp Tyr Lys Asn His Val Leu Leu Glu
355 360 365

Asp Ala His Ser His Thr Leu Arg Leu His Leu Ala Thr Arg Ala Asp
370 375 380

Thr Gly Phe Tyr Phe Cys Glu Val Gln Asn Val His Gly Ser Glu Arg
385 390 395 400

Ser Gly Pro Val Ser Val Val Val Asn His Pro Pro Leu Thr Pro Val
405 410 415

Leu Thr Ala Phe Leu Glu Thr Gln Ala Gly Leu Val Gly Ile Leu His
420 425 430

Cys Ser Val Val Ser Glu Pro Leu Ala Thr Leu Val Leu Ser His Gly
435 440 445

Gly His Ile Leu Ala Ser Thr Ser Gly Asp Ser Asp His Ser Pro Arg
450 455 460

Phe Ser Gly Thr Ser Gly Pro Asn Ser Leu Arg Leu Glu Ile Arg Asp
465 470 475 480

Leu Glu Glu Thr Asp Ser Gly Glu Tyr Lys Cys Ser Ala Thr Asn Ser
485 490 495

Leu Gly Asn Ala Thr Ser Thr Leu Asp Phe His Ala Asn Ala Ala Arg
500 505 510

Leu Leu Ile Ser Pro Ala Ala Glu Val Val Glu Gly Gln Ala Val Thr
515 520 525

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

Trp Tyr Leu Asn Gly Ala Leu Leu His Glu Gly Pro Gly Ser Ser Leu
545 550 555 560

Leu Leu Pro Ala Ala Ser Ser Thr Asp Ala Gly Ser Tyr His Cys Arg
565 570 575

Ala Arg Asp Gly His Ser Ala Ser Gly Pro Ser Ser Pro Ala Val Leu
580 585 590

Thr Val Leu Tyr Pro Pro Arg Gln Pro Thr Phe Thr Thr Arg Leu Asp
595 600 605

Leu Asp Ala Ala Gly Ala Gly Ala Gly Arg Arg Gly Leu Leu Leu Cys
610 615 620

Arg Val Asp Ser Asp Pro Pro Ala Arg Leu Gln Leu Leu His Lys Asp
625 630 635 640

Arg Val Val Ala Thr Ser Leu Pro Ser Gly Gly Gly Cys Ser Thr Cys
645 650 655

Gly Gly Cys Ser Pro Arg Met Lys Val Thr Lys Ala Pro Asn Leu Leu
660 665 670

Arg Val Glu Ile His Asn Pro Leu Leu Glu Glu Glu Gly Leu Tyr Leu
675 680 685

Cys Glu Ala Ser Asn Ala Leu Gly Asn Ala Ser Thr Ser Ala Thr Phe
690 695 700

Asn Gly Gln Ala Thr Val Leu Ala Ile Ala Pro Ser His Thr Leu Gln
705 710 715 720

Glu Gly Thr Glu Ala Asn Leu Thr Cys Asn Val Ser Arg Glu Ala Ala
725 730 735

Gly Ser Pro Ala Asn Phe Ser Trp Phe Arg Asn Gly Val Leu Trp Ala
740 745 750

Gln Gly Pro Leu Glu Thr Val Thr Leu Leu Pro Val Ala Arg Thr Asp
755 760 765

Ala Ala Leu Tyr Ala Cys Arg Ile Leu Thr Glu Ala Gly Ala Gln Leu
770 775 780

Ser Thr Pro Val Leu Leu Ser Val Leu Tyr Pro Pro Asp Arg Pro Lys
785 790 795 800

Leu Ser Ala Leu Leu Asp Met Gly Gln Gly His Met Ala Leu Phe Ile
805 810 815

Cys Thr Val Asp Ser Arg Pro Leu Ala Leu Leu Ala Leu Phe His Gly
820 825 830

Glu His Leu Leu Ala Thr Ser Leu Gly Pro Gln Val Pro Ser His Gly
835 840 845

Arg Phe Gln Ala Lys Ala Glu Ala Asn Ser Leu Lys Leu Glu Val Arg
850 855 860

Glu Leu Gly Leu Gly Asp Ser Gly Ser Tyr Arg Cys Glu Ala Thr Asn
865 870 875 880

Val Leu Gly Ser Ser Asn Thr Ser Leu Phe Phe Gln Val Arg Gly Ala
885 890 895

Trp Val Gln Val Ser Pro Ser Pro Glu Leu Gln Glu Gly Gln Ala Val
900 905 910

Val Leu Ser Cys Gln Val His Thr Gly Val Pro Glu Gly Thr Ser Tyr
915 920 925

Arg Trp Tyr Arg Asp Gly Gln Pro Leu Gln Glu Ser Thr Ser Ala Thr
930 935 940

Leu Arg Phe Ala Ala Ile Thr Leu Thr Gln Ala Gly Ala Tyr His Cys
945 950 955 960

Gln Ala Gln Ala Pro Gly Ser Ala Thr Thr Ser Leu Ala Ala Pro Ile
965 970 975

Ser Leu His Val Ser Tyr Ala Pro Arg His Val Thr Leu Thr Thr Leu
980 985 990

Met Asp Thr Gly Pro Gly Arg Leu Gly Leu Leu Leu Cys Arg Val Asp
995 1000 1005

Ser Asp Pro Pro Ala Gln Leu Arg Leu Leu His Gly Asp Arg Leu
1010 1015 1020

Val Ala Ser Thr Leu Gln Gly Val Gly Gly Pro Glu Gly Ser Ser
1025 1030 1035

Pro Arg Leu His Val Ala Val Ala Pro Asn Thr Leu Arg Leu Glu
1040 1045 1050

Ile His Gly Ala Met Leu Glu Asp Glu Gly Val Tyr Ile Cys Glu
1055 1060 1065

Ala Ser Asn Thr Leu Gly Gln Ala Ser Ala Ser Ala Asp Phe Asp
1070 1075 1080

Ala Gln Ala Val Asn Val Gln Val Trp Pro Gly Ala Thr Val Arg
    1085 1090 1095

Glu Gly Gln Leu Val Asn Leu Thr Cys Leu Val Trp Thr Thr His
    1100 1105 1110

Pro Ala Gln Leu Thr Tyr Thr Trp Tyr Gln Asp Gly Gln Gln Arg
    1115 1120 1125

Leu Asp Ala His Ser Ile Pro Leu Pro Asn Val Thr Val Arg Asp
    1130 1135 1140

Ala Thr Ser Tyr Arg Cys Gly Val Gly Pro Pro Gly Arg Ala Pro
    1145 1150 1155

Arg Leu Ser Arg Pro Ile Thr Leu Asp Val Leu Tyr Ala Pro Arg
    1160 1165 1170

Asn Leu Arg Leu Thr Tyr Leu Leu Glu Ser His Gly Gly Gln Leu
    1175 1180 1185

Ala Leu Val Leu Cys Thr Val Asp Ser Arg Pro Pro Ala Gln Leu
    1190 1195 1200

Ala Leu Ser His Ala Gly Arg Leu Leu Ala Ser Ser Thr Ala Ala
    1205 1210 1215

Ser Val Pro Asn Thr Leu Arg Leu Glu Leu Arg Gly Pro Gln Pro
    1220 1225 1230

Arg Asp Glu Gly Phe Tyr Ser Cys Ser Ala Arg Ser Pro Leu Gly
    1235 1240 1245

Gln Ala Asn Thr Ser Leu Glu Leu Arg Leu Glu Gly Val Arg Val
    1250 1255 1260

Ile Leu Ala Pro Glu Ala Ala Val Pro Glu Gly Ala Pro Ile Thr
    1265 1270 1275

Val Thr Cys Ala Asp Pro Ala Ala His Ala Pro Thr Leu Tyr Thr
    1280 1285 1290

Trp Tyr His Asn Gly Arg Trp Leu Gln Glu Gly Pro Ala Ala Ser
1295 1300 1305

Leu Ser Phe Leu Val Ala Thr Arg Ala His Ala Gly Ala Tyr Ser
1310 1315 1320

Cys Gln Ala Gln Asp Ala Gln Gly Thr Arg Ser Ser Arg Pro Ala
1325 1330 1335

Ala Leu Gln Val Leu Tyr Ala Pro Gln Asp Ala Val Leu Ser Ser
1340 1345 1350

Phe Arg Asp Ser Arg Ala Arg Ser Met Ala Val Ile Gln Cys Thr
1355 1360 1365

Val Asp Ser Glu Pro Pro Ala Glu Leu Ala Leu Ser His Asp Gly
1370 1375 1380

Lys Val Leu Ala Thr Ser Ser Gly Val His Ser Leu Ala Ser Gly
1385 1390 1395

Thr Gly His Val Gln Val Ala Arg Asn Ala Leu Arg Leu Gln Val
1400 1405 1410

Gln Asp Val Pro Ala Gly Asp Asp Thr Tyr Val Cys Thr Ala Gln
1415 1420 1425

Asn Leu Leu Gly Ser Ile Ser Thr Ile Gly Arg Leu Gln Val Glu
1430 1435 1440

Gly Ala Arg Val Val Ala Glu Pro Gly Leu Asp Val Pro Glu Gly
1445 1450 1455

Ala Ala Leu Asn Leu Ser Cys Arg Leu Leu Gly Gly Pro Gly Pro
1460 1465 1470

Val Gly Asn Ser Thr Phe Ala Trp Phe Trp Asn Asp Arg Arg Leu
1475 1480 1485

His Ala Glu Pro Val Pro Thr Leu Ala Phe Thr His Val Ala Arg
1490 1495 1500

Ala Gln Ala Gly Met Tyr His Cys Leu Ala Glu Leu Pro Thr Gly
1505 1510 1515

Ala Ala Ala Ser Ala Pro Val Met Leu Arg Val Leu Tyr Pro Pro
1520 1525 1530

Lys Thr Pro Thr Met Met Val Phe Val Glu Pro Glu Gly Gly Leu
1535 1540 1545

Arg Gly Ile Leu Asp Cys Arg Val Asp Ser Glu Pro Leu Ala Ser
1550 1555 1560

Leu Thr Leu His Leu Gly Ser Arg Leu Val Ala Ser Ser Gln Pro
1565 1570 1575

Gln Gly Ala Pro Ala Glu Pro His Ile His Val Leu Ala Ser Pro
1580 1585 1590

Asn Ala Leu Arg Val Asp Ile Glu Ala Leu Arg Pro Ser Asp Gln
1595 1600 1605

Gly Glu Tyr Ile Cys Ser Ala Ser Asn Val Leu Gly Ser Ala Ser
1610 1615 1620

Thr Ser Thr Tyr Phe Gly Val Arg Ala Leu His Arg Leu His Gln
1625 1630 1635

Phe Gln Gln Leu Leu Trp Val Leu Gly Leu Leu Val Gly Leu Leu
1640 1645 1650

Leu Leu Leu Leu Gly Leu Gly Ala Cys Tyr Thr Trp Arg Arg Arg
1655 1660 1665

Arg Val Cys Lys Gln Ser Met Gly Glu Asn Ser Val Glu Met Ala
1670 1675 1680

Phe Gln Lys Glu Thr Thr Gln Leu Ile Asp Pro Asp Ala Ala Thr
1685 1690 1695

Cys Glu Thr Ser Thr Cys Ala Pro Pro Leu Gly
    1700   1705

<210> 16
<211> 6736
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(6736)
<223> Siglec 1 FL

<400> 16
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tggggcgtct ccagtcccca ggacgtgcag ggtgtgaagg ggtcttgcct gcttatcccc 120

tgcatcttca gcttccctgc cgacgtggag gtgcccgacg gcatcacggc catctggtac 180

tacgactact cgggccagcg gcaggtggtg agccactcgg cggaccccaa gctggtggag 240

gcccgcttcc gcggccgcac cgagttcatg gggaaccccg agcacagggt gtgcaacctg 300

ctgctgaagg acctgcagcc cgaggactct ggttcctaca acttccgctt cgagatcagt 360

gaggtcaacc gctggtcaga tgtgaaaggc accttggtca cagtaacaga ggagcccagg 420

gtgcccacca ttgcctcccc ggtggagctt ctcgagggca cagaggtgga cttcaactgc 480

tccactccct acgtatgcct gcaggagcag gtcagactgc agtggcaagg ccaggaccct 540

gctcgctctg tcaccttcaa cagccagaag tttgagccca ccggcgtcgg ccacctggag 600

accctccaca tggccatgtc ctggcaggac cacggccgga tcctgcgctg ccagctctcc 660

gtggccaatc acagggctca gagcgagatt cacctccaag tgaagtatgc ccccaagggt 720

gtgaagatcc tcctcagccc ctcggggagg aacatccttc caggtgagct ggtcacactc 780

acctgccagg tgaacagcag ctaccctgca gtcagttcca ttaagtggct caaggatggg 840

gtacgcctcc aaaccaagac tggtgtgctg cacctgcccc aggcagcctg gagcgatgct 900

ggcgtctaca cctgccaagc tgagaacggc gtgggctctt tggtctcacc ccccatcagc 960

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<210> 17
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(301)
<223> Siglec 1 Fragment (20-320)

<400> 17

Ser Trp Gly Val Ser Ser Pro Gln Asp Val Gln Gly Val Lys Gly Ser
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Cys Leu Leu Ile Pro Cys Ile Phe Ser Phe Pro Ala Asp Val Glu Val
20 25 30

Pro Asp Gly Ile Thr Ala Ile Trp Tyr Tyr Asp Tyr Ser Gly Gln Arg
35 40 45

Gln Val Val Ser His Ser Ala Asp Pro Lys Leu Val Glu Ala Arg Phe
    50 55 60

Arg Gly Arg Thr Glu Phe Met Gly Asn Pro Glu His Arg Val Cys Asn
65 70 75 80

Leu Leu Leu Lys Asp Leu Gln Pro Glu Asp Ser Gly Ser Tyr Asn Phe
                85 90 95

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

Leu Val Thr Val Thr Glu Glu Pro Arg Val Pro Thr Ile Ala Ser Pro
        115 120 125

Val Glu Leu Leu Glu Gly Thr Glu Val Asp Phe Asn Cys Ser Thr Pro
    130 135 140

Tyr Val Cys Leu Gln Glu Gln Val Arg Leu Gln Trp Gln Gly Gln Asp
145 150 155 160

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

Val Gly His Leu Glu Thr Leu His Met Ala Met Ser Trp Gln Asp His
            180 185 190

Gly Arg Ile Leu Arg Cys Gln Leu Ser Val Ala Asn His Arg Ala Gln
        195 200 205

Ser Glu Ile His Leu Gln Val Lys Tyr Ala Pro Lys Gly Val Lys Ile
    210 215 220

Leu Leu Ser Pro Ser Gly Arg Asn Ile Leu Pro Gly Glu Leu Val Thr
225 230 235 240

Leu Thr Cys Gln Val Asn Ser Ser Tyr Pro Ala Val Ser Ser Ile Lys
                245 250 255

Trp Leu Lys Asp Gly Val Arg Leu Gln Thr Lys Thr Gly Val Leu His
            260 265 270

Leu Pro Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr Cys Gln Ala
275 280 285

Glu Asn Gly Val Gly Ser Leu Val Ser Pro Pro Ile Ser
290 295 300

<210> 18
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 1 Fragment (20-320) SAX (R97A)

<400> 18

Ser Trp Gly Val Ser Ser Pro Gln Asp Val Gln Gly Val Lys Gly Ser
1 5 10 15

Cys Leu Leu Ile Pro Cys Ile Phe Ser Phe Pro Ala Asp Val Glu Val
20 25 30

Pro Asp Gly Ile Thr Ala Ile Trp Tyr Tyr Asp Tyr Ser Gly Gln Arg
35 40 45

Gln Val Val Ser His Ser Ala Asp Pro Lys Leu Val Glu Ala Arg Phe
50 55 60

Arg Gly Arg Thr Glu Phe Met Gly Asn Pro Glu His Arg Val Cys Asn
65 70 75 80

Leu Leu Leu Lys Asp Leu Gln Pro Glu Asp Ser Gly Ser Tyr Asn Phe
85 90 95

Ala Phe Glu Ile Ser Glu Val Asn Arg Trp Ser Asp Val Lys Gly Thr
100 105 110

Leu Val Thr Val Thr Glu Glu Pro Arg Val Pro Thr Ile Ala Ser Pro
115 120 125

Val Glu Leu Leu Glu Gly Thr Glu Val Asp Phe Asn Cys Ser Thr Pro
130 135 140

Tyr Val Cys Leu Gln Glu Gln Val Arg Leu Gln Trp Gln Gly Gln Asp
145 150 155 160

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

Val Gly His Leu Glu Thr Leu His Met Ala Met Ser Trp Gln Asp His
180 185 190

Gly Arg Ile Leu Arg Cys Gln Leu Ser Val Ala Asn His Arg Ala Gln
195 200 205

Ser Glu Ile His Leu Gln Val Lys Tyr Ala Pro Lys Gly Val Lys Ile
210 215 220

Leu Leu Ser Pro Ser Gly Arg Asn Ile Leu Pro Gly Glu Leu Val Thr
225 230 235 240

Leu Thr Cys Gln Val Asn Ser Ser Tyr Pro Ala Val Ser Ser Ile Lys
245 250 255

Trp Leu Lys Asp Gly Val Arg Leu Gln Thr Lys Thr Gly Val Leu His
260 265 270

Leu Pro Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr Cys Gln Ala
275 280 285

Glu Asn Gly Val Gly Ser Leu Val Ser Pro Pro Ile Ser
290 295 300

<210> 19
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 1 Fragment (20-320) / (G4S)2 / hIgG1 Fc N297G

<400> 19

Ser Trp Gly Val Ser Ser Pro Gln Asp Val Gln Gly Val Lys Gly Ser
1 5 10 15

Cys Leu Leu Ile Pro Cys Ile Phe Ser Phe Pro Ala Asp Val Glu Val
20 25 30

Pro Asp Gly Ile Thr Ala Ile Trp Tyr Tyr Asp Tyr Ser Gly Gln Arg
35 40 45

Gln Val Val Ser His Ser Ala Asp Pro Lys Leu Val Glu Ala Arg Phe
50 55 60

Arg Gly Arg Thr Glu Phe Met Gly Asn Pro Glu His Arg Val Cys Asn
65 70 75 80

Leu Leu Leu Lys Asp Leu Gln Pro Glu Asp Ser Gly Ser Tyr Asn Phe
85 90 95

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

Leu Val Thr Val Thr Glu Glu Pro Arg Val Pro Thr Ile Ala Ser Pro
115 120 125

Val Glu Leu Leu Glu Gly Thr Glu Val Asp Phe Asn Cys Ser Thr Pro
130 135 140

Tyr Val Cys Leu Gln Glu Gln Val Arg Leu Gln Trp Gln Gly Gln Asp
145 150 155 160

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

Val Gly His Leu Glu Thr Leu His Met Ala Met Ser Trp Gln Asp His
180 185 190

Gly Arg Ile Leu Arg Cys Gln Leu Ser Val Ala Asn His Arg Ala Gln
195 200 205

Ser Glu Ile His Leu Gln Val Lys Tyr Ala Pro Lys Gly Val Lys Ile
210 215 220

Leu Leu Ser Pro Ser Gly Arg Asn Ile Leu Pro Gly Glu Leu Val Thr
225 230 235 240

Leu Thr Cys Gln Val Asn Ser Ser Tyr Pro Ala Val Ser Ser Ile Lys
245 250 255

Trp Leu Lys Asp Gly Val Arg Leu Gln Thr Lys Thr Gly Val Leu His
260 265 270

Leu Pro Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr Cys Gln Ala
275 280 285

Glu Asn Gly Val Gly Ser Leu Val Ser Pro Pro Ile Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
305 310 315 320

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
325 330 335

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
340 345 350

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
355 360 365

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
370 375 380

Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
385 390 395 400

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
405 410 415

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
420 425 430

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
435 440 445

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    450 455 460

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
465 470 475 480

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                485 490 495

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            500 505 510

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        515 520 525

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    530 535

<210> 20
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 1 Fragment (20-320) / (G4S)2 / hIgG1 Fc N297G

<400> 20
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ccctgcatct tcagcttccc cgccgatgtg gaagtgcccg atggaatcac agccatctgg 120

tactacgact acagcggcca gagacaggtg gtgtcccata gcgccgatcc taagctggtg 180

gaagcccggt ttagaggccg gaccgagttc atgggaaacc ccgagcacag agtgtgcaac 240

ctgctgctga aggacctgca gcctgaggat agcggcagct acaacttcag attcgagatc 300

agcgaagtga accgttggag cgacgtgaag ggcaccctgg tcacagtgac cgaggaaccc 360

agagtgccca caatcgcctc tccagtggaa ctgctggaag gcaccgaggt ggacttcaac 420

tgcagcaccc cttacgtgtg cctgcaagag caagttcggc tgcagtggca gggccaagat 480

cctgccagaa gcgtgacctt caacagccag aagttcgagc ctacaggcgt gggccacctg 540

gaaacactgc atatggccat gagctggcag gaccacggca gaatcctgag atgccagctg 600

agcgtggcca accacagagc ccagtctgag atccatctgc aagtgaagta cgcccctaaa 660

ggcgtgaaga ttctgctgag ccccagcggc agaaacatcc tgcctggcga actcgtgacc 720

ctgacctgcc aagtgaacag cagctaccct gccgtgtcca gcatcaagtg gctgaaagac 780

ggcgtgcggc tgcagacaaa aaccggcgtt ctgcatctgc ctcaggccgc ttggagtgac 840

gctggcgtgt acacttgtca ggccgagaat ggcgtgggca gcctggtgtc tcctcctatc 900

tctggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 960

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1020

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gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1140

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1200

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1260

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1320

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1380

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1440

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1500

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1560

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1614

<210> 21
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 1 Fragment (20-320) SAX / (G4S)2 / hIgG1 Fc
N297G

<400> 21

Ser Trp Gly Val Ser Ser Pro Gln Asp Val Gln Gly Val Lys Gly Ser
1 5 10 15

Cys Leu Leu Ile Pro Cys Ile Phe Ser Phe Pro Ala Asp Val Glu Val
20 25 30

Pro Asp Gly Ile Thr Ala Ile Trp Tyr Tyr Asp Tyr Ser Gly Gln Arg
35 40 45

Gln Val Val Ser His Ser Ala Asp Pro Lys Leu Val Glu Ala Arg Phe
50 55 60

Arg Gly Arg Thr Glu Phe Met Gly Asn Pro Glu His Arg Val Cys Asn
65 70 75 80

Leu Leu Leu Lys Asp Leu Gln Pro Glu Asp Ser Gly Ser Tyr Asn Phe
85 90 95

Ala Phe Glu Ile Ser Glu Val Asn Arg Trp Ser Asp Val Lys Gly Thr
100 105 110

Leu Val Thr Val Thr Glu Glu Pro Arg Val Pro Thr Ile Ala Ser Pro
115 120 125

Val Glu Leu Leu Glu Gly Thr Glu Val Asp Phe Asn Cys Ser Thr Pro
130 135 140

Tyr Val Cys Leu Gln Glu Gln Val Arg Leu Gln Trp Gln Gly Gln Asp
145 150 155 160

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

Val Gly His Leu Glu Thr Leu His Met Ala Met Ser Trp Gln Asp His
180 185 190

Gly Arg Ile Leu Arg Cys Gln Leu Ser Val Ala Asn His Arg Ala Gln
195 200 205

Ser Glu Ile His Leu Gln Val Lys Tyr Ala Pro Lys Gly Val Lys Ile
210 215 220

Leu Leu Ser Pro Ser Gly Arg Asn Ile Leu Pro Gly Glu Leu Val Thr
225 230 235 240

Leu Thr Cys Gln Val Asn Ser Ser Tyr Pro Ala Val Ser Ser Ile Lys

245 250 255

Trp Leu Lys Asp Gly Val Arg Leu Gln Thr Lys Thr Gly Val Leu His
260 265 270

Leu Pro Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr Cys Gln Ala
275 280 285

Glu Asn Gly Val Gly Ser Leu Val Ser Pro Pro Ile Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
305 310 315 320

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
325 330 335

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
340 345 350

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
355 360 365

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
370 375 380

Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
385 390 395 400

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
405 410 415

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
420 425 430

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
435 440 445

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
450 455 460

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
465 470 475 480

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
485 490 495

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
500 505 510

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
515 520 525

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
530 535

<210> 22
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 1 Fragment (20-320) SAX / (G4S)2 / hIgG1 Fc N297G

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ccctgcatct tcagcttccc cgccgatgtg gaagtgcccg atggaatcac agccatctgg 120

tactacgact acagcggcca gagacaggtg gtgtcccata gcgccgatcc taagctggtg 180

gaagcccggt ttagaggccg gaccgagttc atgggaaacc ccgagcacag agtgtgcaac 240

ctgctgctga aggacctgca gcctgaggat agcggcagct acaacttcgc cttcgagatc 300

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agagtgccca caatcgcctc tccagtggaa ctgctggaag gcaccgaggt ggacttcaac 420

tgcagcaccc cttacgtgtg cctgcaagag caagttcggc tgcagtggca gggccaagat 480

cctgccagaa gcgtgacctt caacagccag aagttcgagc ctacaggcgt gggccacctg 540

gaaacactgc atatggccat gagctggcag gaccacggca gaatcctgag atgccagctg 600

agcgtggcca accacagagc ccagtctgag atccatctgc aagtgaagta cgcccctaaa 660

ggcgtgaaga ttctgctgag ccccagcggc agaaacatcc tgcctggcga actcgtgacc 720

ctgacctgcc aagtgaacag cagctaccct gccgtgtcca gcatcaagtg gctgaaagac 780

ggcgtgcggc tgcagacaaa aaccggcgtt ctgcatctgc ctcaggccgc ttggagtgac 840

gctggcgtgt acacttgtca ggccgagaat ggcgtgggca gcctggtgtc tcctcctatc 900

tctggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 960

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1020

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1080

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1140

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1200

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1260

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1320

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1380

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1440

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1500

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1560

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1614

<210> 23
<211> 847
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(847)
<223> Siglec 2 FL

<400> 23

Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
1 5 10 15

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

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala

35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
50 55 60

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

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
195 200 205

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

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
225 230 235 240

Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg
245 250 255

Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro
260 265 270

Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys
275 280 285

Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser
290 295 300

Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
305 310 315 320

Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
325 330 335

Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
340 345 350

Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
355 360 365

Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
370 375 380

Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
385 390 395 400

Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
420 425 430

Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
435 440 445

Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
450 455 460

Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr

465 470 475 480

Thr Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
485 490 495

Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
500 505 510

Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
515 520 525

Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
530 535 540

Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
545 550 555 560

Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser
565 570 575

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

Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu
595 600 605

Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
610 615 620

Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His
625 630 635 640

Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
645 650 655

Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
660 665 670

Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
675 680 685

Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
690 695 700

Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
705 710 715 720

Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys
725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
770 775 780

Arg Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
835 840 845

<210> 24
<211> 2544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2544)
<223> Siglec 2 FL

<400> 24
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tcaagtaaat gggtttttga gcaccctgaa accctctacg cctgggaggg ggcctgcgtc 120

tggatcccct gcacctacag agccctagat ggtgacctgg aaagcttcat cctgttccac 180

aatcctgagt ataacaagaa cacctcgaag tttgatggga caagactcta tgaaagcaca 240

aaggatggga aggttccttc tgagcagaaa agggtgcaat tcctgggaga caagaataag 300

aactgcacac tgagtatcca cccggtgcac ctcaatgaca gtggtcagct ggggctgagg 360

atggagtcca agactgagaa atggatggaa cgaatacacc tcaatgtctc tgaaaggcct 420

tttccacctc atatccagct ccctccagaa attcaagagt cccaggaagt cactctgacc 480

tgcttgctga atttctcctg ctatgggtat ccgatccaat tgcagtggct cctagagggg 540

gttccaatga ggcaggctgc tgtcacctcg acctccttga ccatcaagtc tgtcttcacc 600

cggagcgagc tcaagttctc cccacagtgg agtcaccatg ggaagattgt gacctgccag 660

cttcaggatg cagatgggaa gttcctctcc aatgacacgg tgcagctgaa cgtgaagcac 720

accccgaagt tggagatcaa ggtcactccc agtgatgcca tagtgaggga gggggactct 780

gtgaccatga cctgcgaggt cagcagcagc aacccggagt acacgacggt atcctggctc 840

aaggatggga cctcgctgaa gaagcagaat acattcacgc taaacctgcg cgaagtgacc 900

aaggaccaga gtgggaagta ctgctgtcag gtctccaatg acgtgggccc gggaaggtcg 960

gaagaagtgt tcctgcaagt gcagtatgcc ccggaacctt ccacggttca gatcctccac 1020

tcaccggctg tggagggaag tcaagtcgag tttctttgca tgtcactggc caatcctctt 1080

ccaacaaatt acacgtggta ccacaatggg aaagaaatgc agggaaggac agaggagaaa 1140

gtccacatcc caaagatcct cccctggcac gctgggactt attcctgtgt ggcagaaaac 1200

attcttggta ctggacagag gggcccggga gctgagctgg atgtccagta tcctcccaag 1260

aaggtgacca cagtgattca aaaccccatg ccgattcgag aaggagacac agtgaccctt 1320

tcctgtaact acaattccag taaccccagt gttacccggt atgaatggaa accccatggc 1380

gcctgggagg agccatcgct tggggtgctg aagatccaaa acgttggctg ggacaacaca 1440

accatcgcct gcgcagcttg taatagttgg tgctcgtggg cctcccctgt cgccctgaat 1500

gtccagtatg ccccccgaga cgtgagggtc cggaaaatca agcccctttc cgagattcac 1560

tctggaaact cggtcagcct ccaatgtgac ttctcaagca gccaccccaa agaagtccag 1620

ttcttctggg agaaaaatgg caggcttctg gggaaagaaa gccagctgaa ttttgactcc 1680

atctccccag aagatgctgg gagttacagc tgctgggtga acaactccat aggacagaca 1740

gcgtccaagg cctggacact tgaagtgctg tatgcaccca ggaggctgcg tgtgtccatg 1800

agcccggggg accaagtgat ggaggggaag agtgcaaccc tgacctgtga gagcgacgcc 1860

aaccctcccg tctcccacta cacctggttt gactggaata accaaagcct cccctaccac 1920

agccagaagc tgagattgga gccggtgaag gtccagcact cgggtgccta ctggtgccag 1980

gggaccaaca gtgtgggcaa gggccgttcg cctctcagca ccctcaccgt ctactatagc 2040

ccggagacca tcggcaggcg agtggctgtg ggactcgggt cctgcctcgc catcctcatc 2100

ctggcaatct gtgggctcaa gctccagcga cgttggaaga ggacacagag ccagcagggg 2160

cttcaggaga attccagcgg ccagagcttc tttgtgagga ataaaaaggt tagaagggcc 2220

cccctctctg aaggccccca ctccctggga tgctacaatc caatgatgga agatggcatt 2280

agctacacca ccctgcgctt tcccgagatg aacataccac gaactggaga tgcagagtcc 2340

tcagagatgc agagacctcc cccggactgc gatgacacgg tcacttattc agcattgcac 2400

aagcgccaag tgggcgacta tgagaacgtc attccagatt ttccagaaga tgaggggatt 2460

cattactcag agctgatcca gtttggggtc ggggagcggc ctcaggcaca agaaaatgtg 2520

gactatgtga tcctcaaaca ttga 2544

<210> 25
<211> 364
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(364)
<223> Siglec 3 FL

<400> 25

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
20 25 30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro

35 40 45

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

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

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
85 90 95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
100 105 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
115 120 125

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

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145 150 155 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
165 170 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
180 185 190

His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr
195 200 205

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
210 215 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225 230 235 240

Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
245 250 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
260 265 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
275 280 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
290 295 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305 310 315 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
325 330 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
340 345 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
355 360

<210> 26
<211> 1466
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1466)
<223> Siglec 3 FL

<400> 26
tctgctcaca caggaagccc tggaagctgc ttcctcagac atgccgctgc tgctactgct 60

gcccctgctg tgggcagggg ccctggctat ggatccaaat ttctggctgc aagtgcagga 120

gtcagtgacg gtacaggagg gtttgtgcgt cctcgtgccc tgcactttct tccatcccat 180

accctactac gacaagaact ccccagttca tggttactgg ttccgggaag gagccattat 240

atccagggac tctccagtgg ccacaaacaa gctagatcaa gaagtacagg aggagactca 300

gggcagattc cgcctccttg gggatcccag taggaacaac tgctccctga gcatcgtaga 360

cgccaggagg agggataatg gttcatactt ctttcggatg gagagaggaa gtaccaaata 420

cagttacaaa tctccccagc tctctgtgca tgtgacagac ttgacccaca ggcccaaaat 480

cctcatccct ggcactctag aacccggcca ctccaaaaac ctgacctgct ctgtgtcctg 540

ggcctgtgag cagggaacac ccccgatctt ctcctggttg tcagctgccc ccacctccct 600

gggccccagg actactcact cctcggtgct cataatcacc ccacggcccc aggaccacgg 660

caccaacctg acctgtcagg tgaagttcgc tggagctggt gtgactacgg agagaaccat 720

ccagctcaac gtcacctatg ttccacagaa cccaacaact ggtatctttc caggagatgg 780

ctcagggaaa caagagacca gagcaggagt ggttcatggg gccattggag gagctggtgt 840

tacagccctg ctcgctcttt gtctctgcct catcttcttc atagtgaaga cccacaggag 900

gaaagcagcc aggacagcag tgggcaggaa tgacacccac cctaccacag ggtcagcctc 960

cccgaaacac cagaagaagt ccaagttaca tggccccact gaaacctcaa gctgttcagg 1020

tgccgcccct actgtggaga tggatgagga gctgcattat gcttccctca actttcatgg 1080

gatgaatcct tccaaggaca cctccaccga atactcagag gtcaggaccc agtgaggaac 1140

ccacaagagc atcaggctca gctagaagat ccacatcctc tacaggtcgg ggaccaaagg 1200

ctgattcttg gagatttaac accccacagg caatgggttt atagacatta tgtgagtttc 1260

ctgctatatt aacatcatct tagactttgc aagcagagag tcgtggaatc aaatctgtgc 1320

tctttcattt gctaagtgta tgatgtcaca caagctcctt aaccttccat gtctccattt 1380

tcttctctgt gaagtaggta taagaagtcc tatctcatag ggatgctgtg agcattaaat 1440

aaaggtacac atggaaaaca ccagtc 1466

<210> 27
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(117)
<223> Siglec 3 V-Set (23-139)

<400> 27

Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu Gly Leu Cys Val Leu
1 5 10 15

Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr Tyr Asp Lys Asn Ser
20 25 30

Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala Ile Ile Ser Arg Asp
35 40 45

Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu Val Gln Glu Glu Thr
50 55 60

Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro Ser Arg Asn Asn Cys Ser
65 70 75 80

Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn Gly Ser Tyr Phe Phe
85 90 95

Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr Lys Ser Pro Gln Leu
100 105 110

Ser Val His Val Thr
115

<210> 28
<211> 205
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(205)
<223> Siglec 3 V-Set Domain + 1 C2-Set Domain (23-227)

<400> 28

Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu Gly Leu Cys Val Leu
1 5 10 15

Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr Tyr Asp Lys Asn Ser
20 25 30

Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala Ile Ile Ser Arg Asp
35 40 45

Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu Val Gln Glu Glu Thr
    50 55 60

Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro Ser Arg Asn Asn Cys Ser
65 70 75 80

Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn Gly Ser Tyr Phe Phe
                85 90 95

Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr Lys Ser Pro Gln Leu
            100 105 110

Ser Val His Val Thr Asp Leu Thr His Arg Pro Lys Ile Leu Ile Pro
        115 120 125

Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu Thr Cys Ser Val Ser
    130 135 140

Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Leu Ser Ala
145 150 155 160

Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His Ser Ser Val Leu Ile
                165 170 175

Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn Leu Thr Cys Gln Val
            180 185 190

Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg Thr Ile
        195 200 205

<210> 29
<211> 242
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(242)
<223> Siglec 3 Fragment (18-259)

<400> 29

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu

1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His

<210> 30
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) SAX

<400> 30

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Lys Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His

<210> 31
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) SAX / AS / hIgG1 Fc N297G

<400> 31

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Lys Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His Ala Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

275 280 285

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

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

Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

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

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 32
<211> 1413
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) SAX / AS / hIgG1 Fc N297G

<400> 32
gatcccaatt tctggctgca agtgcaagag tccgtgaccg tgcaagaggg cctgtgtgtg 60

ctggtgccct gcaccttctt tcaccccatt ccttactacg acaagaacag ccctgtgcac 120

ggctactggt ttagagaggg cgccatcatc agcagagata gccctgtggc caccaacaag 180

ctggaccaag aggtgcaaga agagacacag ggcagattca gactgctggg cgaccccagc 240

agaaacaact gcagcctgtc tatcgtggac gccaggcgga gagacaacgg cagctacttc 300

ttcaagatgg aacggggcag caccaagtac agctacaaga gccctcagct gtccgtgcac 360

gtgaccgacc tgacacacag acccaagatt ctgatccccg gcacactgga acctggccac 420

agcaagaatc tgacctgctc cgtgtcctgg gcctgcgaac agggaacccc tcctatcttt 480

agctggctga gcgccgctcc tacatctctg ggccctagaa caacacacag cagcgtgctg 540

atcatcaccc ctagacctca ggaccacggc accaacctga cctgccaagt gaaatttgct 600

ggcgctggcg tgaccaccga gagaaccatc cagctgaacg tgacctacgt gccacagaac 660

cctaccaccg gcatctttcc aggcgacggc tctggcaagc aagaaacaag agctggcgtg 720

gtgcacgcta gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1260

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acgcagaaga gcctctccct gtctccgggt aaa 1413

<210> 33
<211> 626
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(626)
<223> Siglec 4 FL

<400> 33

Met Ile Phe Leu Thr Ala Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15

Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30

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

Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60

Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65 70 75 80

Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
85 90 95

Leu Arg Asn Cys Thr Leu Leu Leu Ser Asn Val Ser Pro Glu Leu Gly
100 105 110

Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
115 120 125

Phe Ser Glu His Ser Val Leu Asp Ile Val Asn Thr Pro Asn Ile Val
130 135 140

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

Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
165 170 175

His Glu Gly Leu Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp
180 185 190

Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
195 200 205

Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr
210 215 220

Thr Leu Gln Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro
225 230 235 240

Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
245 250 255

Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
260 265 270

Trp Met Arg Asp Gly Thr Val Leu Arg Glu Ala Val Ala Glu Ser Leu
275 280 285

Leu Leu Glu Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Val Tyr Ala
290 295 300

Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Gly Leu
305 310 315 320

Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Met Val
325 330 335

Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
340 345 350

Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ser Thr
355 360 365

Val Ile Tyr Glu Ser Glu Leu Gln Leu Glu Leu Pro Ala Val Ser Pro
370 375 380

Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
385 390 395 400

Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu
405 410 415

Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
420 425 430

Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
435 440 445

Arg Asn Val Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu
450 455 460

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

Gln Ala Pro Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly Ala
485 490 495

Lys Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met Trp Ala
500 505 510

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

Ile Val Cys Tyr Ile Thr Gln Thr Arg Arg Lys Lys Asn Val Thr Glu
530 535 540

Ser Pro Ser Phe Ser Ala Gly Asp Asn Pro Pro Val Leu Phe Ser Ser
545 550 555 560

Asp Phe Arg Ile Ser Gly Ala Pro Glu Lys Tyr Glu Ser Glu Arg Arg
565 570 575

Leu Gly Ser Glu Arg Arg Leu Leu Gly Leu Arg Gly Glu Pro Pro Glu
580 585 590

Leu Asp Leu Ser Tyr Ser His Ser Asp Leu Gly Lys Arg Pro Thr Lys
595 600 605

Asp Ser Tyr Thr Leu Thr Glu Glu Leu Ala Glu Tyr Ala Glu Ile Arg
610 615 620

Val Lys
625

<210> 34
<211> 1881
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1881)
<223> Siglec 4 FL

<400> 34
atgatattcc tcacggcact gcctctgttc tggattatga tttcagcctc ccgaggggt 60

cactggggtg cctggatgcc ctcgtccatc tcggccttcg aaggcacgtg cgtctccatc 120

ccctgccgct ttgacttccc ggatgagctg cggcccgctg tggtgcatgg tgtctggtac 180

ttcaatagcc cctaccccaa gaactacccc ccggtggtct tcaagtcgcg cacccaagta 240

gtccacgaga gcttccaggg ccgcagccgc ctcctggggg acctgggcct gcgaaactgc 300

accctcctgc tcagcaacgt cagccccgag ctgggcggga agtactactt ccgtggggac 360

ctgggcggct acaaccagta caccttctca gagcacagcg tcctggatat cgtcaacacc 420

cccaacatcg tggtgccccc agaggtggtg gcaggcacgg aggtggaggt cagctgcatg 480

gtgccggaca actgcccaga gctgcgccct gagctgagct ggctgggcca cgaggggctg 540

ggggagcccg ctgtgctggg ccggctgcgg gaggacgagg gcacctgggt gcaggtgtca 600

ctgctgcact tcgtgcccac gagggaggcc aacggccaca ggctgggctg ccaggcctcc 660

ttccccaaca ccaccctgca gttcgagggc tacgccagca tggacgtcaa gtacccccg 720

gtgattgtgg agatgaactc ctcggtggag gccatcgagg gctcccacgt gagcctgctc 780

tgtggggctg acagcaaccc cccgccgctg ctgacctgga tgcgggacgg gacagtcctc 840

cgggaggcgg tggccgagag cctgctcctg gagctggagg aggtgacccc cgccgaagac 900

ggcgtctatg cctgcctggc cgagaatgcc tatggccagg acaaccgcac cgtggggctc 960

agtgtcatgt atgcaccctg gaagccaaca gtgaacggga caatggtggc cgtagagggg 1020

gagacggtct ctatcttgtg ctccacacag agcaacccgg accctattct caccatcttc 1080

aaggagaagc agatcctgtc cacggtcatc tacgagagcg agctgcagct ggagctgccg 1140

gccgtgtcac ccgaggatga tggagagtac tggtgtgtgg ctgagaacca gtatggccag 1200

agggccaccg ccttcaacct gtctgtggag ttcgcccctg tgctcctcct ggagtcccac 1260

tgcgcggcag cccgagacac ggtgcagtgc ctgtgcgtgg tgaagtccaa cccggagccg 1320

tccgtggcct ttgagctgcc atcgcgcaat gtgaccgtga acgagagcga gcgggagttc 1380

gtgtactcgg agcgcagcgg cctcgtgctc accagcatcc tcacgctgcg ggggcaggcc 1440

caggccccgc cccgcgtcat ctgcaccgcg aggaacctct atggcgccaa gagcctggag 1500

ctgcccttcc agggagccca tcgactgatg tgggccaaga tcgggcctgt gggcgccgtg 1560

gtcgcctttg ccatcctgat tgccatcgtc tgctacatta cccagacacg caggaaaaag 1620

aacgtgacag agagccccag cttctcggca ggggacaacc ctcccgtcct gttcagcagc 1680

gacttccgca tctctggggc accagagaag tacgagagcg agaggcgcct gggatctgag 1740

aggaggctgc tgggccttcg gggtgagccc ccagagctgg acctgagcta ttctcactcg 1800

gacctgggga aacggcccac caaggacagc tacacgctga cggaggagct agctgagtat 1860

gctgaaatcc gggtcaagtg a 1881

<210> 35
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(497)
<223> Siglec 4 Fragment (20-516)

<400> 35

Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala Phe Glu Gly
1 5 10 15

Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp Glu Leu Arg
20 25 30

Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro Tyr Pro Lys
35 40 45

Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val Val His Glu
50 55 60

Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly Leu Arg Asn
65 70 75 80

Cys Thr Leu Leu Leu Ser Asn Val Ser Pro Glu Leu Gly Gly Lys Tyr
85 90 95

Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr Phe Ser Glu
100 105 110

His Ser Val Leu Asp Ile Val Asn Thr Pro Asn Ile Val Val Pro Pro
115 120 125

Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met Val Pro Asp
130 135 140

Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly His Glu Gly
145 150 155 160

Leu Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp Glu Gly Thr
165 170 175

Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg Glu Ala Asn
180 185 190

Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr Thr Leu Gln
195 200 205

Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro Val Ile Val
210 215 220

Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His Val Ser Leu
225 230 235 240

Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr Trp Met Arg
245 250 255

Asp Gly Thr Val Leu Arg Glu Ala Val Ala Glu Ser Leu Leu Leu Glu
260 265 270

Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Val Tyr Ala Cys Leu Ala
275 280 285

Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Gly Leu Ser Val Met
290 295 300

Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Met Val Ala Val Glu
305 310 315 320

Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn Pro Asp Pro
325 330 335

Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ser Thr Val Ile Tyr
340 345 350

Glu Ser Glu Leu Gln Leu Glu Leu Pro Ala Val Ser Pro Glu Asp Asp
355 360 365

Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg Ala Thr
370 375 380

Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu Leu Glu Ser
385 390 395 400

His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys Val Val Lys
405 410 415

Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser Arg Asn Val
420 425 430

Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu Arg Ser Gly
435 440 445

Leu Val Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala Gln Ala Pro
450 455 460

Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly Ala Lys Ser Leu
465 470 475 480

Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met Trp Ala Lys Ile Gly
485 490 495

Pro

<210> 36
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 4 Fragment (20-516) SAX

<400> 36

Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala Phe Glu Gly
1 5 10 15

Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp Glu Leu Arg
20 25 30

Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro Tyr Pro Lys
35 40 45

Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val Val His Glu
50 55 60

Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly Leu Arg Asn
65 70 75 80

Cys Thr Leu Leu Leu Ser Asn Val Ser Pro Glu Leu Gly Gly Lys Tyr
85 90 95

Tyr Phe Ala Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr Phe Ser Glu
100 105 110

His Ser Val Leu Asp Ile Val Asn Thr Pro Asn Ile Val Val Pro Pro
115 120 125

Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met Val Pro Asp
130 135 140

Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly His Glu Gly
145 150 155 160

Leu Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp Glu Gly Thr
165 170 175

Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg Glu Ala Asn
180 185 190

Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr Thr Leu Gln
195 200 205

Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro Val Ile Val
210 215 220

Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His Val Ser Leu
225 230 235 240

Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr Trp Met Arg
245 250 255

Asp Gly Thr Val Leu Arg Glu Ala Val Ala Glu Ser Leu Leu Leu Glu
260 265 270

Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Val Tyr Ala Cys Leu Ala
275 280 285

Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Gly Leu Ser Val Met
290 295 300

Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Met Val Ala Val Glu
305 310 315 320

Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn Pro Asp Pro
325 330 335

Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ser Thr Val Ile Tyr
340 345 350

Glu Ser Glu Leu Gln Leu Glu Leu Pro Ala Val Ser Pro Glu Asp Asp
355 360 365

Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg Ala Thr
370 375 380

Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu Leu Glu Ser
385 390 395 400

His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys Val Val Lys
405 410 415

Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser Arg Asn Val
420 425 430

Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu Arg Ser Gly
435 440 445

Leu Val Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala Gln Ala Pro
450 455 460

Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly Ala Lys Ser Leu
465 470 475 480

Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met Trp Ala Lys Ile Gly
485 490 495

Pro

<210> 37
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 4 Fragment (20-516) / (G4S)2 / hIgG1 Fc N297G

<400> 37

Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala Phe Glu Gly
1 5 10 15

Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp Glu Leu Arg
20 25 30

Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro Tyr Pro Lys
35 40 45

Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val Val His Glu
50 55 60

Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly Leu Arg Asn
65 70 75 80

Cys Thr Leu Leu Leu Ser Asn Val Ser Pro Glu Leu Gly Gly Lys Tyr
85 90 95

Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr Phe Ser Glu
100 105 110

His Ser Val Leu Asp Ile Val Asn Thr Pro Asn Ile Val Val Pro Pro
115 120 125

Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met Val Pro Asp
130 135 140

Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly His Glu Gly
145 150 155 160

Leu Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp Glu Gly Thr
165 170 175

Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg Glu Ala Asn
180 185 190

Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr Thr Leu Gln
195 200 205

Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro Val Ile Val
210 215 220

Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His Val Ser Leu
225 230 235 240

Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr Trp Met Arg
245 250 255

Asp Gly Thr Val Leu Arg Glu Ala Val Ala Glu Ser Leu Leu Leu Glu
260 265 270

Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Val Tyr Ala Cys Leu Ala
275 280 285

Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Gly Leu Ser Val Met
290 295 300

Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Met Val Ala Val Glu
305 310 315 320

Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn Pro Asp Pro
325 330 335

Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ser Thr Val Ile Tyr
340 345 350

Glu Ser Glu Leu Gln Leu Glu Leu Pro Ala Val Ser Pro Glu Asp Asp
355 360 365

Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg Ala Thr
370 375 380

Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu Leu Glu Ser
385 390 395 400

His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys Val Val Lys
405 410 415

Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser Arg Asn Val
420 425 430

Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu Arg Ser Gly
435 440 445

Leu Val Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala Gln Ala Pro
450 455 460

Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly Ala Lys Ser Leu
465 470 475 480

Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met Trp Ala Lys Ile Gly
485 490 495

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
500 505 510

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
515 520 525

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
530 535 540

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
545 550 555 560

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
565 570 575

Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val
580 585 590

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
595 600 605

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
610 615 620

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
625 630 635 640

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
645 650 655

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
660 665 670

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
675 680 685

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
690 695 700

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
705 710 715 720

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 38
<211> 2202
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 4 Fragment (20-516) / (G4S)2 / hIgG1 Fc N297G

<400> 38
ggacattggg gagcctggat gcctagcagc atcagcgcct ttgagggaac ctgtgtgtca 60

atcccctgca gattcgactt ccccgacgaa ctgaggcctg ctgtggttca cggcgtgtgg 120

tacttcaaca gcccctatcc taagaactac cctcctgtgg tgttcaagag cagaacccag 180

gtggtgcacg agagcttcca gggcagatct agactgctgg gcgatctggg cctgagaaac 240

tgtacactgc tgctgagcaa cgtgtcccct gaactcggcg gcaagtacta cttcagaggc 300

gatctcggcg gctacaacca gtacaccttt agcgagcaca gcgtgctgga catcgtgaac 360

acccctaaca tcgtggtgcc tccagaagtg gtggccggca cagaggtgga agtgtcctgt 420

atggtgcccg acaactgccc tgagctgagg ccagaactgt cttggctggg acacgaagga 480

ctgggagaac ctgctgttct gggcagactg agagaggacg aaggcacctg ggtgcaagtg 540

tccctgctgc actttgtgcc taccagagag gccaacggcc acagactggg ttgtcaggcc 600

agctttccca acaccacact gcagtttgag ggctacgcca gcatggacgt gaagtaccct 660

ccagtgatcg tggaaatgaa cagcagcgtg gaagccatcg agggctctca tgtgtctctg 720

ctgtgtggcg ccgacagcaa tcctcctcct ctgctgacct ggatgagaga tggcaccgtg 780

ctgagagaag ccgtggccga atctctgctg ctggaactgg aagaagtgac ccctgccgag 840

gatggcgtgt acgcttgtct ggccgagaat gcctacggcc aggacaatag aaccgtgggc 900

ctgtccgtga tgtacgcccc ttggaagcct accgtgaacg gcacaatggt ggccgtggaa 960

ggcgagacag tgtccatcct gtgtagcacc cagagcaacc ccgatcctat cctgaccatc 1020

ttcaaagaga agcagatcct gagcaccgtg atctacgaga gcgaactgca gctcgaactg 1080

cccgctgtgt ccccagagga tgatggcgaa tattggtgcg tggcagagaa ccagtacggc 1140

cagagagcca ccgccttcaa cctgagcgtg gaatttgctc ccgtgctgct gctcgagagc 1200

cattgtgctg ccgccagaga taccgtgcag tgcctgtgtg tggtcaagtc taaccccgag 1260

cctagcgtgg cctttgagct gcccagcaga aacgtgaccg tgaatgagag cgagcgcgag 1320

ttcgtgtaca gcgagagatc tggactggtg ctgaccagca tcctgacact gagaggacag 1380

gctcaggccc ctcctagagt gatctgcacc gccagaaatc tgtacggcgc caagagcctg 1440

gaactgccat ttcagggcgc ccacagactc atgtgggcca agattggacc tggcggaggt 1500

ggaagtggcg gaggcggatc cgacaaaact cacacatgcc caccgtgccc agcacctgaa 1560

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1620

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1680

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1740

gagcagtacg gtagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1800

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1860

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtctacac cctgccccca 1920

tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1980

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 2040

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 2100

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2160

aaccactaca cgcagaagag cctctccctg tctccgggta aa 2202

<210> 39
<211> 734

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 4 Fragment (20-516) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 39

Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala Phe Glu Gly
1 5 10 15

Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp Glu Leu Arg
20 25 30

Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro Tyr Pro Lys
35 40 45

Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val Val His Glu
50 55 60

Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly Leu Arg Asn
65 70 75 80

Cys Thr Leu Leu Leu Ser Asn Val Ser Pro Glu Leu Gly Gly Lys Tyr
85 90 95

Tyr Phe Ala Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr Phe Ser Glu
100 105 110

His Ser Val Leu Asp Ile Val Asn Thr Pro Asn Ile Val Val Pro Pro
115 120 125

Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met Val Pro Asp
130 135 140

Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly His Glu Gly
145 150 155 160

Leu Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp Glu Gly Thr
165 170 175

Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg Glu Ala Asn

180 185 190

Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr Thr Leu Gln
195 200 205

Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro Val Ile Val
210 215 220

Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His Val Ser Leu
225 230 235 240

Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr Trp Met Arg
245 250 255

Asp Gly Thr Val Leu Arg Glu Ala Val Ala Glu Ser Leu Leu Leu Glu
260 265 270

Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Val Tyr Ala Cys Leu Ala
275 280 285

Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Gly Leu Ser Val Met
290 295 300

Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Met Val Ala Val Glu
305 310 315 320

Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn Pro Asp Pro
325 330 335

Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ser Thr Val Ile Tyr
340 345 350

Glu Ser Glu Leu Gln Leu Glu Leu Pro Ala Val Ser Pro Glu Asp Asp
355 360 365

Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg Ala Thr
370 375 380

Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu Leu Glu Ser
385 390 395 400

His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys Val Val Lys
405 410 415

Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser Arg Asn Val
420 425 430

Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu Arg Ser Gly
435 440 445

Leu Val Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala Gln Ala Pro
450 455 460

Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly Ala Lys Ser Leu
465 470 475 480

Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met Trp Ala Lys Ile Gly
485 490 495

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
500 505 510

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
515 520 525

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
530 535 540

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
545 550 555 560

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
565 570 575

Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val
580 585 590

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
595 600 605

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

610 615 620

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
625 630 635 640

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
645 650 655

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
660 665 670

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
675 680 685

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
690 695 700

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
705 710 715 720

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 40
<211> 2202
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 4 Fragment (20-516) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 40
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atcccctgca gattcgactt ccccgacgaa ctgaggcctg ctgtggttca cggcgtgtgg 120

tacttcaaca gcccctatcc taagaactac cctcctgtgg tgttcaagag cagaacccag 180

gtggtgcacg agagcttcca gggcagatct agactgctgg gcgatctggg cctgagaaac 240

tgtacactgc tgctgagcaa cgtgtcccct gaactcggcg gcaagtacta cttcgccggc 300

gatctcggcg gctacaacca gtacaccttt agcgagcaca gcgtgctgga catcgtgaac 360

acccctaaca tcgtggtgcc tccagaagtg gtggccggca cagaggtgga agtgtcctgt 420

atggtgcccg acaactgccc tgagctgagg ccagaactgt cttggctggg acacgaagga 480

ctgggagaac ctgctgttct gggcagactg agagaggacg aaggcacctg ggtgcaagtg 540

tccctgctgc actttgtgcc taccagagag gccaacggcc acagactggg ttgtcaggcc 600

agctttccca acaccacact gcagtttgag ggctacgcca gcatggacgt gaagtaccct 660

ccagtgatcg tggaaatgaa cagcagcgtg gaagccatcg agggctctca tgtgtctctg 720

ctgtgtggcg ccgacagcaa tcctcctcct ctgctgacct ggatgagaga tggcaccgtg 780

ctgagagaag ccgtggccga atctctgctg ctggaactgg aagaagtgac ccctgccgag 840

gatggcgtgt acgcttgtct ggccgagaat gcctacggcc aggacaatag aaccgtgggc 900

ctgtccgtga tgtacgcccc ttggaagcct accgtgaacg gcacaatggt ggccgtggaa 960

ggcgagacag tgtccatcct gtgtagcacc cagagcaacc ccgatcctat cctgaccatc 1020

ttcaaagaga agcagatcct gagcaccgtg atctacgaga gcgaactgca gctcgaactg 1080

cccgctgtgt ccccagagga tgatggcgaa tattggtgcg tggcagagaa ccagtacggc 1140

cagagagcca ccgccttcaa cctgagcgtg gaatttgctc ccgtgctgct gctcgagagc 1200

cattgtgctg ccgccagaga taccgtgcag tgcctgtgtg tggtcaagtc taaccccgag 1260

cctagcgtgg cctttgagct gcccagcaga aacgtgaccg tgaatgagag cgagcgcgag 1320

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tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1980

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 2040

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 2100

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2160

aaccactaca cgcagaagag cctctccctg tctccgggta aa 2202

<210> 41
<211> 551
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(551)
<223> Siglec 5 FL

<400> 41

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
35 40 45

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

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
65 70 75 80

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
85 90 95

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

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
115 120 125

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu

130 135 140

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
145 150 155 160

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
165 170 175

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
180 185 190

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
195 200 205

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
210 215 220

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
225 230 235 240

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
245 250 255

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
260 265 270

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
275 280 285

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
290 295 300

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
305 310 315 320

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
325 330 335

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
340 345 350

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
355 360 365

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
370 375 380

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
385 390 395 400

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
405 410 415

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
420 425 430

Gly Thr Gly Val Val Pro Ala Ala Leu Gly Gly Ala Gly Val Met Ala
435 440 445

Leu Leu Cys Ile Cys Leu Cys Leu Ile Phe Phe Leu Ile Val Lys Ala
450 455 460

Arg Arg Lys Gln Ala Ala Gly Arg Pro Glu Lys Met Asp Asp Glu Asp
465 470 475 480

Pro Ile Met Gly Thr Ile Thr Ser Gly Ser Arg Lys Lys Pro Trp Pro
485 490 495

Asp Ser Pro Gly Asp Gln Ala Ser Pro Pro Gly Asp Ala Pro Pro Leu
500 505 510

Glu Glu Gln Lys Glu Leu His Tyr Ala Ser Leu Ser Phe Ser Glu Met
515 520 525

Lys Ser Arg Glu Pro Lys Asp Gln Glu Ala Pro Ser Thr Thr Glu Tyr
530 535 540

Ser Glu Ile Lys Thr Ser Lys
545 550

<210> 42

<211> 2523
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2523)
<223> Siglec 5 FL

<400> 42
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ggccctggcg gatggagaca tgctgcccct gctgctgctg cccctgctgt ggggggggtc 180

cctgcaggag aagccagtgt acgagctgca agtgcagaag tcggtgacgg tgcaggaggg 240

cctgtgcgtc cttgtgccct gctccttctc ttacccctgg agatcctggt attcctctcc 300

cccactctac gtctactggt tccgggacgg ggagatccca tactacgctg aggttgtggc 360

cacaaacaac ccagacagaa gagtgaagcc agagacccag ggccgattcc gcctccttgg 420

ggatgtccag aagaagaact gctccctgag catcggagat gccagaatgg aggacacggg 480

aagctatttc ttccgcgtgg agagaggaag ggatgtaaaa tatagctacc aacagaataa 540

gctgaacttg gaggtgacag ccctgataga gaaacccgac atccactttc tggagcctct 600

ggagtccggc cgccccacaa ggctgagctg cagccttcca ggatcctgtg aagcgggacc 660

acctctcaca ttctcctgga cggggaatgc cctcagcccc ctggaccccg agaccacccg 720

ctcctcggag ctcaccctca cccccaggcc cgaggaccat ggcaccaacc tcacctgtca 780

gatgaaacgc caaggagctc aggtgaccac ggagagaact gtccagctca atgtctccta 840

tgctccacag accatcacca tcttcaggaa cggcatagcc ctagagatcc tgcaaaacac 900

ctcatacctt ccggtcctgg agggccaggc tctgcggctg ctctgtgatg ctcccagcaa 960

ccccccctgca cacctgagct ggttccaggg ctcccctgcc ctgaacgcca cccccatctc 1020

caataccggg atcttggagc ttcgtcgagt aaggtctgca gaagaaggag gcttcacctg 1080

ccgcgctcag cacccgctgg gcttcctgca aatttttctg aatctctcag tttactccct 1140

cccacagttg ctgggcccct cctgctcctg ggaggctgag ggtctgcact gcagatgctc 1200

ctttcgagcc cggccggccc cctccctgtg ctggcggctt gaggagaagc cgctggaggg 1260

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gtgcctcatc ttctttttaa tagtgaaagc ccgcaggaag caagcagctg ggagaccaga 1560

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tgcccagagt tcagtcctgg ctggaggagc cacagcctgt ctgggggaaa ggacaagtca 1860

gggaccactt gctgaagcac gaagagccct tgtggcaatg ttaacattaa ctgatgttta 1920

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gtc 2523

<210> 43
<211> 453
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(453)
<223> Siglec 6 FL

<400> 43

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

Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala Gln Glu Arg Arg Phe Gln
20 25 30

Leu Glu Gly Pro Glu Ser Leu Thr Val Gln Glu Gly Leu Cys Val Leu
35 40 45

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

Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val Pro Val Ala Thr Asn Asp
65 70 75 80

Pro Asp Glu Glu Val Gln Glu Glu Thr Arg Gly Arg Phe His Leu Leu
85 90 95

Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu Ser Ile Arg Asp Ala Arg
100 105 110

Arg Arg Asp Asn Ala Ala Tyr Phe Phe Arg Leu Lys Ser Lys Trp Met
115 120 125

Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser Val Arg Val Met Ala Leu
130 135 140

Thr His Arg Pro Asn Ile Ser Ile Pro Gly Thr Leu Glu Ser Gly His
145 150 155 160

Pro Ser Asn Leu Thr Cys Ser Val Pro Trp Val Cys Glu Gln Gly Thr
165 170 175

Pro Pro Ile Phe Ser Trp Met Ser Ala Ala Pro Thr Ser Leu Gly Pro
180 185 190

Arg Thr Thr Gln Ser Ser Val Leu Thr Ile Thr Pro Arg Pro Gln Asp
195 200 205

His Ser Thr Asn Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Gly Val
210 215 220

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

Val Ala Ile Ser Ile Phe Gln Gly Asn Ser Ala Ala Phe Lys Ile Leu
245 250 255

Gln Asn Thr Ser Ser Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu
260 265 270

Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala His Leu Ser Trp Phe Gln
275 280 285

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

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

Ala Gln His Pro Leu Gly Ser Leu Gln Ile Ser Leu Ser Leu Phe Val
325 330 335

His Trp Lys Pro Glu Gly Arg Ala Gly Gly Val Leu Gly Ala Val Trp
340 345 350

Gly Ala Ser Ile Thr Thr Leu Val Phe Leu Cys Val Cys Phe Ile Phe
355 360 365

Arg Val Lys Thr Arg Arg Lys Lys Ala Ala Gln Pro Val Gln Asn Thr
370 375 380

Asp Asp Val Asn Pro Val Met Val Ser Gly Ser Arg Gly His Gln His
385 390 395 400

Gln Phe Gln Thr Gly Ile Val Ser Asp His Pro Ala Glu Ala Gly Pro
405 410 415

Ile Ser Glu Asp Glu Gln Glu Leu His Tyr Ala Val Leu His Phe His

420 425 430

Lys Val Gln Pro Gln Glu Pro Lys Val Thr Asp Thr Glu Tyr Ser Glu
435 440 445

Ile Lys Ile His Lys
450

<210> 44
<211> 3815
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(3815)
<223> Siglec 6 FL

<400> 44
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ctgtgagcag gggacgcccc ccatcttctc ctggatgtca gctgccccca cctccctggg 780

ccccaggacc acccagtcct cggtgctcac aatcacccca cggccccagg accacagcac 840

caacctcacc tgtcaggtga cgttccctgg agccggtgtg accatggaga gaaccatcca 900

gctcaatgtc tcctccttca aaatcctgca aaacacctcg tccctccctg tcctggaggg 960

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ccagggcttc cccgccctga acgccacccc catctccaat accggggtcc tggagctgcc 1080

tcaagtaggg tctgcagaag aaggagattt cacctgccgt gctcagcatc ctctgggctc 1140

cctgcaaatc tctctgagtc tctttgtgca ttggaaacca gaaggcaggg ctggtggtgt 1200

cctgggagca gtctggggag ctagcatcac aaccctggtt ttcctctgtg tttgcttcat 1260

cttcagagtg aagactagaa ggaagaaagc agcccagcca gtgcaaaaca cggatgatgt 1320

gaaccccgtc atggtctcag gctccagggg tcatcagcac cagttccaga caggcatagt 1380

ttcagaccac cctgctgagg ctggccccat ctcagaagat gagcaggagc tccactacgc 1440

tgtcctacac ttccacaagg tgcaacctca ggaaccaaag gtcaccgaca ctgagtactc 1500

agaaatcaag atacacaagt gaggaattgt ccaaagccat aaccttgatt ggagagaaca 1560

tggtacctct cagtgtattg gttactaggg ctgccacagc aatgtaccac aaaccgagtg 1620

acataaacac agaactttat tttcgtatag tttcagatgt tagaggtctg agaacaaggt 1680

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tccctgctct gtaaggcagg gaaataattt ccatctaacc agattattgt gaaaggtcaa 2160

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cacaaaggtt ttcataaagt ctgtatattt ttgtaaatga atgccttgta tctggctttg 2280

gctagctttt tttttttttt ttttttctg agatggagtc ttgctgtatc tcccaggctg 2340

gagtgcagtg gtgcgatctt ggctcagtgc aagcttcgcc ccctgggttc acaccattct 2400

cctgcctcag cctcccaagt agctgggact acaggcaccc accaccacac ccggctaatt 2460

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ctcttcacga ctccccaaaa taaggtttcc atccatcatc tttctgctca aggctctcta 2760

catgatcttg tccatccaga tttccccaga tcaattcctc accagtcacc aataccccat 2820

gtccatttcc acagcttcct cttacaaatc ccagtctcca ctattccagt gaaattgaag 2880

aaagcattta atgaagacca actattaagg aaaattctta agagtagcca tgaaaaataa 2940

aaagatagat tacacttaaa agaccacagt tagcagtggc tcacgcctgt aatcccagca 3000

ctttgggagg ctgaggtggg tggatcactg gaggtcagga gttcgagact ggtctggcca 3060

acatggtgaa accccatctc tactaaaata caaaaattag ctcggtgtgg tggcacttgc 3120

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aggttgaagt gagctgagat tgcatcactg cactccagcc tgggcaacag agcgagactc 3240

caactcagaa aaagcaaaac aaaacaaaca aacaagcaaa aaaccacaat tagactgaca 3300

gctgactttt ttaggagcaa tattggaagg ctaaatgcaa tagaaagatg tctttgatgg 3360

cttaagagaa ataaatgttg ttttagaaag cctactcaat gaaaacacat tttaagactg 3420

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tttttgagat ccaaaaaaaa tgaaaaccta ggaaagtagc aaatatgtga gcaaaatgaa 3600

acaaatactt gttgtaaaaa tgatggtttg tagaggggtc aaacatcaaa tgtaatattg 3660

aaataccaat attatatagc ccagaaacta taataacata aagttcagaa gagtgtaaat 3720

agaatttata ttacataaag tctttatatt tttccagaga aaattaaatg ttatgatgaa 3780

tgttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 3815

<210> 45
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(321)
<223> Siglec 6 Fragment (27-347)

<400> 45

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg
50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Arg
85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser
100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile
260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val

<210> 46
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX

<400> 46

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg
    50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Ala
                85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser
            100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
        115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
    130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
                165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
            180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
        195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
    210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
                245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile

260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val

<210> 47
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) / (G4S)2 / hIgG1 Fc N297G

<400> 47

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg
50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Arg
85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser

100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile
260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

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

530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 48
<211> 1674
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) / (G4S)2 / hIgG1 Fc N297G

<400> 48
caagagcggc ggtttcagct ggaaggacct gagagcctga cagtgcaaga gggcctgtgt 60

gtgctggtgc cttgtagact gcctaccaca ctgcccgcca gctactacgg ctacggctat 120

tggtttctgg aaggcgccga tgtgcccgtg gccaccaatg atcctgacga ggaagtgcaa 180

gaagagacac ggggcagatt ccatctgctg tgggacccca gacggaagaa ctgcagcctg 240

agcatcagag atgccagaag gcgggataac gccgcctact tcttccggct gaagtccaag 300

tggatgaagt acggctacac cagcagcaag ctgagcgtca gagtgatggc cctgacacac 360

agacccaaca tcagcatccc cggcacactg gaaagcggac accctagcaa tctgacctgc 420

agcgtgccat gggtttgcga gcagggaacc cctcctatct tctcctggat gtctgccgct 480

cctacctctc tgggccctag aacaacacag agcagcgtgc tgaccatcac acccagacct 540

caggaccaca gcaccaacct gacctgccaa gtgacctttc ctggcgctgg cgtgaccatg 600

gaaagaacca tccagctcaa cgtgtcctac gctccccaga aggtggccat cagcattttc 660

cagggcaaca gcgccgcctt caagatcctg cagaatacca gcagcctgcc tgtgctggaa 720

ggccaggctc tgagactgct gtgtgacgcc gatggcaatc ctcctgctca cctgagctgg 780

ttccagggct tcccagctct gaacgccaca cctatcagca acaccggcgt gctggaactg 840

cctcaagtgg gatctgccga ggaaggcgac ttcacctgta gagcccaaca tcctctgggc 900

agcctgcaga tctccctgag cctgtttgtg cactggaagc ccgaaggcag agctggcgga 960

gtgggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1020

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1080

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1140

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1200

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1260

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1320

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1380

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1440

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1500

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1560

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1620

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1674

<210> 49
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 49

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg
50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Ala
85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser
100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile
260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 50
<211> 1674
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 50
caagagcggc ggtttcagct ggaaggacct gagagcctga cagtgcaaga gggcctgtgt 60

gtgctggtgc cttgtagact gcctaccaca ctgcccgcca gctactacgg ctacggctat 120

tggtttctgg aaggcgccga tgtgcccgtg gccaccaatg atcctgacga ggaagtgcaa 180

gaagagacac ggggcagatt ccatctgctg tgggacccca gacggaagaa ctgcagcctg 240

agcatcagag atgccagaag gcgggataac gccgcctact tcttcgccct gaagtccaag 300

tggatgaagt acggctacac cagcagcaag ctgagcgtca gagtgatggc cctgacacac 360

agacccaaca tcagcatccc cggcacactg gaaagcggac accctagcaa tctgacctgc 420

agcgtgccat gggtttgcga gcagggaacc cctcctatct tctcctggat gtctgccgct 480

cctacctctc tgggccctag aacaacacag agcagcgtgc tgaccatcac acccagacct 540

caggaccaca gcaccaacct gacctgccaa gtgacctttc ctggcgctgg cgtgaccatg 600

gaaagaacca tccagctcaa cgtgtcctac gctccccaga aggtggccat cagcattttc 660

cagggcaaca gcgccgcctt caagatcctg cagaatacca gcagcctgcc tgtgctggaa 720

ggccaggctc tgagactgct gtgtgacgcc gatggcaatc ctcctgctca cctgagctgg 780

ttccagggct tcccagctct gaacgccaca cctatcagca acaccggcgt gctggaactg 840

cctcaagtgg gatctgccga ggaaggcgac ttcacctgta gagcccaaca tcctctgggc 900

agcctgcaga tctccctgag cctgtttgtg cactggaagc ccgaaggcag agctggcgga 960

gtgggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1020

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1080

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1140

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1200

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1260

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1320

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1380

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1440

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1500

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1560

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1620

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1674

<210> 51
<211> 467
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(467)
<223> Siglec 7 FL

<400> 51

Met Leu Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Val
1 5 10 15

Glu Gly Gln Lys Ser Asn Arg Lys Asp Tyr Ser Leu Thr Met Gln Ser
20 25 30

Ser Val Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe
35 40 45

Ser Tyr Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr
50 55 60

Trp Phe Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr
65 70 75 80

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

Leu Leu Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp
100 105 110

Ala Arg Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly
115 120 125

Asn Ile Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr
130 135 140

Ala Leu Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser
145 150 155 160

Gly Cys Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln
165 170 175

Gly Thr Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu
180 185 190

His Pro Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro
195 200 205

Gln His His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala
210 215 220

Gly Val Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro
225 230 235 240

Gln Asn Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr
245 250 255

Ala Leu Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu
260 265 270

Arg Leu Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp
275 280 285

Thr Trp Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu
290 295 300

Val Leu Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys
305 310 315 320

Arg Ala Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser
325 330 335

Leu Gln Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu
340 345 350

Leu Gly Ala Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Ser
355 360 365

Phe Cys Val Ile Phe Ile Val Val Arg Ser Cys Arg Lys Lys Ser Ala
370 375 380

Arg Pro Ala Ala Asp Val Gly Asp Ile Gly Met Lys Asp Ala Asn Thr
385 390 395 400

Ile Arg Gly Ser Ala Ser Gln Gly Asn Leu Thr Glu Ser Trp Ala Asp
405 410 415

Asp Asn Pro Arg His His Gly Leu Ala Ala His Ser Ser Gly Glu Glu
420 425 430

Arg Glu Ile Gln Tyr Ala Pro Leu Ser Phe His Lys Gly Glu Pro Gln
435 440 445

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

Ile Pro Lys
465

<210> 52
<211> 1769
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(1769)
<223> Siglec 7 FL

<400> 52
gcagttcctg agagaagaac cctgaggaac agacgttccc tcgcggccct ggcacctcca 60

accccagata tgctgctgct gctgctgctg cccctgctct gggggaggga gagggtggaa 120

ggacagaaga gtaaccggaa ggattactcg ctgacgatgc agagttccgt gaccgtgcaa 180

gagggcatgt gtgtccatgt gcgctgctcc ttctcctacc cagtggacag ccagactgac 240

tctgacccag ttcatggcta ctggttccgg gcagggaatg atataagctg gaaggctcca 300

gtggccacaa acaacccagc ttgggcagtg caggaggaaa ctcgggaccg attccacctc 360

cttggggacc cacagaccaa aaattgcacc ctgagcatca gagatgccag aatgagtgat 420

gcggggagat acttctttcg tatggagaaa ggaaatataa aatggaatta taaatatgac 480

cagctctctg tgaacgtgac agccttgacc cacaggccca acatccttat ccccggtacc 540

ctggagtctg gctgcttcca gaatctgacc tgctctgtgc cctgggcctg tgagcagggg 600

acgcccccta tgatctcctg gatggggacc tctgtgtccc ccctgcaccc ctccaccacc 660

cgctcctcag tgctcaccct catcccacag ccccagcacc acggcaccag cctcacctgt 720

caggtgacct tgcctggggc cggcgtgacc acgaacagga ccatccaact caatgtgtcc 780

taccctcctc agaacttgac tgtgactgtc ttccaaggag aaggcacagc atccacagct 840

ctggggaaca gctcatctct ttcagtccta gagggccagt ctctgcgctt ggtctgtgct 900

gttgacagca atccccctgc caggctgagc tggacctgga ggagtctgac cctgtacccc 960

tcacagccct caaaccctct ggtactggag ctgcaagtgc acctgggggga tgaaggggaa 1020

ttcacctgtc gagctcagaa ctctctgggt tcccagcacg tttccctgaa cctctccctg 1080

caacaggagt acacaggcaa aatgaggcct gtatcaggag tgttgctggg ggcggtcggg 1140

ggagctggag ccacagccct ggtcttcctc tccttctgtg tcatcttcat tgtagtgagg 1200

tcctgcagga agaaatcggc aaggccagca gcggacgtgg gagacatagg catgaaggat 1260

gcaaacacca tcaggggctc agcctctcag ggtaacctga ctgagtcctg ggcagatgat 1320

aacccccgac accatggcct ggctgcccac tcctcagggg aggaaagaga gatccagtat 1380

gcacccctca gctttcataa gggggagcct caggacctat caggacaaga agccaccaac 1440

aatgagtact cagagatcaa gatccccaag taagaaaatg cagaggctcg ggcttgtttg 1500

agggttcacg acccctccag caaaggagtc tgaggctgat tccagtagaa ttagcagccc 1560

tcaatgctgt gcaacaagac atcagaactt attcctcttg tctaactgaa aatgcatgcc 1620

tgatgaccaa actctccctt tccccatcca atcggtccac actccccgcc ctggcctctg 1680

gtacccacca ttctcctctg tacttctcta aggatgacta ctttagattc cgaatatagt 1740

gagattgtaa cgtgaaaaaa aaaaaaaaa 1769

<210> 53
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(119)
<223> Siglec 7 V-Set (26-144)

<400> 53

Tyr Ser Leu Thr Met Gln Ser Ser Val Thr Val Gln Glu Gly Met Cys
1 5 10 15

Val His Val Arg Cys Ser Phe Ser Tyr Pro Val Asp Ser Gln Thr Asp
20 25 30

Ser Asp Pro Val His Gly Tyr Trp Phe Arg Ala Gly Asn Asp Ile Ser
35 40 45

Trp Lys Ala Pro Val Ala Thr Asn Asn Pro Ala Trp Ala Val Gln Glu
50 55 60

Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro Gln Thr Lys Asn
65 70 75 80

Cys Thr Leu Ser Ile Arg Asp Ala Arg Met Ser Asp Ala Gly Arg Tyr
85 90 95

Phe Phe Arg Met Glu Lys Gly Asn Ile Lys Trp Asn Tyr Lys Tyr Asp
100 105 110

Gln Leu Ser Val Asn Val Thr
115

<210> 54
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(92)
<223> Siglec 7 V-Set (Alt. boundary) (31-122)

<400> 54

Gln Ser Ser Val Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys
1 5 10 15

Ser Phe Ser Tyr Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His
20 25 30

Gly Tyr Trp Phe Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val
35 40 45

Ala Thr Asn Asn Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg
50 55 60

Phe His Leu Leu Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile
65 70 75 80

Arg Asp Ala Arg Met Ser Asp Ala Gly Arg Tyr Phe
85 90

<210> 55
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(221)
<223> Siglec 7 V-Set + 1 C2-Set Domain (19-239)

<400> 55

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro
210 215 220

<210> 56
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(339)
<223> Siglec 7 V-Set Domain + 2 C2-Set Domains (Full ECD) (19-357)

<400> 56

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro

165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly

<210> 57
<211> 339
<212> PRT
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(339)
<223> Siglec 7 Fragment (19-357)

<400> 57

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly

<210> 58
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) SAX

<400> 58

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly

<210> 59
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) / AS / hIgG1 Fc N297G

<400> 59

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly Ala Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
340 345 350

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
355 360 365

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
370 375 380

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
385 390 395 400

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
405 410 415

Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
420 425 430

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
435 440 445

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
450 455 460

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
465 470 475 480

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
485 490 495

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
500 505 510

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
515 520 525

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
545 550 555 560

Ser Leu Ser Leu Ser Pro Gly Lys
565

<210> 60
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) / AS / hIgG1 Fc N297G

<400> 60
cagaagtcca acagaaagga ctacagcctg accatgcaga gcagcgtgac agtgcaagag 60

gggatgtgcg tccacgtccg gtgcagcttt agctaccctg tggacagcca gaccgacagc 120

gatcctgtgc acggctactg gttcagagcc ggcaacgaca tctcttggaa agccccagtg 180

gccaccaaca atcctgcctg ggctgtgcaa gaagagacac gggacagatt ccatctgctg 240

ggcgaccctc agaccaagaa ctgcacactg agcatccggg acgccagaat gtctgacgcc 300

ggcagatact tcttcagaat ggaaaagggc aacatcaagt ggaactataa gtacgaccag 360

ctgagcgtga acgtgacagc cctgacacac agacccaaca ttctgatccc cggcacactg 420

gaaagcggct gcttccagaa tctgacctgc tctgtgcctt gggcctgcga gcagggaaca 480

cctcctatga tcagctggat gggaaccagc gtgtcccctc tgcaccctag caccacaaga 540

tccagcgtgc tgacactgat ccctcagcct cagcaccacg gcacaagcct gacctgtcaa 600

gttacacttc ctggcgctgg cgtgaccacc aacagaacaa tccagctcaa cgtgtcctat 660

cctcctcaga acctgaccgt gaccgtgttc caaggcgagg gcacagcttc tacagccctg 720

ggcaatagca gcagcctgtc tgtgctggaa ggccagtctc tgagactcgt gtgcgccgtg 780

gatagcaacc ctcctgctag actgagctgg acttggcgga gcctgacact gtaccctagc 840

cagcctagca atcccctggt gctggaactg caagtgcacc tgggagatga gggcgagttc 900

acctgtagag cccagaatag cctgggcagc cagcacgtgt ccctgaacct gtctctgcag 960

caagagtaca ccggcaagat gaggcctgtg tctggcgttc tgctgggagc cgtgggagct 1020

agcgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 1080

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1140

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1200

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta cggtagcacg 1260

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1320

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1380

aaagggcagc cccgagaacc acaggtctac accctgcccc catcccggga ggagatgacc 1440

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1500

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1560

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1620

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1680

agcctctccc tgtctccggg taaa 1704

<210> 61
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) SAX / AS / hIgG1 Fc N297G

<400> 61

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly Ala Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
340 345 350

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
355 360 365

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
370 375 380

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
385 390 395 400

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
405 410 415

Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
420 425 430

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
435 440 445

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
450 455 460

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
465 470 475 480

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
485 490 495

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
500 505 510

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
515 520 525

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
545 550 555 560

Ser Leu Ser Leu Ser Pro Gly Lys
565

<210> 62
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) SAX / AS / hIgG1 Fc N297G

<400> 62
cagaagtcca acagaaagga ctacagcctg accatgcaga gcagcgtgac agtgcaagag 60

gggatgtgcg tccacgtccg gtgcagcttt agctaccctg tggacagcca gaccgacagc 120

gatcctgtgc acggctactg gttcagagcc ggcaacgaca tctcttggaa agccccagtg 180

gccaccaaca atcctgcctg ggctgtgcaa gaagagacac gggacagatt ccatctgctg 240

ggcgaccctc agaccaagaa ctgcacactg agcatccggg acgccagaat gtctgacgcc 300

ggcagatact tcttcaagat ggaaaagggc aacatcaagt ggaactataa gtacgaccag 360

ctgagcgtga acgtgacagc cctgacacac agacccaaca ttctgatccc cggcacactg 420

gaaagcggct gcttccagaa tctgacctgc tctgtgcctt gggcctgcga gcagggaaca 480

cctcctatga tcagctggat gggaaccagc gtgtcccctc tgcaccctag caccacaaga 540

tccagcgtgc tgacactgat ccctcagcct cagcaccacg gcacaagcct gacctgtcaa 600

gttacacttc ctggcgctgg cgtgaccacc aacagaacaa tccagctcaa cgtgtcctat 660

cctcctcaga acctgaccgt gaccgtgttc caaggcgagg gcacagcttc tacagccctg 720

ggcaatagca gcagcctgtc tgtgctggaa ggccagtctc tgagactcgt gtgcgccgtg 780

gatagcaacc ctcctgctag actgagctgg acttggcgga gcctgacact gtaccctagc 840

cagcctagca atcccctggt gctggaactg caagtgcacc tgggagatga gggcgagttc 900

acctgtagag cccagaatag cctgggcagc cagcacgtgt ccctgaacct gtctctgcag 960

caagagtaca ccggcaagat gaggcctgtg tctggcgttc tgctgggagc cgtgggagct 1020

agcgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 1080

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1140

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1200

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta cggtagcacg 1260

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1320

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1380

aaagggcagc cccgagaacc acaggtctac accctgcccc catcccggga ggagatgacc 1440

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1500

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1560

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1620

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1680

agcctctccc tgtctccggg taaa 1704

<210> 63
<211> 499
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(499)
<223> Siglec 8 FL

<400> 63

Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Thr Lys Gly
1 5 10 15

Met Glu Gly Asp Arg Gln Tyr Gly Asp Gly Tyr Leu Leu Gln Val Gln
20 25 30

Glu Leu Val Thr Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser
35 40 45

Phe Ser Tyr Pro Gln Asp Gly Trp Thr Asp Ser Asp Pro Val His Gly
50 55 60

Tyr Trp Phe Arg Ala Gly Asp Arg Pro Tyr Gln Asp Ala Pro Val Ala
65 70 75 80

Thr Asn Asn Pro Asp Arg Glu Val Gln Ala Glu Thr Gln Gly Arg Phe
85 90 95

Gln Leu Leu Gly Asp Ile Trp Ser Asn Asp Cys Ser Leu Ser Ile Arg
100 105 110

Asp Ala Arg Lys Arg Asp Lys Gly Ser Tyr Phe Phe Arg Leu Glu Arg
115 120 125

Gly Ser Met Lys Trp Ser Tyr Lys Ser Gln Leu Asn Tyr Lys Thr Lys
130 135 140

Gln Leu Ser Val Phe Val Thr Ala Leu Thr His Arg Pro Asp Ile Leu
145 150 155 160

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

Val Pro Trp Ala Cys Lys Gln Gly Thr Pro Pro Met Ile Ser Trp Ile
180 185 190

Gly Ala Ser Val Ser Ser Pro Gly Pro Thr Thr Ala Arg Ser Ser Val
195 200 205

Leu Thr Leu Thr Pro Lys Pro Gln Asp His Gly Thr Ser Leu Thr Cys

210 215 220

Gln Val Thr Leu Pro Gly Thr Gly Val Thr Thr Thr Ser Thr Val Arg
225 230 235 240

Leu Asp Val Ser Tyr Pro Pro Trp Asn Leu Thr Met Thr Val Phe Gln
245 250 255

Gly Asp Ala Thr Ala Ser Thr Ala Leu Gly Asn Gly Ser Ser Leu Ser
260 265 270

Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Ala Val Asn Ser Asn
275 280 285

Pro Pro Ala Arg Leu Ser Trp Thr Arg Gly Ser Leu Thr Leu Cys Pro
290 295 300

Ser Arg Ser Ser Asn Pro Gly Leu Leu Glu Leu Pro Arg Val His Val
305 310 315 320

Arg Asp Glu Gly Glu Phe Thr Cys Arg Ala Gln Asn Ala Gln Gly Ser
325 330 335

Gln His Ile Ser Leu Ser Leu Ser Leu Gln Asn Glu Gly Thr Gly Thr
340 345 350

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

Ala Thr Ala Leu Ala Phe Leu Ser Phe Cys Ile Ile Phe Ile Ile Val
370 375 380

Arg Ser Cys Arg Lys Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp
385 390 395 400

Thr Gly Met Glu Asp Ala Lys Ala Ile Arg Gly Ser Ala Ser Gln Gly
405 410 415

Pro Leu Thr Glu Ser Trp Lys Asp Gly Asn Pro Leu Lys Lys Pro Pro
420 425 430

Pro Ala Val Ala Pro Ser Ser Gly Glu Glu Gly Glu Leu His Tyr Ala
435 440 445

Thr Leu Ser Phe His Lys Val Lys Pro Gln Asp Pro Gln Gly Gln Glu
450 455 460

Ala Thr Asp Ser Glu Tyr Ser Glu Ile Lys Ile His Lys Arg Glu Thr
465 470 475 480

Ala Glu Thr Gln Ala Cys Leu Arg Asn His Asn Pro Ser Ser Lys Glu
485 490 495

Val Arg Gly

<210> 64
<211> 2967
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2967)
<223> Siglec 8 FL

<400> 64
agtttctgag agaagaaccc tgaggaacag acgttccctg gcggccctgg cgccttcaaa 60

cccagacatg ctgctgctgc tgctgctgct gcccctgctc tgggggacaa aggggatgga 120

gggagacaga caatatgggg atggttactt gctgcaagtg caggagctgg tgacggtgca 180

ggagggcctg tgtgtccatg tgccctgctc cttctcctac ccccaggatg gctggactga 240

ctctgaccca gttcatggct actggttccg ggcaggagac agaccatacc aagacgctcc 300

agtggccaca aacaacccag acagagaagt gcaggcagag acccagggcc gattccaact 360

ccttggggac atttggagca acgactgctc cctgagcatc agagacgcca ggaagaggga 420

taaggggtca tatttctttc ggctagagag aggaagcatg aaatggagtt acaaatcaca 480

gttgaattac aaaactaagc agctgtctgt gtttgtgaca gccctgaccc ataggcctga 540

catcctcatc ctagggaccc tagagtctgg ccactccagg aacctgacct gctctgtgcc 600

ctgggcctgt aagcagggga cacccccat gatctcctgg attggggcct ccgtgtcctc 660

cccgggcccc actactgccc gctcctcagt gctcaccctt accccaaagc cccaggacca 720

cggcaccagc ctcacctgtc aggtgacctt gcctgggaca ggtgtgacca cgaccagtac 780

cgtccgcctc gatgtgtcct accctccttg gaacttgacc atgactgtct tccaaggaga 840

tgccacagca tccacagccc tgggaaatgg ctcatctctt tcagtccttg agggccagtc 900

tctgcgcctg gtctgtgctg tcaacagcaa tccccctgcc aggctgagct ggacccgggg 960

gagcctgacc ctgtgcccct cacggtcctc aaaccctggg ctgctggagc tgcctcgagt 1020

gcacgtgagg gatgaagggg aattcacctg ccgagctcag aacgctcagg gctcccagca 1080

catttccctg agcctctccc tgcagaatga gggcacaggc acctcaagac ctgtatcaca 1140

agtgacactg gcagcagtcg ggggagctgg agccacagcc ctggccttcc tgtccttctg 1200

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gactgaatcc tggaaagatg gcaacccccct gaagaagcct cccccagctg ttgccccctc 1380

gtcaggggag gaaggagagc tccattatgc aaccctcagc ttccataaag tgaagcctca 1440

ggacccgcag ggacaggagg ccactgacag tgaatactcg gagatcaaga tccacaagcg 1500

agaaactgca gagactcagg cctgtttgag gaatcacaac ccctccagca aagaagtcag 1560

aggctgattc tcatagaaca agaaccctct agagccccat gctatgcagt aggtcaccag 1620

ggctccctcc tcctgtctaa ccaaaacttg gaccaatgtc tccccttttcc ccggctacca 1680

gggacccatc cctgcctcta gcttctacta cccaccattc tcctctcgac ctctctgagg 1740

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gctcatttta cacaaaaaaa tatcccctag gttcatccat gttctctcaa atgacagaat 1860

caagcactga atatttttt ttctttgaga gatggagttt cgctctgttg cccaggctgg 1920

agtgcagtgg ttcaatctct gctcactgca acctccacct cctgggttca aacgattctc 1980

ctgcctcagc ttcccaagta gctggtacta caggcgtgtg tcaccacgcc cagctaattt 2040

ttgtattttt tagtagagac ggggtttcac tataagtggg ccaggctagt ctcaaactcc 2100

tgacctcaag tgatctgcct gccttggcct cccaaagtgc tgggatttca ggcatgagcc 2160

accgcaccca gcttgcattg aatattttca aggagctaaa agaagatttt aaatggtctc 2220

acaaaaacag ataaatattt gcacagatgg gtgtgctaat cattgtgcct tgatggttcc 2280

acgatgtatc cgggtgtgga aatctcactg ggtctctctc aaggccactc ggctactcag 2340

gacagggctg gaatttaaag cctgtccgat tctgaggtct cttctctcat ctagcactga 2400

gtcaagcaat cagcaggctg ggcacccctt agccataagt tttcaggaaa taaattcctt 2460

gagggcattg acttttacaa aagagggagc agcaatggcc tagagtctca ggaacaagac 2520

aggtgcactg aggagatgaa ggccgggacc ccctgcccaa cctgtatggc gggtctgtac 2580

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tgtgttgggg gagggacctg gtgggaggtg ataggatcat gggggtggtt cccccatgct 2760

gttctgatag tgagtgagtt atcacgagat ctgatggttt tgtaagtggt ggtttcccct 2820

gctcttctct cttgcctgcc accatgtaag atgtgcctgg ttccccttcc gccatgattg 2880

taagtttcct gaggcctccc ccgccatgtg gaactgtgag tcaattacac ctctttcatt 2940

tataaattaa aaaaaaaaaa aaaaaaa 2967

<210> 65
<211> 463
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(463)
<223> Siglec 9 FL

<400> 65

Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala Glu
1 5 10 15

Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr Val Gln
20 25 30

Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His
35 40 45

Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr Trp Phe Arg Glu
50 55 60

Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala
65 70 75 80

Arg Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp
85 90 95

Pro His Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser
100 105 110

Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp
115 120 125

Asn Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His
130 135 140

Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln
145 150 155 160

Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro
165 170 175

Met Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr
180 185 190

Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly
195 200 205

Thr Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr
210 215 220

Asn Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr
225 230 235 240

Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn
245 250 255

Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys
260 265 270

Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser

275 280 285

Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val
290 295 300

Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys
305 310 315 320

Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser
325 330 335

Leu Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Val Val Gly Gly
340 345 350

Ala Gly Ala Thr Ala Leu Val Phe Leu Ser Phe Cys Val Ile Phe Val
355 360 365

Val Val Arg Ser Cys Arg Lys Lys Ser Ala Arg Pro Ala Ala Gly Val
370 375 380

Gly Asp Thr Gly Ile Glu Asp Ala Asn Ala Val Arg Gly Ser Ala Ser
385 390 395 400

Gln Gly Pro Leu Thr Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln
405 410 415

Pro Pro Pro Ala Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln
420 425 430

Tyr Ala Ser Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly
435 440 445

Gln Glu Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
450 455 460

<210> 66
<211> 1737
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(1737)
<223> Siglec 9 FL

<400> 66
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gttccctcgc ggccctggca cctctaaccc cagacatgct gctgctgctg ctgcccctgc 120

tctgggggag ggagagggcg gaaggacaga caagtaaact gctgacgatg cagagttccg 180

tgacggtgca ggaaggcctg tgtgtccatg tgccctgctc cttctcctac ccctcgcatg 240

gctggattta ccctggccca gtagttcatg gctactggtt ccgggaaggg gccaatacag 300

accaggatgc tccagtggcc acaaacaacc cagctcgggc agtgtgggag gagactcggg 360

accgattcca cctccttggg gacccacata ccaagaattg caccctgagc atcagagatg 420

ccagaagaag tgatgcgggg agatacttct ttcgtatgga gaaaggaagt ataaaatgga 480

attataaaca tcaccggctc tctgtgaatg tgacagcctt gacccacagg cccaacatcc 540

tcatcccagg caccctggag tccggctgcc cccagaatct gacctgctct gtgccctggg 600

cctgtgagca ggggacaccc cctatgatct cctggatagg gacctccgtg tccccccctgg 660

acccctccac cacccgctcc tcggtgctca ccctcatccc acagccccag gaccatggca 720

ccagcctcac ctgtcaggtg accttccctg gggccagcgt gaccacgaac aagaccgtcc 780

atctcaacgt gtcctacccg cctcagaact tgaccatgac tgtcttccaa ggagacggca 840

cagtatccac agtcttggga aatggctcat ctctgtcact cccagagggc cagtctctgc 900

gcctggtctg tgcagttgat gcagttgaca gcaatccccc tgccaggctg agcctgagct 960

ggagaggcct gaccctgtgc ccctcacagc cctcaaaccc gggggtgctg gagctgcctt 1020

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tgtagaatta acagccctca acgtgatgag ctatgataac actatgaatt atgtgcagag 1620

tgaaaagcac acaggcttta gagtcaaagt atctcaaacc tgaatccaca ctgtgccctc 1680

ccttttattt ttttaactaa aagacagaca aattcctaaa aaaaaaaaaa aaaaaaa 1737

<210> 67
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(122)
<223> Siglec 9 V-Set (23-144)

<400> 67

Leu Thr Met Gln Ser Ser Val Thr Val Gln Glu Gly Leu Cys Val His
1 5 10 15

Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly Trp Ile Tyr Pro Gly
20 25 30

Pro Val Val His Gly Tyr Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln
35 40 45

Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu
50 55 60

Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys
65 70 75 80

Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe
85 90 95

Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg
100 105 110

Leu Ser Val Asn Val Thr Ala Leu Thr His
115 120

<210> 68
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(118)
<223> Siglec 9 V-Set (Alt. boundary) (23-140)

<400> 68

Leu Thr Met Gln Ser Ser Val Thr Val Gln Glu Gly Leu Cys Val His
1 5 10 15

Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly Trp Ile Tyr Pro Gly
20 25 30

Pro Val Val His Gly Tyr Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln
35 40 45

Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu
50 55 60

Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys
65 70 75 80

Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe
85 90 95

Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg
100 105 110

Leu Ser Val Asn Val Thr
115

<210> 69
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(218)
<223> Siglec 9 V-Set + 1 C2-Set Domain (18-235)

<400> 69

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn

195 200 205

Lys Thr Val His Leu Asn Val Ser Tyr Pro
210 215

<210> 70
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(331)
<223> Siglec 9 V-Set Domain + 2 C2-Set Domains (Full ECD) (18-348)

<400> 70

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly
325 330

<210> 71
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y

<400> 71

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser
325 330

<210> 72
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX

<400> 72

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser
325 330

<210> 73
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / AS / hIgG1 Fc N297G

<400> 73

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

His Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp

85 90 95

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
325 330 335

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
340 345 350

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
355 360 365

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
370 375 380

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
385 390 395 400

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
420 425 430

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
435 440 445

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
450 455 460

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
465 470 475 480

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
485 490 495

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
500 505 510

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

515 520 525

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
530 535 540

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555 560

<210> 74
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / AS / hIgG1 Fc N297G

<400> 74
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcagga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

agcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

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agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtaccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

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ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 1080

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gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1320

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1380

gtctacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 1440

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1500

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctat 1560

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1620

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1680

<210> 75
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX / AS / hIgG1 Fc N297G

<400> 75

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg

290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
325 330 335

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
340 345 350

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
355 360 365

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
370 375 380

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
385 390 395 400

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
420 425 430

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
435 440 445

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
450 455 460

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
465 470 475 480

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
485 490 495

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
500 505 510

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
515 520 525

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
530 535 540

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555 560

<210> 76
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX / AS / hIgG1 Fc N297G

<400> 76
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcaaga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

agcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtaccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

cagagtaagg ccaccagcgg cgtgacccaa ggagctagcg acaaaactca cacatgccca 1020

ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 1080

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 1140

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1200

aagacaaagc cgcgggagga gcagtacggt agcacgtacc gtgtggtcag cgtcctcacc 1260

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1320

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1380

gtctacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 1440

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1500

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctat 1560

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1620

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1680

<210> 77
<211> 357
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-145) / AS / hIgG1 Fc (w/ monovalent mutations)

<400> 77

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro

65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

Ala Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
130 135 140

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
260 265 270

Val Asn Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290 295 300

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Asn Ser Thr Leu
305 310 315 320

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325 330 335

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340 345 350

Leu Ser Pro Gly Lys
        355

<210> 78
<211> 1071
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-145) / AS / hIgG1 Fc (w/
       monovalent mutations)

<400> 78
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcagga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccgggctagc gacaaaactc acacatgccc accgtgccca 420

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 720

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtctacacc 780

ctgcccccat cccgggagga gatgaccaag aaccaggtca acctgacctg cctggtcaaa 840

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcaa tagcacgctc 960

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1071

<210> 79
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / His Tag

<400> 79

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly His His His His His
325 330 335

His His His His His
340

<210> 80
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / His Tag

<400> 80
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcaaga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

agcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtaccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

cagagtaagg ccaccagcgg cgtgacccaa ggacaccatc accatcatca ccaccaccat 1020

caccat 1026

<210> 81
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (146-348) / AS / hIgG1 Fc N297G

<400> 81

Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn
1 5 10 15

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
20 25 30

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
35 40 45

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
50 55 60

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
65 70 75 80

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr Met
85 90 95

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
100 105 110

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

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
130 135 140

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
145 150 155 160

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
165 170 175

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

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
195 200 205

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
210 215 220

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
225 230 235 240

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
245 250 255

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
260 265 270

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val
275 280 285

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
290 295 300

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
305 310 315 320

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
325 330 335

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
340 345 350

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
355 360 365

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
370 375 380

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
385 390 395 400

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
405 410 415

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
420 425 430

<210> 82
<211> 1296
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (146-348) / AS / hIgG1 Fc N297G

<400> 82
cccaatatcc tcatccccgg caccctggag agcggctgcc cccagaatct tacctgcagc 60

gtaccctggg cctgcgagca gggcacccct ccaatgatca gctggatcgg caccagcgtg 120

agccccctgg accctagtac caccaggagc agcgtgctga ccctgatccc ccagccccag 180

gaccacggaa ccagcctgac ctgccaggtg accttccccg gagccagcgt aaccaccaac 240

aagaccgtgc acctgaacgt gagctaccca ccccaaaacc tgaccatgac cgtgttccag 300

ggcgacggca cggtgagcac cgtactgggc aacggcagct ctctgagcct gcccgagggc 360

cagagcttgc ggctggtctg cgccgtggat gctgtggaca gcaaccctcc cgccaggctg 420

agcctgagct ggaggggcct gaccctgtgc cccagccagc ccagcaatcc cggcgtgctg 480

gagctgccct gggttcacct gagggacgct gccgagttca catgtagggc ccagaacccc 540

ctgggctctc agcaggtgta cctgaacgtg tctcttcaga gtaaggccac cagcggcgtg 600

acccaaggag ctagcgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 660

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 720

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 780

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 840

tacggtagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 900

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 960

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1020

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1080

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1140

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1200

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1260

tacacgcaga agagcctctc cctgtctccg ggtaaa 1296

<210> 83
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) K131Q / AS / hIgG1 Fc N297G

<400> 83

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Gln His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
325 330 335

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
340 345 350

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
355 360 365

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
370 375 380

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
385 390 395 400

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
420 425 430

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
435 440 445

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
450 455 460

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
465 470 475 480

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
485 490 495

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
500 505 510

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
515 520 525

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
530 535 540

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555 560

<210> 84
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic: Siglec 9 Fragment (18-348) K131Q / AS / hIgG1 Fc N297G

<400> 84

cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcagga tggagaaggg gtctatcaag tggaactacc agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

tgcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtgccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

cagagtaagg ccaccagcgg cgtgacccaa ggagctagcg acaaaactca cacatgccca 1020

ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 1080

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 1140

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1200

aagacaaagc cgcgggagga gcagtacggt agcacgtacc gtgtggtcag cgtcctcacc 1260

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1320

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1380

gtctacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 1440

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1500

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctat 1560

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1620

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1680

<210> 85
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) K100E, A315E / AS / hIgG1 Fc N297G

<400> 85

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

His Thr Glu Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp
85 90 95

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met

145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Glu Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
325 330 335

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
340 345 350

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
355 360 365

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
370 375 380

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
385 390 395 400

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
420 425 430

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
435 440 445

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
450 455 460

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
465 470 475 480

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
485 490 495

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
500 505 510

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
515 520 525

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
530 535 540

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555 560

<210> 86
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) K100E, A315E / AS / hIgG1 Fc N297G

<400> 86
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccgaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcagga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

tgcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtgccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgaagccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

cagagtaagg ccaccagcgg cgtgacccaa ggagctagcg acaaaactca cacatgccca 1020

ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 1080

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 1140

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1200

aagacaaagc cgcgggagga gcagtacggt agcacgtacc gtgtggtcag cgtcctcacc 1260

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1320

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1380

gtctacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 1440

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1500

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctat 1560

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1620

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1680

<210> 87
<211> 697
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(697)
<223> Siglec 10 FL

<400> 87

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
1 5 10 15

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
20 25 30

Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln
35 40 45

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

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

Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro
85 90 95

Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp
100 105 110

Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr
115 120 125

Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln

130 135 140

Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val
145 150 155 160

Thr Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro
165 170 175

Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Ser Gln Gly Thr Lys Pro
180 185 190

Thr Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
195 200 205

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val
210 215 220

Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp
225 230 235 240

Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu Glu Pro Gln
245 250 255

Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe Leu
260 265 270

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
275 280 285

Val Leu Gln Asn Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
290 295 300

Pro Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg
305 310 315 320

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu
325 330 335

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
340 345 350

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
355 360 365

Pro Val Leu Glu Gly Gln Ser Leu Cys Leu Val Cys Val Thr His Ser
370 375 380

Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser
385 390 395 400

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln
405 410 415

Val Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly
420 425 430

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Ser Pro Lys Leu
435 440 445

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
450 455 460

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
465 470 475 480

Glu Leu Leu Glu Gly Asn Ser Ser Gln Asp Ser Phe Glu Val Thr Pro
485 490 495

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
500 505 510

Leu Ser Ser Gly Leu Arg Leu Arg Cys Glu Ala Trp Asn Val His Gly
515 520 525

Ala Gln Ser Gly Ser Ile Leu Gln Leu Pro Asp Lys Lys Gly Leu Ile
530 535 540

Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile Thr Ala
545 550 555 560

Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile Leu Pro Lys

565 570 575

Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe Ser Arg His Ser
580 585 590

Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr Ala Gly Pro Leu Ala
595 600 605

Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn Ser Pro Arg Thr Pro Leu
610 615 620

Pro Pro Gly Ala Pro Ser Pro Glu Ser Lys Lys Asn Gln Lys Lys Gln
625 630 635 640

Tyr Gln Leu Pro Ser Phe Pro Glu Pro Lys Ser Ser Thr Gln Ala Pro
645 650 655

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

Pro Gly Val Arg Pro Arg Pro Glu Ala Arg Met Pro Lys Gly Thr Gln
675 680 685

Ala Asp Tyr Ala Glu Val Lys Phe Gln
690 695

<210> 88
<211> 3400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(3400)
<223> Siglec 10 FL

<400> 88
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aaggagttct gtgagctcag cgtctgaagc tcatttcatg catcaggccc cagggctcag 120

cttccgcctt cggcttcccc ttctgccaag agccctgagc cactcacagc acgaccagag 180

aacaggcctg tctcaggcag gccctgcgcc tcctatgcgg agatgctact gccactgctg 240

ctgtcctcgc tgctgggcgg gtcccaggct atggatggga gattctggat acgagtgcag 300

gagtcagtga tggtgccgga gggcctgtgc atctctgtgc cctgctcttt ctcctacccc 360

cgacaagact ggacagggtc taccccagct tatggctact ggttcaaagc agtgactgag 420

acaaccaagg gtgctcctgt ggccacaaac caccagagtc gagaggtgga aatgagcacc 480

cggggccgat tccagctcac tggggatccc gccaagggga actgctcctt ggtgatcaga 540

gacgcgcaga tgcaggatga gtcacagtac ttctttcggg tggagagagg aagctatgtg 600

agatataatt tcatgaacga tgggttcttt ctaaaagtaa cagccctgac tcagaagcct 660

gatgtctaca tccccgagac cctggagccc gggcagccgg tgacggtcat ctgtgtgttt 720

aactgggcct ttgaggaatg tccacccccct tctttctcct ggacgggggc tgccctctcc 780

tcccaaggaa ccaaaccaac gacctcccac ttctcagtgc tcagcttcac gcccagaccc 840

caggaccaca acaccgacct cacctgccat gtggacttct ccagaaaggg tgtgagcgca 900

cagaggaccg tccgactccg tgtggcctat gcccccagag accttgttat cagcatttca 960

cgtgacaaca cgccagccct ggagccccag ccccagggaa atgtcccata cctggaagcc 1020

caaaaaggcc agttcctgcg gctcctctgt gctgctgaca gccagccccc tgccacactg 1080

agctgggtcc tgcagaacag agtcctctcc tcgtcccatc cctggggccc tagacccctg 1140

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aacaggcttg gctcccagca gcgagccctg gacctctctg tgcagtatcc tccagagaac 1260

ctgagagtga tggtttccca agcaaacagg acagtcctgg aaaaccttgg gaacggcacg 1320

tctctcccag tactggaggg ccaaagcctg tgcctggtct gtgtcacaca cagcagcccc 1380

ccagccaggc tgagctggac ccagagggga caggttctga gcccctccca gccctcagac 1440

cccggggtcc tggagctgcc tcgggttcaa gtggagcacg aaggagagtt cacctgccac 1500

gctcggcacc cactgggctc ccagcacgtc tctctcagcc tctccgtgca ctactccccg 1560

aagctgctgg gcccctcctg ctcctgggag gctgagggtc tgcactgcag ctgctcctcc 1620

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ggtgctccct ccccagaatc aaagaagaac cagaaaaagc agtatcagtt gcccagtttc 2160

ccagaaccca aatcatccac tcaagcccca gaatcccagg agagccaaga ggagctccat 2220

tatgccacgc tcaacttccc aggcgtcaga cccaggcctg aggcccggat gcccaagggc 2280

acccaggcgg attatgcaga agtcaagttc caatgagggt ctcttaggct ttaggactgg 2340

gacttcggct agggaggaag gtagagtaag aggttgaaga taacagagtg caaagtttcc 2400

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tgggaagctg aggcaggaga atcacttgaa cctgggagac ggaggttgca gtgagccaag 2700

atcacaccat tgcacgccag cctgggcaac aaagcgagac tccatctcaa aaaaaaaatc 2760

ctccaaatgg gttgggtgtc tgtaatccca gcactttggg aggctaaggt gggtggattg 2820

cttgagccca ggagttcgag accagcctgg gcaacatggt gaaaccccat ctctacaaaa 2880

aatacaaaac atagctgggc ttggtggtgt gtgcctgtag tcccagctgt cagacattta 2940

aaccagagca actccatctg gaataggagc tgaataaaat gaggctgaga cctactgggc 3000

tgcattctca gacagtggag gcattctaag tcacaggatg agacaggagg tccgtacaag 3060

atacaggtca taaagacttt gctgataaaa cagattgcag taaagaagcc aaccaaatcc 3120

caccaaaacc aagttggcca cgagagtgac ctctggtcgt cctcactgct acactcctga 3180

cagcaccatg acagtttaca aatgccatgg caacatcagg aagttacccg atatgtccca 3240

aaagggggag gaatgaataa tccacccctt gtttagcaaa taagcaagaa ataaccataa 3300

aagtgggcaa ccagcagctc taggcgctgc tcttgtctat ggagtagcca ttcttttgtt 3360

cctttacttt cttaataaac ttgctttcac cttaaaaaaa 3400

<210> 89
<211> 533
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(533)
<223> Siglec 10 Fragment (18-550)

<400> 89

Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro Glu
1 5 10 15

Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln Asp
20 25 30

Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val Thr
35 40 45

Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg Glu
50 55 60

Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro Ala
65 70 75 80

Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp Glu
85 90 95

Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr Asn
100 105 110

Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln Lys
115 120 125

Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val Thr
130 135 140

Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro Ser
145 150 155 160

Phe Ser Trp Thr Gly Ala Ala Leu Ser Ser Gln Gly Thr Lys Pro Thr

165 170 175

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

Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val Ser
195 200 205

Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp Leu
210 215 220

Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu Glu Pro Gln Pro
225 230 235 240

Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe Leu Arg
245 250 255

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
260 265 270

Leu Gln Asn Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Pro
275 280 285

Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg Tyr
290 295 300

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
305 310 315 320

Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser Gln
325 330 335

Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro
340 345 350

Val Leu Glu Gly Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser
355 360 365

Pro Pro Ala Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro
370 375 380

Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val
385 390 395 400

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
405 410 415

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Ser Pro Lys Leu Leu
420 425 430

Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys Ser
435 440 445

Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu Glu
450 455 460

Leu Leu Glu Gly Asn Ser Ser Gln Asp Ser Phe Glu Val Thr Pro Ser
465 470 475 480

Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly Leu
485 490 495

Ser Ser Gly Leu Arg Leu Arg Cys Glu Ala Trp Asn Val His Gly Ala
500 505 510

Gln Ser Gly Ser Ile Leu Gln Leu Pro Asp Lys Lys Gly Leu Ile Ser
515 520 525

Thr Ala Phe Ser Asn
530

<210> 90
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 10 Fragment (18-550) / (G4S)2 / hIgG1 Fc N297G

<400> 90

Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro Glu
1 5 10 15

Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln Asp
20 25 30

Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val Thr
35 40 45

Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg Glu
50 55 60

Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro Ala
65 70 75 80

Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp Glu
85 90 95

Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr Asn
100 105 110

Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln Lys
115 120 125

Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val Thr
130 135 140

Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro Ser
145 150 155 160

Phe Ser Trp Thr Gly Ala Ala Leu Ser Ser Gln Gly Thr Lys Pro Thr
165 170 175

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

Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val Ser
195 200 205

Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp Leu
210 215 220

Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu Glu Pro Gln Pro

225 230 235 240

Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe Leu Arg
245 250 255

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
260 265 270

Leu Gln Asn Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Pro
275 280 285

Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg Tyr
290 295 300

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
305 310 315 320

Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser Gln
325 330 335

Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro
340 345 350

Val Leu Glu Gly Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser
355 360 365

Pro Pro Ala Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro
370 375 380

Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val
385 390 395 400

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
405 410 415

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Ser Pro Lys Leu Leu
420 425 430

Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys Ser
435 440 445

Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu Glu
    450 455 460

Leu Leu Glu Gly Asn Ser Ser Gln Asp Ser Phe Glu Val Thr Pro Ser
465 470 475 480

Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly Leu
                485 490 495

Ser Ser Gly Leu Arg Leu Arg Cys Glu Ala Trp Asn Val His Gly Ala
            500 505 510

Gln Ser Gly Ser Ile Leu Gln Leu Pro Asp Lys Lys Gly Leu Ile Ser
        515 520 525

Thr Ala Phe Ser Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
    530 535 540

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
545 550 555 560

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                565 570 575

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            580 585 590

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        595 600 605

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
625 630 635 640

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                645 650 655

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

660 665 670

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
675 680 685

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
690 695 700

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
705 710 715 720

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
725 730 735

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
740 745 750

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
755 760 765

Gly Lys
770

<210> 91
<211> 2310
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 10 Fragment (18-550) / (G4S)2 / hIgG1 Fc N297G

<400> 91
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agcgtgccct gcagcttcag ctaccccaga caggattgga caggcagcac accagcctac 120

ggctactggt ttaaggccgt gaccgaaacc accaagggcg ctccagtggc cacaaaccac 180

cagagcagag aagtggaaat gagcacccgg ggcagattcc agctgacagg cgatcctgcc 240

aagggcaatt gcagcctggt catcagagat gcccagatgc aggacgagag ccagtacttc 300

ttcagagtgg aacggggcag ctacgtgcgg tacaacttta tgaacgacgg attcttcctg 360

aaagtgacgg ccctgacaca gaaacccgac gtgtacatcc ccgagacact ggaacctggc 420

cagcctgtga cagtgatctg cgtgttcaac tgggccttcg aggaatgccc tccaccttcc 480

ttttcttgga ctggcgccgc tctgtctagc cagggcacaa agcctaccac cagccacttt 540

agcgtgctga gcttcacccc tagacctcag gaccacaaca ccgacctgac ctgccacgtg 600

gacttcagca gaaaaggcgt gtcagcccag agaaccgtgc ggctgagagt ggcctatgct 660

cccagagatc tcgtgatcag catcagccgg gacaacaccc ctgctctgga acctcagcct 720

cagggcaatg tgccttacct ggaagcccag aagggccagt tcctgagact gctgtgtgcc 780

gccgattctc agcctcctgc tacactgtct tgggtgctgc agaacagagt gctgagcagc 840

tctcaccctt ggggccctag accactggga cttgaactgc ctggtgtcaa ggcaggcgac 900

agcggcagat acacatgcag agccgagaac agactgggca gccagcagag agcactggat 960

ctgagcgtgc agtaccctcc tgagaacctg agagtgatgg tgtcccaggc caaccggacc 1020

gtgctggaaa atctcggcaa tggcacaagc ctgcctgtgc tggaaggcca gtctctgtgt 1080

ctcgtgtgtg tgacccacag cagccctcca gccagactct cttggacaca gcgaggacag 1140

gtgctgtctc ctagccagcc ttctgatcct ggcgtcctgg aactgcctag agtgcaggtt 1200

gagcacgagg gcgagttcac ctgtcacgcc agacatcctc tgggctctca gcacgtttcc 1260

ctgagcctgt ctgtgcacta cagccctaag ctgctgggcc ctagctgttc ttgggaagcc 1320

gaaggcctgc actgcagctg tagctctcaa gcctctcctg ctcctagcct gagatggtgg 1380

ctgggcgaag aactgctcga gggcaatagc tcccaggaca gcttcgaagt gaccccttct 1440

tctgccggac cttgggccaa tagctctctg tctctgcacg gcggactgag cagtggactg 1500

agactgagat gcgaggcctg gaatgtgcac ggtgctcagt ctggctctat cctgcagctg 1560

cccgataaga agggcctgat cagcaccgcc ttcagcaacg gcggaggtgg aagtggcgga 1620

ggcggatccg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 1680

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 1740

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1800

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggt 1860

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1920

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1980

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 2040

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 2100

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 2160

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 2220

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 2280

cagaagagcc tctccctgtc tccgggtaaa 2310

<210> 92
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(698)
<223> Siglec 11 FL

<400> 92

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

Pro Leu Leu Leu Pro Val Leu Gly Ala Gly Ser Leu Asn Lys Asp Pro
20 25 30

Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro Val Pro Glu Gly Leu
35 40 45

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

Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys Gly Arg Thr Ser Pro
65 70 75 80

Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln Ser Arg Glu Val Glu
85 90 95

Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly Asp Pro Gly Lys Gly
100 105 110

Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg Glu Asp Glu Ala Trp
115 120 125

Tyr Phe Phe Arg Val Glu Arg Gly Ser Arg Val Arg His Ser Phe Leu
130 135 140

Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu Thr Lys Lys Pro Asp
145 150 155 160

Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val Thr Val Ile
165 170 175

Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro Ala Pro Ser Phe Ser
180 185 190

Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr Arg Pro Ser Thr Ser
195 200 205

His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro Gln Asp His Asp Thr
210 215 220

Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val Ser Ala Gln
225 230 235 240

Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Lys Asp Leu Ile Ile
245 250 255

Ser Ile Ser His Asp Asn Thr Ser Ala Leu Glu Leu Gln Gly Asn Val
260 265 270

Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu Arg Leu Leu Cys Ala
275 280 285

Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val Leu Gln Asp Arg
290 295 300

Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Thr Leu Gly Leu Glu
305 310 315 320

Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala
325 330 335

Glu Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu Asp Leu Ser Val Gln
340 345 350

Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr
355 360 365

Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly
370 375 380

Gln Ser Leu Arg Leu Val Cys Val Thr His Ser Ser Pro Pro Ala Arg
385 390 395 400

Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly Pro Ser Gln Pro Ser
405 410 415

Asp Pro Gly Val Leu Glu Leu Pro Pro Ile Gln Met Glu His Glu Gly
420 425 430

Glu Phe Thr Cys His Ala Gln His Pro Leu Gly Ser Gln His Val Ser
435 440 445

Leu Ser Leu Ser Val His Tyr Pro Pro Gln Leu Leu Gly Pro Ser Cys
450 455 460

Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys Ser Ser Gln Ala Ser
465 470 475 480

Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu Glu Leu Leu Glu Gly
485 490 495

Asn Ser Ser Gln Gly Ser Phe Glu Val Thr Pro Ser Ser Ala Gly Pro
500 505 510

Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly Leu Ser Ser Gly Leu
515 520 525

Arg Leu Arg Cys Lys Ala Trp Asn Val His Gly Ala Gln Ser Gly Ser
530 535 540

Val Phe Gln Leu Leu Pro Gly Lys Leu Glu His Gly Gly Gly Leu Gly
545 550 555 560

Leu Gly Ala Ala Leu Gly Ala Gly Val Ala Ala Leu Leu Ala Phe Cys
565 570 575

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

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

Ser Gln Gly His Gln His Glu Cys Ser Ala Gly Ser Ser Gln Asp His
610 615 620

Pro Pro Pro Gly Ala Ala Thr Tyr Thr Pro Gly Lys Gly Glu Glu Gln
625 630 635 640

Glu Leu His Tyr Ala Ser Leu Ser Phe Gln Gly Leu Arg Leu Trp Glu
645 650 655

Pro Ala Asp Gln Glu Ala Pro Ser Thr Thr Glu Tyr Ser Glu Ile Lys
660 665 670

Ile His Thr Gly Gln Pro Leu Arg Gly Pro Gly Phe Gly Leu Gln Leu
675 680 685

Glu Arg Glu Met Ser Gly Met Val Pro Lys
690 695

<210> 93
<211> 3183
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(3183)
<223> Siglec 11 FL

<400> 93
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tccttcccag ccaggccggc ccagaagcca gatggtcccg ggacaggccc agccccagag 120

cccagagatg ctgctgctgc ccctgctgct gcccgtgctg ggggcggggt ccctgaacaa 180

ggatcccagt tacagtcttc aagtgcagag gcaggtgccg gtgccggagg gcctgtgtgt 240

catcgtgtct tgcaacctct cctacccccg ggatggctgg gacgagtcta ctgctgctta 300

tggctactgg ttcaaaggac ggaccagccc aaagacgggt gctcctgtgg ccactaacaa 360

ccagagtcga gaggtggaaa tgagcacccg ggaccgattc cagctcactg gggatcccgg 420

caaagggagc tgctccttgg tgatcagaga cgcgcagagg gaggatgagg catggtactt 480

ctttcgggtg gagagaggaa gccgtgtgag acatagtttc ctgagcaatg cgttctttct 540

aaaagtaaca gccctgacta agaagcctga tgtctacatc cccgagaccc tggagcccgg 600

gcagccggtg acggtcatct gtgtgtttaa ctgggctttc aagaaatgtc cagccccttc 660

tttctcctgg acgggggctg ccctctcccc tagaagaacc agaccaagca cctcccactt 720

ctcagtgctc agcttcacgc ccagccccca ggaccacgac accgacctca cctgccatgt 780

ggacttctcc agaaagggtg tgagcgcaca gaggaccgtc cgactccgtg tggcctatgc 840

ccccaaagac cttattatca gcatttcaca tgacaacacg tcagccctgg aactccaggg 900

aaacgtcata tatctggaag ttcagaaagg ccagttcctg cggctcctct gtgctgctga 960

cagccagccc cctgccacgc tgagctgggt cctgcaggac agagtcctct cctcgtccca 1020

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ctgtgtcacc cacagcagcc ccccagccag gctgagctgg acccggtggg gacagaccgt 1320

gggcccctcc cagccctcag accccggggt cctggagctg ccacccattc aaatggagca 1380

cgaaggagag ttcacctgcc acgctcagca ccctctgggc tcccagcacg tctctctcag 1440

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gggtcaccag catgaatgct cggcaggcag ctcccaagac cacccgcccc caggtgcagc 1980

cacctacacc ccggggaagg gggaagagca ggagctccac tatgcctccc tcagcttcca 2040

gggcctgagg ctctgggagc ctgcggacca ggaggccccc agcaccaccg agtactcgga 2100

gatcaagatc cacacaggac agcccctgag gggcccaggc tttgggcttc aattggagag 2160

ggagatgtca gggatggttc caaagtgaag aggtctccat ggcaacagga caccagcaag 2220

tgtgtgggag tcgcactggt gtgacggcca gaactggact cagatttcag ccccatcccc 2280

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gctcattgtt atatttttag tagagacagg gttttgccat gtttccctgg ctggtctcag 2520

actcctgggc tcaagcaatc tgcccgcctc tgcctcccaa agtgctggga ttacagacgt 2580

gagccaccac agctggctga agattatact ttcaattcag agcgagtttg aagatgacac 2640

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ggaaaccagg cagaggaggc acagggtgct ctccagaacg agaagccagc tcctggagtt 2760

gtttgctgca actgccattc cccgttgatg accatgctct tccttcagaa gagggagagt 2820

gagaggacca agtccaagtg gttcccattt gaacatttaa aaaaaaaaaa aaggctgggc 2880

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caggagttca agaccagcct gggcaagatg gtgaaacccc atctctacta aaaatacaaa 3000

aattagccgg gcatggtggc gggcgcctaa aatcccagct actcgggaga ctaggcagag 3060

aattggttga acccgggagg tggaggttgc agtgagccga gatcgtccca ctgcactcca 3120

gcctgggcaa cagagtgaga ctctgtttct aaataaataa atgaaaaaaa aaaaaaaaaa 3180

aaa 3183

<210> 94
<211> 534
<212> PRT

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(534)
<223> Siglec 11 Fragment (28-561)

<400> 94

Leu Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro
1 5 10 15

Val Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro
20 25 30

Arg Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys
35 40 45

Gly Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln
50 55 60

Ser Arg Glu Val Glu Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly
65 70 75 80

Asp Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg
85 90 95

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

Arg His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu
115 120 125

Thr Lys Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln
130 135 140

Pro Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro
145 150 155 160

Ala Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr
165 170 175

Arg Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro
180 185 190

Gln Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys
195 200 205

Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
210 215 220

Lys Asp Leu Ile Ile Ser Ile Ser His Asp Asn Thr Ser Ala Leu Glu
225 230 235 240

Leu Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu
245 250 255

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
260 265 270

Val Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
275 280 285

Thr Leu Gly Leu Glu Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg
290 295 300

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu
305 310 315 320

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
325 330 335

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
340 345 350

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

Ser Pro Pro Ala Arg Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly
370 375 380

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Pro Ile Gln
385 390 395 400

Met Glu His Glu Gly Glu Phe Thr Cys His Ala Gln His Pro Leu Gly
405 410 415

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Pro Pro Gln Leu
420 425 430

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
435 440 445

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
450 455 460

Glu Leu Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Glu Val Thr Pro
465 470 475 480

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
485 490 495

Leu Ser Ser Gly Leu Arg Leu Arg Cys Lys Ala Trp Asn Val His Gly
500 505 510

Ala Gln Ser Gly Ser Val Phe Gln Leu Leu Pro Gly Lys Leu Glu His
515 520 525

Gly Gly Gly Leu Gly Leu
530

<210> 95
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 11 Fragment (28-561) SAX

<400> 95

Leu Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro
1 5 10 15

Val Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro
20 25 30

Arg Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys
35 40 45

Gly Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln
50 55 60

Ser Arg Glu Val Glu Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly
65 70 75 80

Asp Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg
85 90 95

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

Arg His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu
115 120 125

Thr Lys Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln
130 135 140

Pro Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro
145 150 155 160

Ala Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr
165 170 175

Arg Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro
180 185 190

Gln Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys
195 200 205

Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
210 215 220

Lys Asp Leu Ile Ile Ser Ile Ser His Asp Asn Thr Ser Ala Leu Glu
225 230 235 240

Leu Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu
245 250 255

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
260 265 270

Val Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
275 280 285

Thr Leu Gly Leu Glu Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg
290 295 300

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu
305 310 315 320

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
325 330 335

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
340 345 350

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

Ser Pro Pro Ala Arg Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly
370 375 380

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Pro Ile Gln
385 390 395 400

Met Glu His Glu Gly Glu Phe Thr Cys His Ala Gln His Pro Leu Gly
405 410 415

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Pro Pro Gln Leu
420 425 430

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
435 440 445

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
450 455 460

Glu Leu Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Glu Val Thr Pro
465 470 475 480

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
485 490 495

Leu Ser Ser Gly Leu Arg Leu Arg Cys Lys Ala Trp Asn Val His Gly
500 505 510

Ala Gln Ser Gly Ser Val Phe Gln Leu Leu Pro Gly Lys Leu Glu His
515 520 525

Gly Gly Gly Leu Gly Leu
530

<210> 96
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 11 Fragment (28-561) / (G4S)2 / hIgG1 Fc N297G

<400> 96

Leu Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro
1 5 10 15

Val Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro
20 25 30

Arg Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys
35 40 45

Gly Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln
50 55 60

Ser Arg Glu Val Glu Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly
65 70 75 80

Asp Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg
85 90 95

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

Arg His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu
115 120 125

Thr Lys Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln
130 135 140

Pro Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro
145 150 155 160

Ala Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr
165 170 175

Arg Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro
180 185 190

Gln Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys
195 200 205

Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
210 215 220

Lys Asp Leu Ile Ile Ser Ile Ser His Asp Asn Thr Ser Ala Leu Glu
225 230 235 240

Leu Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu
245 250 255

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
260 265 270

Val Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
275 280 285

Thr Leu Gly Leu Glu Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg
290 295 300

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu
305 310 315 320

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
325 330 335

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
340 345 350

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

Ser Pro Pro Ala Arg Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly
370 375 380

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Pro Ile Gln
385 390 395 400

Met Glu His Glu Gly Glu Phe Thr Cys His Ala Gln His Pro Leu Gly
405 410 415

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Pro Pro Gln Leu
420 425 430

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
435 440 445

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
450 455 460

Glu Leu Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Glu Val Thr Pro
465 470 475 480

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
485 490 495

Leu Ser Ser Gly Leu Arg Leu Arg Cys Lys Ala Trp Asn Val His Gly
500 505 510

Ala Gln Ser Gly Ser Val Phe Gln Leu Leu Pro Gly Lys Leu Glu His
515 520 525

Gly Gly Gly Leu Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
530 535 540

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
545 550 555 560

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
565 570 575

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
580 585 590

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
595 600 605

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr
610 615 620

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
625 630 635 640

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
645 650 655

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
660 665 670

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
675 680 685

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
690 695 700

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
705 710 715 720

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
725 730 735

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
740 745 750

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
755 760 765

Pro Gly Lys
770

<210> 97
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 11 Fragment (28-561) / (G4S)2 / hIgG1 Fc N297G

<400> 97
ctgaacaagg accccagcta tagcctgcag gtccagagac aggtgccagt gcctgaaggc 60

ctgtgtgtga tcgtgtcctg caacctgagc taccccagag atggctggga tgagagcaca 120

gccgcctacg gctactggtt caagggcaga acaagcccca aaacaggcgc cccagtggcc 180

accaacaacc agagcagaga agtggaaatg agcacccggg acagattcca gctgacaggc 240

gatcctggca agggcagctg ttctctggtc atcagagatg cccagagaga ggacgaggcc 300

tggtacttct tcagagtgga acggggctct agagtgcggc acagctttct gagcaacgca 360

ttcttcctga aagtgacggc cctgaccaag aaacccgacg tgtacatccc cgagacactg 420

gaacctggcc agcctgtgac agtgatctgc gtgttcaact gggccttcaa gaagtgcccc 480

gctcctagct ttagctggac aggcgctgct ctgagcccca gaagaaccag acctagcacc 540

agccacttca gcgtgctgag cttcacccca tctccacagg accacgacac cgatctgacc 600

tgccacgtgg acttcagcag aaagggcgtg tcagcccaga gaaccgtcag actgagagtg 660

gcctacgctc ccaaggacct gatcatcagc atcagccacg acaacacaag cgccctggaa 720

ctgcagggca acgtgatcta cctggaagtg cagaagggcc agttcctgag actgctgtgt 780

gccgccgatt ctcagcctcc tgctacactg tcttgggtgc tgcaggacag agtgctgagc 840

agcagtcatc cttggggccc tagaacactg ggcctcgaac tgagaggtgt cagagccggc 900

gatagcggca gatacacatg cagagccgag aacagactgg gctctcagca gcaggctctg 960

gatctgagcg tgcagtaccc tcctgagaac ctgagagtga tggtgtccca ggccaaccgg 1020

accgtgctgg aaaatctcgg caatggcaca agcctgcctg tgctggaagg ccagagtctg 1080

agactcgtgt gtgtgaccca cagcagccct ccagccagac tgagttggac aagatggggc 1140

cagacagtgg gccctagcca gccttctgat cctggcgttt tggagctgcc tcctatccag 1200

atggaacacg agggcgagtt cacctgtcac gcccaacatc ctctcggcag ccagcatgtg 1260

tctctgagcc tgtctgtgca ctacccacct cagctgctgg gcccttcttg ttcttgggaa 1320

gccgagggcc tgcactgcag ctgtagttct caagcctctc ctgctcctag cctgagatgg 1380

tggctgggcg aagaactgct cgagggcaat agcagccagg gcagctttga agtgacccct 1440

tcttctgccg gaccttgggc caatagctct ctgtctctgc acggcggact gagcagtgga 1500

ctgagactga gatgcaaggc ctggaatgtg cacggcgctc agagcggctc tgtgtttcaa 1560

ctgctgcccg gcaagctgga acatggcgga ggacttggac ttggcggagg tggaagtggc 1620

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cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 1800

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1860

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1920

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1980

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 2040

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 2100

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 2160

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 2220

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 2280

acgcagaaga gcctctccct gtctccgggt aaa 2313

<210> 98
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 11 Fragment (28-561) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 98

Leu Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro
1 5 10 15

Val Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro
20 25 30

Arg Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys
35 40 45

Gly Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln
50 55 60

Ser Arg Glu Val Glu Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly
65 70 75 80

Asp Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg
85 90 95

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

Arg His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu
115 120 125

Thr Lys Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln
130 135 140

Pro Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro
145 150 155 160

Ala Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr
165 170 175

Arg Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro
180 185 190

Gln Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys
195 200 205

Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
210 215 220

Lys Asp Leu Ile Ile Ser Ile Ser His Asp Asn Thr Ser Ala Leu Glu
225 230 235 240

Leu Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu
245 250 255

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
260 265 270

Val Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
275 280 285

Thr Leu Gly Leu Glu Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg
290 295 300

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu
305 310 315 320

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
325 330 335

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
340 345 350

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

Ser Pro Pro Ala Arg Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly
370 375 380

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Pro Ile Gln
385 390 395 400

Met Glu His Glu Gly Glu Phe Thr Cys His Ala Gln His Pro Leu Gly
405 410 415

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Pro Pro Gln Leu

420 425 430

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
435 440 445

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
450 455 460

Glu Leu Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Glu Val Thr Pro
465 470 475 480

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
485 490 495

Leu Ser Ser Gly Leu Arg Leu Arg Cys Lys Ala Trp Asn Val His Gly
500 505 510

Ala Gln Ser Gly Ser Val Phe Gln Leu Leu Pro Gly Lys Leu Glu His
515 520 525

Gly Gly Gly Leu Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
530 535 540

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
545 550 555 560

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
565 570 575

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
580 585 590

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
595 600 605

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr
610 615 620

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
625 630 635 640

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
645 650 655

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
660 665 670

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
675 680 685

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
690 695 700

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
705 710 715 720

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
725 730 735

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
740 745 750

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
755 760 765

Pro Gly Lys
770

<210> 99
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 11 Fragment (28-561) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 99
ctgaacaagg accccagcta tagcctgcag gtccagagac aggtgccagt gcctgaaggc 60

ctgtgtgtga tcgtgtcctg caacctgagc taccccagag atggctggga tgagagcaca 120

gccgcctacg gctactggtt caagggcaga acaagcccca aaacaggcgc cccagtggcc 180

accaacaacc agagcagaga agtggaaatg agcacccggg acagattcca gctgacaggc 240

gatcctggca agggcagctg ttctctggtc atcagagatg cccagagaga ggacgaggcc 300

tggtacttct tcgccgtgga acggggctct agagtgcggc acagctttct gagcaacgca 360

ttcttcctga aagtgacggc cctgaccaag aaacccgacg tgtacatccc cgagacactg 420

gaacctggcc agcctgtgac agtgatctgc gtgttcaact gggccttcaa gaagtgcccc 480

gctcctagct ttagctggac aggcgctgct ctgagcccca gaagaaccag acctagcacc 540

agccacttca gcgtgctgag cttcacccca tctccacagg accacgacac cgatctgacc 600

tgccacgtgg acttcagcag aaagggcgtg tcagcccaga gaaccgtcag actgagagtg 660

gcctacgctc ccaaggacct gatcatcagc atcagccacg acaacacaag cgccctggaa 720

ctgcagggca acgtgatcta cctggaagtg cagaagggcc agttcctgag actgctgtgt 780

gccgccgatt ctcagcctcc tgctacactg tcttgggtgc tgcaggacag agtgctgagc 840

agcagtcatc cttggggccc tagaacactg ggcctcgaac tgagaggtgt cagagccggc 900

gatagcggca gatacacatg cagagccgag aacagactgg gctctcagca gcaggctctg 960

gatctgagcg tgcagtaccc tcctgagaac ctgagagtga tggtgtccca ggccaaccgg 1020

accgtgctgg aaaatctcgg caatggcaca agcctgcctg tgctggaagg ccagagtctg 1080

agactcgtgt gtgtgaccca cagcagccct ccagccagac tgagttggac aagatggggc 1140

cagacagtgg gccctagcca gccttctgat cctggcgttt tggagctgcc tcctatccag 1200

atggaacacg agggcgagtt cacctgtcac gcccaacatc ctctcggcag ccagcatgtg 1260

tctctgagcc tgtctgtgca ctacccacct cagctgctgg gcccttcttg ttcttgggaa 1320

gccgagggcc tgcactgcag ctgtagttct caagcctctc ctgctcctag cctgagatgg 1380

tggctgggcg aagaactgct cgagggcaat agcagccagg gcagctttga agtgacccct 1440

tcttctgccg gaccttgggc caatagctct ctgtctctgc acggcggact gagcagtgga 1500

ctgagactga gatgcaaggc ctggaatgtg cacggcgctc agagcggctc tgtgtttcaa 1560

ctgctgcccg gcaagctgga acatggcgga ggacttggac ttggcggagg tggaagtggc 1620

ggaggcggat ccgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 1680

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 1740

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 1800

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1860

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1920

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1980

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 2040

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 2100

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 2160

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 2220

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 2280

acgcagaaga gcctctccct gtctccgggt aaa 2313

<210> 100
<211> 595
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(595)
<223> Siglec 12 FL

<400> 100

Met Leu Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Cys Gly Arg Val
1 5 10 15

Gly Ala Lys Glu Gln Lys Asp Tyr Leu Leu Thr Met Gln Lys Ser Val
20 25 30

Thr Val Gln Glu Gly Leu Cys Val Ser Val Leu Cys Ser Phe Ser Tyr
35 40 45

Pro Gln Asn Gly Trp Thr Ala Ser Asp Pro Val His Gly Tyr Trp Phe
50 55 60

Arg Ala Gly Asp His Val Ser Arg Asn Ile Pro Val Ala Thr Asn Asn
65 70 75 80

Pro Ala Arg Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
85 90 95

Gly Asp Pro Gln Asn Lys Asp Cys Thr Leu Ser Ile Arg Asp Thr Arg
100 105 110

Glu Ser Asp Ala Gly Thr Tyr Val Phe Cys Val Glu Arg Gly Asn Met
115 120 125

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Ser
130 135 140

Gln Asp Leu Leu Ser Arg Tyr Arg Leu Glu Val Pro Glu Ser Val Thr
145 150 155 160

Val Gln Glu Gly Leu Cys Val Ser Val Pro Cys Ser Val Leu Tyr Pro
165 170 175

His Tyr Asn Trp Thr Ala Ser Ser Pro Val Tyr Gly Ser Trp Phe Lys
180 185 190

Glu Gly Ala Asp Ile Pro Trp Asp Ile Pro Val Ala Thr Asn Thr Pro
195 200 205

Ser Gly Lys Val Gln Glu Asp Thr His Gly Arg Phe Leu Leu Leu Gly
210 215 220

Asp Pro Gln Thr Asn Asn Cys Ser Leu Ser Ile Arg Asp Ala Arg Lys
225 230 235 240

Gly Asp Ser Gly Lys Tyr Tyr Phe Gln Val Glu Arg Gly Ser Arg Lys
245 250 255

Trp Asn Tyr Ile Tyr Asp Lys Leu Ser Val His Val Thr Ala Leu Thr
260 265 270

His Met Pro Thr Phe Ser Ile Pro Gly Thr Leu Glu Ser Gly His Pro
275 280 285

Arg Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro
290 295 300

Pro Thr Ile Thr Trp Met Gly Ala Ser Val Ser Ser Leu Asp Pro Thr

305 310 315 320

Ile Thr Arg Ser Ser Met Leu Ser Leu Ile Pro Gln Pro Gln Asp His
325 330 335

Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val Thr
340 345 350

Met Thr Arg Ala Val Arg Leu Asn Ile Ser Tyr Pro Pro Gln Asn Leu
355 360 365

Thr Met Thr Val Phe Gln Gly Asp Gly Thr Ala Ser Thr Thr Leu Arg
370 375 380

Asn Gly Ser Ala Leu Ser Val Leu Glu Gly Gln Ser Leu His Leu Val
385 390 395 400

Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp Gly
405 410 415

Ser Leu Thr Leu Ser Pro Ser Gln Ser Ser Asn Leu Gly Val Leu Glu
420 425 430

Leu Pro Arg Val His Val Lys Asp Glu Gly Glu Phe Thr Cys Arg Ala
435 440 445

Gln Asn Pro Leu Gly Ser Gln His Ile Ser Leu Ser Leu Ser Leu Gln
450 455 460

Asn Glu Tyr Thr Gly Lys Met Arg Pro Ile Ser Gly Val Thr Leu Gly
465 470 475 480

Ala Phe Gly Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Tyr Phe Cys
485 490 495

Ile Ile Phe Val Val Val Arg Ser Cys Arg Lys Lys Ser Ala Arg Pro
500 505 510

Ala Val Gly Val Gly Asp Thr Gly Met Glu Asp Ala Asn Ala Val Arg
515 520 525

Gly Ser Ala Ser Gln Gly Pro Leu Ile Glu Ser Pro Ala Asp Asp Ser
    530 535 540

Pro Pro His His Ala Pro Pro Ala Leu Ala Thr Pro Ser Pro Glu Glu
545 550 555 560

Gly Glu Ile Gln Tyr Ala Ser Leu Ser Phe His Lys Ala Arg Pro Gln
                565 570 575

Tyr Pro Gln Glu Gln Glu Ala Ile Gly Tyr Glu Tyr Ser Glu Ile Asn
            580 585 590

Ile Pro Lys
        595

<210> 101
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1788)
<223> Siglec 12 FL

<400> 101
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cagaaggatt acctgctgac aatgcagaag tccgtgacgg tgcaggaggg cctgtgtgtc 120

tctgtgcttt gctccttctc ctacccccaa aatggctgga ctgcctccga tccagttcat 180

ggctactggt tccgggcagg ggaccatgta agccggaaca ttccagtggc cacaaacaac 240

ccagctcgag cagtgcagga ggagactcgg gaccgattcc acctccttgg ggacccacag 300

aacaaggatt gtaccctgag catcagagac accagagaga gtgatgcagg gacatacgtc 360

ttttgtgtag agagaggaaa tatgaaatgg aattataaat atgaccagct ctctgtgaat 420

gtgacagcgt cccaggacct actgtcaaga tacaggctgg aggtgccaga gtcggtgact 480

gtgcaggagg gtctgtgtgt ctctgtgccc tgcagtgtcc tttacccccca ttacaactgg 540

actgcctcta gccctgttta tggatcctgg ttcaaggaag gggccgatat accatgggat 600

attccagtgg ccacaaacac cccaagtgga aaagtgcaag aggataccca cggtcgattc 660

ctcctccttg gggacccaca gaccaacaac tgctccctga gcatcagaga tgccaggaag 720

ggggattcag ggaagtacta cttccaggtg gagagaggaa gcaggaaatg gaactacata 780

tatgacaagc tctctgtgca tgtgacagcc ctgactcaca tgcccacctt ctccatcccg 840

gggaccctgg agtctggcca ccccaggaac ctgacctgct ctgtgccctg ggcctgtgaa 900

caggggacgc cccccacgat cacctggatg ggggcctccg tgtcctccct ggaccccact 960

atcactcgct cctcgatgct cagcctcatc ccacagcccc aggaccatgg caccagcctc 1020

acctgtcagg tgaccttgcc tggggccggc gtgaccatga ccagggctgt ccgactcaac 1080

atatcctatc ctcctcagaa cttgaccatg actgtcttcc aaggagatgg cacagcatcc 1140

acaaccttga ggaatggctc ggccctttca gtcctggagg gccagtccct gcaccttgtc 1200

tgtgctgtcg acagcaatcc ccctgccagg ctgagctgga cctgggggag cctgaccctg 1260

agcccctcac agtcctcgaa ccttggggtg ctggagctgc ctcgagtgca tgtgaaggat 1320

gaaggggaat tcacctgccg agctcagaac cctctaggct cccagcacat ttccctgagc 1380

ctctccctgc aaaacgagta cacaggcaaa atgaggccta tatcaggagt gacgctaggg 1440

gcattcgggg gagctggagc cacagccctg gtcttcctgt acttctgcat catcttcgtt 1500

gtagtgaggt cctgcaggaa gaaatcggca aggccagcag tgggcgtggg ggatacaggc 1560

atggaggacg caaacgctgt caggggctca gcctctcagg gacccctgat tgaatccccg 1620

gcagatgaca gccccccaca ccatgctccg ccagccctgg ccacccccctc cccagaggaa 1680

ggagagatcc agtatgcatc cctcagcttc cacaaagcga ggcctcagta cccacaggaa 1740

caggaggcca tcggctatga gtactccgag atcaacatcc ccaagtga 1788

<210> 102
<211> 396
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(396)
<223> Siglec 14 FL

<400> 102

Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp Gly Gly Ser Leu Gln

1 5 10 15

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
35 40 45

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

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
65 70 75 80

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
85 90 95

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

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
115 120 125

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
130 135 140

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
145 150 155 160

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
165 170 175

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
180 185 190

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
195 200 205

Thr Asn Leu Thr Cys Gln Val Lys Arg Gln Gly Ala Gln Val Thr Thr
210 215 220

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

Ile Ser Ile Phe Phe Arg Asn Gly Thr Gly Thr Ala Leu Arg Ile Leu
245 250 255

Ser Asn Gly Met Ser Val Pro Ile Gln Glu Gly Gln Ser Leu Phe Leu
260 265 270

Ala Cys Thr Val Asp Ser Asn Pro Pro Ala Ser Leu Ser Trp Phe Arg
275 280 285

Glu Gly Lys Ala Leu Asn Pro Ser Gln Thr Ser Met Ser Gly Thr Leu
290 295 300

Glu Leu Pro Asn Ile Gly Ala Arg Glu Gly Gly Glu Phe Thr Cys Arg
305 310 315 320

Val Gln His Pro Leu Gly Ser Gln His Leu Ser Phe Ile Leu Ser Val
325 330 335

Gln Arg Ser Ser Ser Ser Cys Ile Cys Val Thr Glu Lys Gln Gln Gly
340 345 350

Ser Trp Pro Leu Val Leu Thr Leu Ile Arg Gly Ala Leu Met Gly Ala
355 360 365

Gly Phe Leu Leu Thr Tyr Gly Leu Thr Trp Ile Tyr Tyr Thr Arg Cys
370 375 380

Gly Gly Pro Gln Gln Ser Arg Ala Glu Arg Pro Gly
385 390 395

<210> 103
<211> 1191
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1191)

<223> Siglec 14 FL

<400> 103
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tacgagctgc aagtgcagaa gtcggtgacg gtgcaggagg gcctgtgcgt ccttgtgccc 120

tgctccttct cttacccctg gagatcctgg tattcctctc ccccactcta cgtctactgg 180

ttccgggacg gggagatccc atactacgct gaggttgtgg ccacaaacaa cccagacaga 240

agagtgaagc cagagaccca gggccgattc cgcctccttg gggatgtcca gaagaagaac 300

tgctccctga gcatcggaga tgccagaatg gaggacacgg gaagctattt cttccgcgtg 360

gagagaggaa gggatgtaaa atatagctac caacagaata agctgaactt ggaggtgaca 420

gccctgatag agaaacccga catccacttt ctggagcctc tggagtccgg ccgccccaca 480

aggctgagct gcagccttcc aggatcctgt gaagcgggac cacctctcac attctcctgg 540

acggggaatg ccctcagccc cctggacccc gagaccaccc gctcctcgga gctcaccctc 600

acccccaggc ccgaggacca tggcaccaac ctcacctgtc aggtgaaacg ccaaggagct 660

caggtgacca cggagagaac tgtccagctc aatgtctcct atgctccaca gaacctcgcc 720

atcagcatct tcttcagaaa tggcacaggc acagccctgc ggatcctgag caatggcatg 780

tcggtgccca tccaggaggg ccagtccctg ttcctcgcct gcacagttga cagcaacccc 840

cctgcctcac tgagctggtt ccgggaggga aaagccctca atccttccca gacctcaatg 900

tctgggaccc tggagctgcc taacatagga gctagagagg gaggggaatt cacctgccgg 960

gttcagcatc cgctgggctc ccagcacctg tccttcatcc tttctgtgca gagaagctcc 1020

tcttcctgca tatgtgtaac tgagaaacag cagggctcct ggcccctcgt cctcaccctg 1080

atcagggggg ctctcatggg ggctggcttc ctcctcacct atggcctcac ctggatctac 1140

tataccaggt gtggaggccc ccagcagagc agggctgaga ggcctggctg a 1191

<210> 104
<211> 328
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(328)
<223> Siglec 15 FL

<400> 104

Met Glu Lys Ser Ile Trp Leu Leu Ala Cys Leu Ala Trp Val Leu Pro
1 5 10 15

Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu
20 25 30

Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala
85 90 95

Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
100 105 110

Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
115 120 125

Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
130 135 140

Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val
145 150 155 160

Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
165 170 175

Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
180 185 190

Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu
195 200 205

Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala
    210   215   220

Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala
225   230   235   240

Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His
                245   250   255

Gly Ala Ser Gly Ala Ser Thr Val Ala Leu Leu Leu Gly Ala Leu Gly
            260   265   270

Phe Lys Ala Leu Leu Leu Leu Gly Val Leu Ala Ala Arg Ala Ala Arg
        275   280   285

Arg Arg Pro Glu His Leu Asp Thr Pro Asp Thr Pro Pro Arg Ser Gln
    290   295   300

Ala Gln Glu Ser Asn Tyr Glu Asn Leu Ser Gln Met Asn Pro Arg Ser
305   310   315   320

Pro Pro Ala Thr Met Cys Ser Pro
                325

<210> 105
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(987)
<223> Siglec 15 FL

<400> 105
atggaaaagt ccatctggct gctggcctgc ttggcgtggg ttctcccgac aggctcattt 60

gtgagaacta aaatagatac tacggagaac ttgctcaaca cagaggtgca cagctcgcca 120

gcgcagcgct ggtccatgca ggtgccaccc gaggtgagcg cggaggcagg cgacgcggca 180

gtgctgccct gcaccttcac gcacccgcac cgccactacg acgggccgct gacggccatc 240

tggcgcgcgg gcgagcccta tgcgggcccg caggtgttcc gctgcgctgc ggcgcggggc 300

agcgagctct gccagacggc gctgagcctg cacggccgct tccggctgct gggcaacccg 360

cgccgcaacg acctctcgct gcgcgtcgag cgcctcgccc tggctgacga ccgccgctac 420

ttctgccgcg tcgagttcgc cggcgacgtc catgaccgct acgagagccg ccacggcgtc 480

cggctgcacg tgacagccgc gccgcggatc gtcaacatct cggtgctgcc cagtccggct 540

cacgccttcc gcgcgctctg cactgccgaa ggggagccgc cgcccgccct cgcctggtcc 600

ggcccggccc tgggcaacag cttggcagcc gtgcggagcc cgcgtgaggg tcacggccac 660

ctagtgaccg ccgaactgcc cgcactgacc catgacggcc gctacacgtg tacggccgcc 720

aacagcctgg gccgctccga ggccagcgtc tacctgttcc gcttccatgg cgccagcggg 780

gcctcgacgg tcgccctcct gctcggcgct ctcggcttca aggcgctgct gctgctcggg 840

gtcctggccg cccgcgctgc ccgccgccgc ccagagcatc tggacacccc ggacacccca 900

ccacggtccc aggcccagga gtccaattat gaaaatttga gccagatgaa cccccggagc 960

ccaccagcca ccatgtgctc accgtga 987

<210> 106
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(244)
<223> Siglec 15 Fragment (20-263)

<400> 106

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Pro Glu
20 25 30

Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys Thr Phe Thr
35 40 45

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg
65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val Glu Phe Ala
115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Arg Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu Pro Ser Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu Ala Ala Val
180 185 190

Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala Glu Leu Pro
195 200 205

Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr

<210> 107
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) SAX

<400> 107

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Pro Glu
20 25 30

Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys Thr Phe Thr
35 40 45

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg
65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val Glu Phe Ala
115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Ala Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu Pro Ser Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu Ala Ala Val
180 185 190

Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala Glu Leu Pro

195 200 205

Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr

<210> 108
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) / (G4S)2 / hIgG1 Fc N297G

<400> 108

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Pro Glu
20 25 30

Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys Thr Phe Thr
35 40 45

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg
65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val Glu Phe Ala

115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Arg Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu Pro Ser Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu Ala Ala Val
180 185 190

Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala Glu Leu Pro
195 200 205

Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys
245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val
325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 109
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) / (G4S)2 / hIgG1 Fc N297G

<400> 109
tttgtgcgga ccaagatcga caccaccgag aacctgctga acaccgaggt gcactctagc 60

cctgctcagc ggtggtctat gcaggtccca cctgaagtgt ctgccgaagc tggggatgct 120

gctgtgctgc cttgcacctt tacacaccct caccggcact acgatggccc tctgacagcc 180

atttggagag ccggcgaacc ttatgccgga ccacaggtgt tcagatgcgc tgccgctaga 240

ggctctgagc tgtgtcagac agccctgtct ctgcacggca gattcagact gctgggcaac 300

cccagaagaa acgacctgag cctgagagtg gaaagactgg ccctggccga cgacagacgg 360

tacttctgca gagtggaatt tgccggcgac gtgcacgaca gatacgagtc tagacacggc 420

gtgcggctgc acgttacagc cgctcctaga atcgtgaaca tcagcgtgct gccctctcca 480

gctcacgcct ttagagccct gtgtacagcc gaaggcgaac ctcctcctgc tcttgcttgg 540

agtggacccg ctctgggaaa ttctctggcc gccgtcagaa gccctagaga aggacacgga 600

cacctggtca cagccgaact gcctgctctg acacacgacg gcagatacac atgcacagcc 660

gccaatagcc tgggcagatc tgaggccagc gtgtacctgt tcagattcca tggcgccagc 720

ggcgcctcta caggcggagg tggaagtggc ggaggcggat ccgacaaaac tcacacatgc 780

ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagtac ggtagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1080

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140

caggtctaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 110
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) SAX / (G4S)2 / hIgG1 Fc

N297G

<400> 110

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Pro Glu
20 25 30

Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys Thr Phe Thr
35 40 45

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg
65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Ala Val Glu Phe Ala
115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Arg Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu Pro Ser Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu Ala Ala Val
180 185 190

Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala Glu Leu Pro
195 200 205

Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys
245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val
325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 111
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) SAX / (G4S)2 / hIgG1 Fc N297G

<400> 111
tttgtgcgga ccaagatcga caccaccgag aacctgctga acaccgaggt gcactctagc 60

cctgctcagc ggtggtctat gcaggtccca cctgaagtgt ctgccgaagc tggggatgct 120

gctgtgctgc cttgcacctt tacacaccct caccggcact acgatggccc tctgacagcc 180

atttggagag ccggcgaacc ttatgccgga ccacaggtgt tcagatgcgc tgccgctaga 240

ggctctgagc tgtgtcagac agccctgtct ctgcacggca gattcagact gctgggcaac 300

cccagaagaa acgacctgag cctgagagtg gaaagactgg ccctggccga cgacagacgg 360

tacttctgcg ccgtggaatt tgccggcgac gtgcacgaca gatacgagtc tagacacggc 420

gtgcggctgc acgttacagc cgctcctaga atcgtgaaca tcagcgtgct gccctctcca 480

gctcacgcct ttagagccct gtgtacagcc gaaggcgaac ctcctcctgc tcttgcttgg 540

agtggacccg ctctgggaaa ttctctggcc gccgtcagaa gccctagaga aggacacgga 600

cacctggtca cagccgaact gcctgctctg acacacgacg gcagatacac atgcacagcc 660

gccaatagcc tgggcagatc tgaggccagc gtgtacctgt tcagattcca tggcgccagc 720

ggcgcctcta caggcggagg tggaagtggc ggaggcggat ccgacaaaac tcacacatgc 780

ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagtac ggtagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1080

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140

caggtctaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 112
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Mouse Siglec 15 Fragment / (G4S)2 / hIgG1 Fc N297G

<400> 112

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Ala Glu
20 25 30

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

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg

65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val Glu Phe Ala
115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Arg Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Ile Asn Ile Ser Val Leu Pro Gly Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Gly Ser Ala Ala Val
180 185 190

Pro Ser Ser Gly Gln Gly His Gly His Leu Val Thr Ala Glu Leu Pro
195 200 205

Ala Leu Asn His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys
245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val
                325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    370 375 380

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 113

<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Mouse Siglec 15 Fragment / (G4S)2 / hIgG1 Fc N297G

<400> 113
ttcgtgcgga ccaagatcga caccaccgag aacctgctga acaccgaggt gcactctagc 60

cctgctcagc ggtggtctat gcaggtccca gctgaagtgt ctgctgctgc tggggatgct 120

gctgtgctgc cttgcacctt tacacaccct caccggcact acgatggccc tctgacagcc 180

atttggagag ccggcgaacc ttatgccgga ccacaggtgt tcagatgcgc tgccgctaga 240

ggctctgagc tgtgtcagac agccctgtct ctgcacggca gattcagact gctgggcaac 300

cccagaagaa acgacctgag cctgagagtg gaaagactgg ccctggccga cgacagacgg 360

tacttctgca gagtggaatt tgccggcgac gtgcacgaca gatacgagtc tagacacggc 420

gtgcggctgc acgttacagc cgctcctaga atcatcaaca tcagcgtgct gcccggacct 480

gctcacgctt ttagagccct gtgtacagcc gagggcgaac ctcctcctgc tcttgcttgg 540

agtggacccg ctctcggaaa tggatctgcc gccgttccta gctctggcca aggacacgga 600

catctggtca cagccgaact gcccgctctg aaccacgacg gcagatacac atgtaccgcc 660

gccaatagcc tgggcagatc tgaggctagc gtgtacctgt tcagattcca cggcgccagc 720

ggagcctcta caggcggagg tggaagtggc ggaggcggat ccgacaaaac tcacacatgc 780

ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagtac ggtagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1080

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140

caggtctaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 114
<211> 481
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(481)
<223> Siglec 16 FL

<400> 114

Met Leu Leu Leu Pro Leu Leu Leu Pro Val Leu Gly Ala Gly Ser Leu
1 5 10 15

Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro Val
20 25 30

Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro Arg
35 40 45

Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys Gly
50 55 60

Trp Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln Ser
65 70 75 80

Arg Glu Val Glu Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly Asp
85 90 95

Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg Glu
100 105 110

Asp Glu Ala Trp Tyr Phe Phe Arg Val Glu Arg Gly Ser Arg Val Arg
115 120 125

His Ser Phe Val Asn Asn Leu Phe Phe Leu Lys Val Thr Ala Leu Thr
130 135 140

Gln Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro
145 150 155 160

Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro Ala
165 170 175

Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr Arg
180 185 190

Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro Gln
195 200 205

Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
210 215 220

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Ser Leu Glu Leu
225 230 235 240

Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu Arg
245 250 255

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
260 265 270

Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Thr
275 280 285

Leu Gly Leu Glu Leu Arg Gly Val Arg Ala Gly Asp Ser Gly Arg Tyr
290 295 300

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
305 310 315 320

Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser Gln
325 330 335

Ala Asn Arg Thr Val Leu Glu Asn Leu Arg Asn Gly Thr Ser Leu Arg
340 345 350

Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Val Thr His Ser Ser
355 360 365

Pro Pro Ala Arg Leu Ser Trp Thr Arg Trp Gly Gln Thr Val Gly Pro
370 375 380

Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Met
385 390 395 400

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
405 410 415

Gln Arg Val Ser Leu Ser Phe Ser Val His Cys Lys Ser Gly Pro Met
420 425 430

Thr Gly Val Val Leu Val Ala Val Gly Glu Val Ala Met Lys Ile Leu
435 440 445

Leu Leu Cys Leu Cys Leu Ile Leu Leu Arg Val Arg Ser Cys Arg Arg
450 455 460

Lys Ala Ala Arg Ala Ala Leu Gly Met Glu Ala Ala Asp Ala Val Thr
465 470 475 480

Asp

<210> 115
<211> 3811
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(3811)
<223> Siglec 16 FL

<400> 115
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ggcaggtgcc ggtgccggag ggcctgtgtg tcatcgtgtc ttgcaacctc tcctaccccc 180

gggatggctg ggacgagtct actgctgctt atggctactg gttcaaagga tggaccagcc 240

caaagacggg tgctcctgtg gccactaaca accagagtcg agaggtggaa atgagcaccc 300

gggaccgatt ccagctcact ggggatcccg gcaaagggag ctgctccttg gtgatcagag 360

acgcgcagag ggaggatgag gcatggtact tctttcgggt ggagagagga agccgtgtga 420

gacatagttt cgtgaacaat ttgttctttc taaaagtaac agccctgact cagaagcctg 480

atgtctacat ccccgagacc ctggagcccg ggcagccggt gacggtcatc tgtgtgttta 540

actgggcttt caagaaatgt ccagcccctt ctttctcctg gacgggggct gccctctccc 600

ctagaagaac cagaccaagc acctcccact tctcagtgct cagcttcacg cccagccccc 660

aggaccacga caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 720

agaggaccgt ccgactccgt gtggcctccc tggaactcca gggaaacgtc atatatctgg 780

aagttcagaa aggccagttc ctgcggctcc tctgtgctgc tgacagccag ccccctgcca 840

cgctgagctg ggtcctgcag gacagagtcc tctcctcgtc ccacccctgg ggccccagaa 900

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cggagaacag gcttggctcc cagcagcgag ccctggacct ctctgtgcag tatcctccag 1020

agaacctgag agtgatggtt tcccaagcaa acaggacagt cctggaaaac ctgaggaacg 1080

gcacatccct ccgggtcctg gagggccaaa gcctgcgtct ggtctgtgtc acacacagca 1140

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cagaccctgg ggtcctggag ctgcctcggg ttcaaatgga gcacgaagga gagttcacct 1260

gccacgctcg gcacccgctg ggctcccagc gcgtctctct cagcttctcc gtgcactgca 1320

aatcagggcc catgacgggg gtggttctgg tggctgttgg ggaggtggct atgaagatcc 1380

tgcttctctg cctctgcctc atcctcctca gagtgaggtc ttgcaggagg aaggcagcaa 1440

gggcagcatt gggcatggag gctgcagacg ctgtcacgga ctaatctcca gactccagac 1500

tgcttccaga tgcctcctca tccagttcct ccacagtctg agcggccgtg tttcctctgc 1560

aggctttgca tggtctgtcc cctgctggac tctcctgatc cctcctttcc ctgtcaccca 1620

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gatccgccag cctcggcctc ccaaagtggt ggggttacat gtgtgagcca ccgtgcccag 2040

ccagctgtgt cttctttttg caggatttac ttacaaaatt ccttgcagct gcagtctgcg 2100

ttccacccac atcctaatat ggtgtttgcg gtggtcacat ccaacttcct tcctcctcca 2160

tccatggaac gtgcattagg gaggaaccac acgcaccacg tgcaagatga gccagttccc 2220

tgaacggccg gccacggcgt taaccgcgct gctctgggct ctgcacgtct catctgctga 2280

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gtggtggctc atgcctgtaa tcccagcact ttgggaggcc aaggcaggca gatcacaagg 2640

tcaggagttt gagaccagcc tggccaatat ggtgaaaccc agtctctact aaaaatacaa 2700

aaattagccg ggtgtggtgg cgggcgcctg tagtcccagc tactcgggag gctgaggcag 2760

aagaatcatt tgaaccagga ggtggaggtt gcagtgagcc gagatcgcat cactgcactc 2820

cagcctgggc gacagagcaa gactgtctca aaaactaaaa caaaaaaaca ccaccaccac 2880

caccaatgtc tgattaaatc taagccacgg ttccattttg gggcaagggg cagggtgtgg 2940

gtgtggtgga cagagaacgg gctccagcca ccatcagctg cacgtcctgg tagcacctga 3000

gccattccca gtctcctgtg ctgggagatc atcatctaat cctgatgatg acgccctcct 3060

ctcagagctc gggggatgag ctgccaaaac ccatggaggt tcaaaacccg ggctctggag 3120

acagaagaca ctgggctcag agacatgggg ccactgtcca ggctttccct gggcctggac 3180

ctgggctcct tccactgtct gagcagggtc agcctgggct ggctgtgctg gttcaagaga 3240

tgagggagga ggacacagcg gttgccagga ccctgaggca ctggactggg cactgcccca 3300

aggggcagag gatggaaccc ggtgttgata ttgtgatgct gacccgtctg ctcacctgat 3360

ttgggtgctg aagggcagct gaccccccta atcttttata gacttgtgaa acgaaaataa 3420

ataaaagtca agctgggaac agcttagggc aaacctgcct cccattctat tcaaagccac 3480

ccctctgctc actgagatag atgcatgtct gatcacctca gttgggaaag gctaatcaga 3540

aactccaaag aatgcatctg ttcatctctc acccatctgt gacctggaag ccccctcccc 3600

acttcgagtc ttcctgcctt tgcttcaagt tttcccgcct ttccaaatgg aaccaaagta 3660

cttcttacat atagtgactc atgtctcaag tctccctaaa acgtataaaa ctaagctgtg 3720

ccccaaccac gctgaccatg tcatcaggac ctcctgaggc tgtgtcacgg cctgtgtcct 3780

caaccttggc aaaataaact ttctaaatta a 3811

<210> 116
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(418)
<223> Siglec 16 Fragment (15-434)

<400> 116

Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro Val
1 5 10 15

Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro Arg
20 25 30

Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys Gly
35 40 45

Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln Ser
50 55 60

Arg Glu Val Ala Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly Asp
65 70 75 80

Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg Glu
85 90 95

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

His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu Thr
115 120 125

Gln Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro
130 135 140

Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro Ala
145 150 155 160

Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr Arg
165 170 175

Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro Gln
180 185 190

Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
195 200 205

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Ser Leu Glu Leu
210 215 220

Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu Arg
225 230 235 240

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
245 250 255

Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Thr
260 265 270

Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg Tyr
275 280 285

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
290 295 300

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

Ala Asn Arg Thr Val Leu Glu Asn Leu Arg Asn Gly Thr Ser Leu Arg
325 330 335

Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Val Thr His Ser Ser
340 345 350

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

Ser Gln Pro Ser Asp Pro Gly Val Leu Gln Leu Pro Arg Val Gln Met
370 375 380

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
385 390 395 400

Gln Arg Val Ser Leu Ser Phe Ser Val His Cys Lys Ser Gly Pro Met
405 410 415

Thr Gly

<210> 117
<211> 655
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 16 Fragment (15-434) (G4S)2 / hIgG1 Fc N297G

<400> 117

Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro Val
1 5 10 15

Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro Arg
20 25 30

Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys Gly
35 40 45

Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln Ser
50 55 60

Arg Glu Val Ala Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly Asp
65 70 75 80

Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg Glu
85 90 95

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

His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu Thr
115 120 125

Gln Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro
130 135 140

Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro Ala
145 150 155 160

Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr Arg
165 170 175

Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro Gln
180 185 190

Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
195 200 205

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Ser Leu Glu Leu
210 215 220

Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu Arg
225 230 235 240

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
245 250 255

Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Thr
260 265 270

Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg Tyr
275 280 285

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
290 295 300

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

Ala Asn Arg Thr Val Leu Glu Asn Leu Arg Asn Gly Thr Ser Leu Arg
325 330 335

Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Val Thr His Ser Ser
340 345 350

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

Ser Gln Pro Ser Asp Pro Gly Val Leu Gln Leu Pro Arg Val Gln Met
370 375 380

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
385 390 395 400

Gln Arg Val Ser Leu Ser Phe Ser Val His Cys Lys Ser Gly Pro Met
405 410 415

Thr Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His
420 425 430

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
435 440 445

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
450 455 460

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
465 470 475 480

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
485 490 495

Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser
500 505 510

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
515 520 525

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
530 535 540

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
545 550 555 560

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
565 570 575

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
580 585 590

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
595 600 605

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
610 615 620

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
625 630 635 640

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650 655

<210> 118
<211> 1965
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 16 Fragment (15-434) (G4S)2 / hIgG1 Fc N297G

<400> 118
aacaaggacc ccagctacag cctgcaggtc cagagacagg tgccagtgcc tgaaggcctg 60

tgtgtgatcg tgtcctgcaa cctgagctac cccagagatg gctgggatga gagcacagcc 120

gcctacggct actggttcaa gggcagaaca agccccaaaa caggcgcccc agtggccacc 180

aacaaccagt ctagagaagt ggccatgagc acccgggaca gattccagtt gacaggcgat 240

cctggcaagg gcagctgtag cctggttatc agagatgccc agagagagga cgaggcctgg 300

tacttcttca gagtggaacg gggctctaga gtgcggcaca gctttctgag caacgcattc 360

ttcctgaaag tgacggccct gacacagaaa cccgacgtgt acatccccga gacactggaa 420

cctggccagc ctgtgacagt gatctgcgtg ttcaactggg ccttcaagaa gtgccccgct 480

cctagcttta gctggacagg cgctgctctg agccccagaa gaaccagacc tagcaccagc 540

cacttcagcg tgctgagctt caccccatct ccacaggacc acgacaccga tctgacctgc 600

cacgtggact tcagcagaaa gggcgtgtca gcccagagaa ccgtcagact gagagtggcc 660

agtctcgagc tgcagggcaa cgtgatctac ctggaagtgc agaagggcca gttcctgaga 720

ctgctgtgtg ccgccgattc tcagcctcct gctacactgt cttgggtgct gcaggacaga 780

gtgctgagca gcagtcatcc ttggggccct agaacactgg gcctcgaatt gcctggtgtc 840

aaggccggcg atagcggcag atacacatgc agagccgaga acagactggg cagccagcag 900

agagcactgg atctgagcgt gcagtaccct cctgagaacc tgagagtgat ggtgtcccag 960

gccaaccgga ccgtgctgga aaacctgaga aatggcacca gcctgagggt gctcgaggga 1020

cagtctctga gactcgtgtg tgtgacccac agcagccctc cagccagact ctcttggaca 1080

tggggagagc agacagtggg ccctagccag ccttctgatc ctggtgttct gcagctgccc 1140

cgggtgcaga tggaacacga aggcgagttt acctgtcacg ccagacatcc tctgggctcc 1200

cagagagtgt ctctgagctt tagcgtgcac tgcaagagcg gccctatgac aggaggcgga 1260

ggtggaagtg gcggaggcgg atccgacaaa actcacacat gcccaccgtg cccagcacct 1320

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 1380

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 1440

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1500

gaggagcagt acggtagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1560

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1620

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtcta caccctgccc 1680

ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1740

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1800

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1860

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1920

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1965

<210> 119
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: HSA-binding protein

<400> 119

Leu Lys Glu Ala Lys Glu Lys Ala Ile Glu Glu Leu Lys Lys Ala Gly
1 5 10 15

Ile Thr Ser Asp Tyr Tyr Phe Asp Leu Ile Asn Lys Ala Lys Thr Val
20 25 30

Glu Gly Val Asn Ala Leu Lys Asp Glu Ile Leu Lys Ala
35 40 45

<210> 120
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / AS / hIgG1
Fc

<400> 120

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu

275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Ala Ser Asp Lys Thr
325 330 335

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
340 345 350

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
355 360 365

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
370 375 380

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
385 390 395 400

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
420 425 430

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
435 440 445

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
450 455 460

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
465 470 475 480

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
485 490 495

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
500 505 510

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
515 520 525

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
530 535 540

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555 560

<210> 121
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / AS / hIgG1 Fc

<400> 121
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcagga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

agcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtaccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

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cagagtaagg ccaccagcgg cgtgacccaa ggagctagcg acaaaactca cacatgccca 1020

ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 1080

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 1140

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1200

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1260

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1320

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1380

gtctacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 1440

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1500

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctat 1560

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1620

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1680

<210> 122
<211> 563
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX / EPKSS / hIgG1 Fc N297G

<400> 122

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg

50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Glu Pro Lys Ser Ser
325 330 335

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
340 345 350

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
355 360 365

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
370 375 380

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
385 390 395 400

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr
405 410 415

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
420 425 430

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
435 440 445

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
450 455 460

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
465 470 475 480

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

485 490 495

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
500 505 510

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
515 520 525

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
530 535 540

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
545 550 555 560

Pro Gly Lys

<210> 123
<211> 1689
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX / EPKSS / hIgG1 Fc N297G

<400> 123
cagaccagca agctgctgac catgcagagc agcgtgaccg tgcaggaggg cctgtgcgtg 60

catgtgccct gcagcttcag ctaccccagc cacggctgga tctaccccgg tcccgtagtg 120

cacggctact ggttcaggga gggcgccaac accgaccagg acgctcccgt ggcaaccaac 180

aaccccgcca gggccgtgtg ggaggagacc agggacaggt tccacctgct gggcgacccc 240

cacaccaaga actgcaccct gagcatcagg gacgccagga ggagcgacgc cggcaggtac 300

ttcttcaaga tggagaaggg gtctatcaag tggaactaca agcaccaccg gctgagcgtg 360

aatgtgaccg ccctgaccca ccggcccaat atcctcatcc ccggcaccct ggagagcggc 420

agcccccaga atcttacctg cagcgtaccc tgggcctgcg agcagggcac ccctccaatg 480

atcagctgga tcggcaccag cgtgagcccc ctggacccta gtaccaccag gagcagcgtg 540

ctgaccctga tcccccagcc ccaggaccac ggaaccagcc tgacctgcca ggtgaccttc 600

cccggagcca gcgtaaccac caacaagacc gtgcacctga acgtgagcta cccaccccaa 660

aacctgacca tgaccgtgtt ccagggcgac ggcacggtga gcaccgtact gggcaacggc 720

agctctctga gcctgcccga gggccagagc ttgcggctgg tctgcgccgt ggatgctgtg 780

gacagcaacc ctcccgccag gctgagcctg agctggaggg gcctgaccct gtaccccagc 840

cagcccagca atcccggcgt gctggagctg ccctgggttc acctgaggga cgctgccgag 900

ttcacatgta gggcccagaa ccccctgggc tctcagcagg tgtacctgaa cgtgtctctt 960

cagagtaagg ccaccagcgg cgtgacccaa ggagagccca aatcttctga caaaactcac 1020

acatgcccac cgtgcccagc acctgaactc ctgggggac cgtcagtctt cctcttcccc 1080

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 1140

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1200

cataatgcca agacaaagcc gcgggaggag cagtacggta gcacgtaccg tgtggtcagc 1260

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1320

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1380

gaaccacagg tctacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1440

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1500

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1560

ttcctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1620

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1680

ccgggtaaa 1689

<210> 124
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) / (G4S)2 / hIgG1 Fc

<400> 124

Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu Asn Thr Glu
1 5 10 15

Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val Pro Pro Glu
20 25 30

Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys Thr Phe Thr
35 40 45

His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile Trp Arg Ala
50 55 60

Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala Ala Ala Arg
65 70 75 80

Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly Arg Phe Arg
85 90 95

Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg Val Glu Arg
100 105 110

Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val Glu Phe Ala
115 120 125

Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val Arg Leu His
130 135 140

Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu Pro Ser Pro
145 150 155 160

Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu Pro Pro Pro
165 170 175

Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu Ala Ala Val
180 185 190

Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala Glu Leu Pro
195 200 205

Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser Leu
210 215 220

Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala Ser
225 230 235 240

Gly Ala Ser Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys
245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 125
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 15 Fragment (20-263) / (G4S)2 / hIgG1 Fc

<400> 125
tttgtgcgga ccaagatcga caccaccgag aacctgctga acaccgaggt gcactctagc 60

cctgctcagc ggtggtctat gcaggtccca cctgaagtgt ctgccgaagc tggggatgct 120

gctgtgctgc cttgcacctt tacacaccct caccggcact acgatggccc tctgacagcc 180

atttggagag ccggcgaacc ttatgccgga ccacaggtgt tcagatgcgc tgccgctaga 240

ggctctgagc tgtgtcagac agccctgtct ctgcacggca gattcagact gctgggcaac 300

cccagaagaa acgacctgag cctgagagtg gaaagactgg ccctggccga cgacagacgg 360

tacttctgca gagtggaatt tgccggcgac gtgcacgaca gatacgagtc tagacacggc 420

gtgcggctgc acgttacagc cgctcctaga atcgtgaaca tcagcgtgct gccctctcca 480

gctcacgcct ttagagccct gtgtacagcc gaaggcgaac ctcctcctgc tcttgcttgg 540

agtggacccg ctctgggaaa ttctctggcc gccgtcagaa gccctagaga aggacacgga 600

cacctggtca cagccgaact gcctgctctg acacacgacg gcagatacac atgcacagcc 660

gccaatagcc tgggcagatc tgaggccagc gtgtacctgt tcagattcca tggcgccagc 720

ggcgcctcta caggcggagg tggaagtggc ggaggcggat ccgacaaaac tcacacatgc 780

ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1080

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140

caggtctaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 126
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) SAX / hIgG1 Fc N297G

<400> 126

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Lys Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

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

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

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

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

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

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys
465

<210> 127
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) / hIgG1 Fc N297G

<400> 127

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
340 345 350

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
355 360 365

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
370 375 380

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
385 390 395 400

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly
405 410 415

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

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
435 440 445

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
450 455 460

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
465 470 475 480

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
485 490 495

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
515 520 525

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
530 535 540

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
545 550 555 560

Ser Leu Ser Pro Gly Lys
565

<210> 128
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 7 Fragment (19-357) SAX / hIgG1 Fc N297G

<400> 128

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

Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser Tyr
20 25 30

Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp Phe
35 40 45

Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn Asn
50 55 60

Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu
65 70 75 80

Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg
85 90 95

Met Ser Asp Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Asn Ile
100 105 110

Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu
115 120 125

Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys
130 135 140

Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr
145 150 155 160

Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His Pro
165 170 175

Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln His
180 185 190

His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val
195 200 205

Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln Asn
210 215 220

Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala Leu
225 230 235 240

Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu
245 250 255

Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp
260 265 270

Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val Leu
275 280 285

Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg Ala
290 295 300

Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu Gln
305 310 315 320

Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly
325 330 335

Ala Val Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
340 345 350

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
355 360 365

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
370 375 380

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
385 390 395 400

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly
405 410 415

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

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
435 440 445

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
450 455 460

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
465 470 475 480

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
485 490 495

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
515 520 525

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
530 535 540

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
545 550 555 560

Ser Leu Ser Pro Gly Lys
565

<210> 129
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / hIgG1 Fc N297G

<400> 129

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

His Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp

85 90 95

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

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

515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 130
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y, SAX / hIgG1 Fc N297G

<400> 130

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Lys Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145   150   155   160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
                165   170   175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
            180   185   190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
        195   200   205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225   230   235   240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
                245   250   255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
            260   265   270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
        275   280   285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
    290   295   300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305   310   315   320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr
                325   330   335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            340   345   350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 131
<211> 355
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-145) / hIgG1 Fc (w/ monovalent mutations)

<400> 131

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
130 135 140

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
145 150 155 160

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
165 170 175

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
180 185 190

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
195 200 205

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
210 215 220

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
225 230 235 240

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
245 250 255

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Asn
260 265 270

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
290 295 300

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Asn Ser Thr Leu Thr Val
305 310 315 320

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
325 330 335

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

Pro Gly Lys
355

<210> 132
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (146-348) / hIgG1 Fc N297G

<400> 132

Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn
1 5 10 15

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
20 25 30

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
35 40 45

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
50 55 60

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
65 70 75 80

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr Met
85 90 95

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
100 105 110

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

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
130 135 140

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
145 150 155 160

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
165 170 175

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

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr

195 200 205

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
210 215 220

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
225 230 235 240

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
245 250 255

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
260 265 270

Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val
275 280 285

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
290 295 300

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
305 310 315 320

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
325 330 335

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
340 345 350

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
355 360 365

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
385 390 395 400

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
405 410 415

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
420 425 430

<210> 133
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) K131Q / hIgG1 Fc N297G

<400> 133

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Gln His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 134
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) K100E, A315E / hIgG1 Fc

N297G

<400> 134

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

His Thr Glu Asn Cys Thr Leu Ser Ile Arg Asp Ala Arg Arg Ser Asp
85 90 95

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala
245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Glu Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 135
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 9 Fragment (18-348) C158S, C295Y / AS / hIgG1 Fc

<400> 135

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

Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr Pro Ser His Gly
20 25 30

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

Ala Asn Thr Asp Gln Asp Ala Pro Val Ala Thr Asn Asn Pro Ala Arg
50 55 60

Ala Val Trp Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro
65 70 75 80

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

Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Ser Ile Lys Trp Asn
100 105 110

Tyr Lys His His Arg Leu Ser Val Asn Val Thr Ala Leu Thr His Arg
115 120 125

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

Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met
145 150 155 160

Ile Ser Trp Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr
165 170 175

Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr
180 185 190

Ser Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
195 200 205

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

Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly Asn Gly
225 230 235 240

Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu Val Cys Ala

245 250 255

Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Leu Ser Trp
260 265 270

Arg Gly Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Gly Val Leu
275 280 285

Glu Leu Pro Trp Val His Leu Arg Asp Ala Ala Glu Phe Thr Cys Arg
290 295 300

Ala Gln Asn Pro Leu Gly Ser Gln Gln Val Tyr Leu Asn Val Ser Leu
305 310 315 320

Gln Ser Lys Ala Thr Ser Gly Val Thr Gln Gly Asp Lys Thr His Thr
325 330 335

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
340 345 350

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
370 375 380

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
385 390 395 400

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
420 425 430

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
435 440 445

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
450 455 460

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
465 470 475 480

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
485 490 495

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
500 505 510

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
515 520 525

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
530 535 540

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 136
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(22)
<223> N-terminal signal sequence

<400> 136

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys
20

<210> 137
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(4)
<223> C terminal lysosomal signal motif

<400> 137

Tyr Gly Thr Leu
1

<210> 138
<211> 481
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(481)
<223> Siglec 16 FL (uniprot A6NMB1)

<400> 138

Met Leu Leu Leu Pro Leu Leu Leu Pro Val Leu Gly Ala Gly Ser Leu
1 5 10 15

Asn Lys Asp Pro Ser Tyr Ser Leu Gln Val Gln Arg Gln Val Pro Val
20 25 30

Pro Glu Gly Leu Cys Val Ile Val Ser Cys Asn Leu Ser Tyr Pro Arg
35 40 45

Asp Gly Trp Asp Glu Ser Thr Ala Ala Tyr Gly Tyr Trp Phe Lys Gly
50 55 60

Arg Thr Ser Pro Lys Thr Gly Ala Pro Val Ala Thr Asn Asn Gln Ser
65 70 75 80

Arg Glu Val Ala Met Ser Thr Arg Asp Arg Phe Gln Leu Thr Gly Asp
85 90 95

Pro Gly Lys Gly Ser Cys Ser Leu Val Ile Arg Asp Ala Gln Arg Glu
100 105 110

Asp Glu Ala Trp Tyr Phe Phe Arg Val Glu Arg Gly Ser Arg Val Arg
115 120 125

His Ser Phe Leu Ser Asn Ala Phe Phe Leu Lys Val Thr Ala Leu Thr
    130 135 140

Gln Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro
145 150 155 160

Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Lys Lys Cys Pro Ala
                165 170 175

Pro Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Pro Arg Arg Thr Arg
            180 185 190

Pro Ser Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Ser Pro Gln
        195 200 205

Asp His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
    210 215 220

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Ser Leu Glu Leu
225 230 235 240

Gln Gly Asn Val Ile Tyr Leu Glu Val Gln Lys Gly Gln Phe Leu Arg
                245 250 255

Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp Val
            260 265 270

Leu Gln Asp Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg Thr
        275 280 285

Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg Tyr
    290 295 300

Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu Asp
305 310 315 320

Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser Gln
                325 330 335

Ala Asn Arg Thr Val Leu Glu Asn Leu Arg Asn Gly Thr Ser Leu Arg
            340 345 350

Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Val Thr His Ser Ser
355 360 365

Pro Pro Ala Arg Leu Ser Trp Thr Trp Gly Glu Gln Thr Val Gly Pro
370 375 380

Ser Gln Pro Ser Asp Pro Gly Val Leu Gln Leu Pro Arg Val Gln Met
385 390 395 400

Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
405 410 415

Gln Arg Val Ser Leu Ser Phe Ser Val His Cys Lys Ser Gly Pro Met
420 425 430

Thr Gly Val Val Leu Val Ala Val Gly Glu Val Ala Met Lys Ile Leu
435 440 445

Leu Leu Cys Leu Cys Leu Ile Leu Leu Arg Val Arg Ser Cys Arg Arg
450 455 460

Lys Ala Ala Arg Ala Ala Leu Gly Met Glu Ala Ala Asp Ala Val Thr
465 470 475 480

Asp

<210> 139
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) / AS / hIgG1 Fc N297G

<400> 139

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His Ala Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

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

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

Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

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

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 140
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) / AS / hIgG1 Fc

<400> 140
gatcccaatt tctggctgca agtgcaagag tccgtgaccg tgcaagaggg cctgtgtgtg 60

ctggtgccct gcaccttctt tcaccccatt ccttactacg acaagaacag ccctgtgcac 120

ggctactggt ttagagaggg cgccatcatc agcagagata gccctgtggc caccaacaag 180

ctggaccaag aggtgcaaga agagacacag ggcagattca gactgctggg cgaccccagc 240

agaaacaact gcagcctgtc tatcgtggac gccaggcgga gagacaacgg cagctacttc 300

ttcaggatgg aacggggcag caccaagtac agctacaaga gccctcagct gtccgtgcac 360

gtgaccgacc tgacacacag acccaagatt ctgatccccg gcacactgga acctggccac 420

agcaagaatc tgacctgctc cgtgtcctgg gcctgcgaac agggaacccc tcctatcttt 480

agctggctga gcgccgctcc tacatctctg ggccctagaa caacacacag cagcgtgctg 540

atcatcaccc ctagacctca ggaccacggc accaacctga cctgccaagt gaaatttgct 600

ggcgctggcg tgaccaccga gagaaccatc cagctgaacg tgacctacgt gccacagaac 660

cctaccaccg gcatctttcc aggcgacggc tctggcaagc aagaaacaag agctggcgtg 720

gtgcacgcta gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1260

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acgcagaaga gcctctccct gtctccgggt aaa 1413

<210> 141
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 5 Fragment (17-441) / AS / hIgG1 Fc N297G

<400> 141

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
210 215 220

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
225 230 235 240

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
245 250 255

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
260 265 270

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
275 280 285

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
290 295 300

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
305 310 315 320

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
325 330 335

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
340 345 350

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
355 360 365

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
370 375 380

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
385 390 395 400

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
405 410 415

Gly Thr Gly Val Val Pro Ala Ala Leu Ala Ser Asp Lys Thr His Thr
420 425 430

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
435 440 445

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
450 455 460

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
465 470 475 480

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
485 490 495

Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val
500 505 510

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
515 520 525

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
530 535 540

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
545 550 555 560

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
565 570 575

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
580 585 590

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
595 600 605

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
610 615 620

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
625 630 635 640

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 142
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 5 Fragment (17-441) / AS / hIgG1 Fc N297G

<400> 142
gagaagcccg tgtatgagct gcaggtccag aaaagcgtga ccgtgcaaga gggcctgtgt 60

gtgctggtgc cttgcagctt tagctaccct tggcggagct ggtacagcag ccctcctctg 120

tacgtgtact ggttcagaga tggcgagatc ccctactacg ccgaggtggt ggccacaaac 180

aaccccgaca gaagagtgaa gcccgagaca cagggcagat tcagactgct gggcgacgtg 240

cagaagaaga actgcagcct gagcatcggc gacgcccgga tggaagatac cggcagctac 300

ttcttcagag tggaacgcgg cagggacgtg aagtacagct accagcagaa caagctgaac 360

ctggaagtga cagccctgat cgagaagcct gacatccact ttctggaacc cctggaaagc 420

ggcagaccca ccagactgtc ttgtagcctg cctggcagct gtgaagctgg ccctccactg 480

acctttagct ggaccggcaa tgccctgtct cctctggacc ctgagacaac cagaagcagc 540

gagctgaccc tgacacctag acctgaggac cacggcacca atctgacctg ccagatgaag 600

aggcagggcg cccaagtgac caccgagaga acagtgcagc tgaacgtgtc ctacgctccc 660

cagaccatca ccatcttccg gaacggaatc gccctggaaa tcctgcagaa caccagctac 720

ctgcctgtgc tggaaggcca ggctctgaga ctgctgtgtg acgcccctag caatcctcct 780

gctcacctga gctggtttca gggcagccca gctctgaacg ccacacctat cagcaacacc 840

ggcatcctgg aactgagaag agtgcggagc gctgaggaag gcggcttcac ttgtagagcc 900

cagcatcctc tgggctttct gcagatcttc ctgaacctga gcgtgtacag cctgccacag 960

ctgctgggac ctagctgttc ttgggaagcc gagggcctgc actgccggtg tagctttaga 1020

gctagacccg ctcctagcct gtgttggcgg ctggaagaga aacctctgga aggcaatagc 1080

agccagggca gcttcaaagt gaacagcagc tctgccggac cttgggccaa tagctctctg 1140

attctgcacg gcggcctgag cagcgatctg aaggtgtcat gcaaggcctg gaacatctac 1200

ggcagccagt ctggctctgt gctgctgctt cagggaagaa gcaatctcgg cacaggcgtg 1260

gtgcctgctg ctctggctag cgacaaaact cacacatgcc caccgtgccc agcacctgaa 1320

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1380

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1440

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1500

gagcagtacg gtagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1560

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1620

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtctacac cctgccccca 1680

tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1740

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1800

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 1860

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1920

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1962

<210> 143
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 5 Fragment (17-441) SAX / AS / hIgG1 Fc N297G

<400> 143

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Ala Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
210 215 220

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
225 230 235 240

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
245 250 255

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
260 265 270

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
275 280 285

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
290 295 300

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
305 310 315 320

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
325 330 335

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
340 345 350

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
355 360 365

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
370 375 380

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
385 390 395 400

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
405 410 415

Gly Thr Gly Val Val Pro Ala Ala Leu Ala Ser Asp Lys Thr His Thr
420 425 430

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
435 440 445

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
450 455 460

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
465 470 475 480

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
485 490 495

Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val
500 505 510

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
515 520 525

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
530 535 540

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
545 550 555 560

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
565 570 575

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
580 585 590

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
595 600 605

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
610 615 620

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
625 630 635 640

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 144
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 5 Fragment (17-441) SAX / AS / hIgG1 Fc N297G

<400> 144
gagaagcccg tgtatgagct gcaggtccag aaaagcgtga ccgtgcaaga gggcctgtgt 60

gtgctggtgc cttgcagctt tagctaccct tggcggagct ggtacagcag ccctcctctg 120

tacgtgtact ggttcagaga tggcgagatc ccctactacg ccgaggtggt ggccacaaac 180

aaccccgaca gaagagtgaa gcccgagaca cagggcagat tcagactgct gggcgacgtg 240

cagaagaaga actgcagcct gagcatcggc gacgcccgga tggaagatac cggcagctac 300

ttcttcgccg tggaacgcgg cagggacgtg aagtacagct accagcagaa caagctgaac 360

ctggaagtga cagccctgat cgagaagcct gacatccact ttctggaacc cctggaaagc 420

ggcagaccca ccagactgtc ttgtagcctg cctggcagct gtgaagctgg ccctccactg 480

acctttagct ggaccggcaa tgccctgtct cctctggacc ctgagacaac cagaagcagc 540

gagctgaccc tgacacctag acctgaggac cacggcacca atctgacctg ccagatgaag 600

aggcagggcg cccaagtgac caccgagaga acagtgcagc tgaacgtgtc ctacgctccc 660

cagaccatca ccatcttccg gaacggaatc gccctggaaa tcctgcagaa caccagctac 720

ctgcctgtgc tggaaggcca ggctctgaga ctgctgtgtg acgcccctag caatcctcct 780

gctcacctga gctggtttca gggcagccca gctctgaacg ccacacctat cagcaacacc 840

ggcatcctgg aactgagaag agtgcggagc gctgaggaag gcggcttcac ttgtagagcc 900

cagcatcctc tgggctttct gcagatcttc ctgaacctga gcgtgtacag cctgccacag 960

ctgctgggac ctagctgttc ttgggaagcc gagggcctgc actgccggtg tagctttaga 1020

gctagacccg ctcctagcct gtgttggcgg ctggaagaga aacctctgga aggcaatagc 1080

agccagggca gcttcaaagt gaacagcagc tctgccggac cttgggccaa tagctctctg 1140

attctgcacg gcggcctgag cagcgatctg aaggtgtcat gcaaggcctg gaacatctac 1200

ggcagccagt ctggctctgt gctgctgctt cagggaagaa gcaatctcgg cacaggcgtg 1260

gtgcctgctg ctctggctag cgacaaaact cacacatgcc caccgtgccc agcacctgaa 1320

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1380

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1440

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1500

gagcagtacg gtagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1560

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1620

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtctacac cctgccccca 1680

tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1740

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1800

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 1860

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1920

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1962

<210> 145
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) / AS / hIgG1 Fc N297G

<400> 145

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Val Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Asn Leu Ala
210 215 220

Ile Ser Ile Phe Phe Arg Asn Gly Thr Gly Thr Ala Leu Arg Ile Leu
225 230 235 240

Ser Asn Gly Met Ser Val Pro Ile Gln Glu Gly Gln Ser Leu Phe Leu
245 250 255

Ala Cys Thr Val Asp Ser Asn Pro Pro Ala Ser Leu Ser Trp Phe Arg
260 265 270

Glu Gly Lys Ala Leu Asn Pro Ser Gln Thr Ser Met Ser Gly Thr Leu
275 280 285

Glu Leu Pro Asn Ile Gly Ala Arg Glu Gly Gly Glu Phe Thr Cys Arg
290 295 300

Val Gln His Pro Leu Gly Ser Gln His Leu Ser Phe Ile Leu Ser Val
305 310 315 320

Gln Arg Ser Ser Ser Ser Cys Ile Cys Val Thr Glu Lys Gln Gln Gly
325 330 335

Ser Trp Pro Leu Val Leu Ala Ser Asp Lys Thr His Thr Cys Pro Pro
340 345 350

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
355 360 365

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
385 390 395 400

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
405 410 415

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
420 425 430

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
435 440 445

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
450 455 460

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
465 470 475 480

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
485 490 495

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
500 505 510

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
545 550 555 560

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
565 570

<210> 146
<211> 1713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) / AS / hIgG1 Fc N297G

<400> 146
gagaagcccg tgtatgagct gcaggtccag aaaagcgtga ccgtgcaaga gggcctgtgt 60

gtgctggtgc cttgcagctt tagctaccct tggcggagct ggtacagcag ccctcctctg 120

tacgtgtact ggttcagaga tggcgagatc ccctactacg ccgaggtggt ggccacaaac 180

aaccccgaca gaagagtgaa gcccgagaca cagggcagat tcagactgct gggcgacgtg 240

cagaagaaga actgcagcct gagcatcggc gacgcccgga tggaagatac cggcagctac 300

ttcttcagag tggaacgcgg cagggacgtg aagtacagct accagcagaa caagctgaac 360

ctggaagtga cagccctgat cgagaagcct gacatccact ttctggaacc cctggaaagc 420

ggcagaccca ccagactgtc ttgtagcctg cctggcagct gtgaagctgg ccctccactg 480

acctttagct ggaccggcaa tgccctgtct cctctggacc ctgagacaac cagaagcagc 540

gagctgaccc tgacacctag acctgaggac cacggcacca acctgacctg ccaagtgaaa 600

agacagggcg cccaagtgac caccgagaga acagtgcagc tgaacgtgtc ctacgctccc 660

cagaacctgg ccatcagcat ctttttcaga aacggcaccg gcacagccct gcggatcctg 720

tctaatggca tgagcgtgcc catccaagag ggacagtctc tgttcctggc ctgcaccgtg 780

gactctaatc ctccagctag cctgagctgg tttagagagg gcaaagccct gaatcctagc 840

cagaccagca tgagcggcac cctggaactg cctaatatcg gcgctagaga aggcggcgag 900

ttcacctgta gagtgcagca ccctctgggc agccagcacc tgagctttat cctgagcgtg 960

cagagaagca gcagcagctg catctgcgtg accgagaaac agcaaggcag ctggcctctg 1020

gttctggcta gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 1080

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 1140

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 1200

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1260

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1320

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1380

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 1440

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1500

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1560

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1620

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1680

acgcagaaga gcctctccct gtctccgggt aaa 1713

<210> 147
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) SAX / AS / hIgG1 Fc N297G

<400> 147

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Ala Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Val Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Asn Leu Ala
210 215 220

Ile Ser Ile Phe Phe Arg Asn Gly Thr Gly Thr Ala Leu Arg Ile Leu
225 230 235 240

Ser Asn Gly Met Ser Val Pro Ile Gln Glu Gly Gln Ser Leu Phe Leu
245 250 255

Ala Cys Thr Val Asp Ser Asn Pro Pro Ala Ser Leu Ser Trp Phe Arg
260 265 270

Glu Gly Lys Ala Leu Asn Pro Ser Gln Thr Ser Met Ser Gly Thr Leu
275 280 285

Glu Leu Pro Asn Ile Gly Ala Arg Glu Gly Gly Glu Phe Thr Cys Arg
290 295 300

Val Gln His Pro Leu Gly Ser Gln His Leu Ser Phe Ile Leu Ser Val
305 310 315 320

Gln Arg Ser Ser Ser Ser Cys Ile Cys Val Thr Glu Lys Gln Gln Gly
325 330 335

Ser Trp Pro Leu Val Leu Ala Ser Asp Lys Thr His Thr Cys Pro Pro
340 345 350

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
355 360 365

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
385 390 395 400

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
405 410 415

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
420 425 430

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
435 440 445

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
450 455 460

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
465 470 475 480

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
485 490 495

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
500 505 510

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
545 550 555 560

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
565 570

<210> 148
<211> 1713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) SAX / AS / hIgG1 Fc N297G

<400> 148
gagaagcccg tgtatgagct gcaggtccag aaaagcgtga ccgtgcaaga gggcctgtgt 60

gtgctggtgc cttgcagctt tagctaccct tggcggagct ggtacagcag ccctcctctg 120

tacgtgtact ggttcagaga tggcgagatc ccctactacg ccgaggtggt ggccacaaac 180

aaccccgaca gaagagtgaa gcccgagaca cagggcagat tcagactgct gggcgacgtg 240

cagaagaaga actgcagcct gagcatcggc gacgcccgga tggaagatac cggcagctac 300

ttcttcgccg tggaacgcgg cagggacgtg aagtacagct accagcagaa caagctgaac 360

ctggaagtga cagccctgat cgagaagcct gacatccact ttctggaacc cctggaaagc 420

ggcagaccca ccagactgtc ttgtagcctg cctggcagct gtgaagctgg ccctccactg 480

acctttagct ggaccggcaa tgccctgtct cctctggacc ctgagacaac cagaagcagc 540

gagctgaccc tgacacctag acctgaggac cacggcacca acctgacctg ccaagtgaaa 600

agacagggcg cccaagtgac caccgagaga acagtgcagc tgaacgtgtc ctacgctccc 660

cagaacctgg ccatcagcat ctttttcaga aacggcaccg gcacagccct gcggatcctg 720

tctaatggca tgagcgtgcc catccaagag ggacagtctc tgttcctggc ctgcaccgtg 780

gactctaatc ctccagctag cctgagctgg tttagagagg gcaaagccct gaatcctagc 840

cagaccagca tgagcggcac cctggaactg cctaatatcg gcgctagaga aggcggcgag 900

ttcacctgta gagtgcagca ccctctgggc agccagcacc tgagctttat cctgagcgtg 960

cagagaagca gcagcagctg catctgcgtg accgagaaac agcaaggcag ctggcctctg 1020

gttctggcta gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 1080

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 1140

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 1200

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1260

ggtagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1320

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1380

tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgccccc atcccgggag 1440

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1500

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1560

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1620

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1680

acgcagaaga gcctctccct gtctccgggt aaa 1713

<210> 149
<211> 652
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 5 Fragment (17-441) / hIgG1 Fc N297G

<400> 149

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
210 215 220

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
225 230 235 240

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
245 250 255

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
260 265 270

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
275 280 285

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
290 295 300

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
305 310 315 320

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
325 330 335

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
340 345 350

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
355 360 365

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
370 375 380

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
385 390 395 400

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
405 410 415

Gly Thr Gly Val Val Pro Ala Ala Leu Asp Lys Thr His Thr Cys Pro
420 425 430

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
435 440 445

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
450 455 460

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
465 470 475 480

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
485 490 495

Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr
500 505 510

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
515 520 525

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
530 535 540

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
545 550 555 560

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
565 570 575

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
580 585 590

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
595 600 605

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
610 615 620

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
625 630 635 640

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 150
<211> 652
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Siglec 5 Fragment (17-441) SAX / hIgG1 Fc N297G

<400> 150

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Ala Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
210 215 220

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
225 230 235 240

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
245 250 255

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
260 265 270

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
275 280 285

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
290 295 300

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
305 310 315 320

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
325 330 335

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
340 345 350

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
355 360 365

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
370 375 380

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
385 390 395 400

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
405 410 415

Gly Thr Gly Val Val Pro Ala Ala Leu Asp Lys Thr His Thr Cys Pro
420 425 430

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
435 440 445

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
450 455 460

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
465 470 475 480

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
485 490 495

Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr
500 505 510

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
515 520 525

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
530 535 540

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
545 550 555 560

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
565 570 575

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
580 585 590

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
595 600 605

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
610 615 620

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
625 630 635 640

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 151
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) SAX / hIgG1 Fc N297G

<400> 151

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
85 90 95

Thr Gly Ser Tyr Phe Phe Ala Val Glu Arg Gly Arg Asp Val Lys Tyr
100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Val Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Asn Leu Ala
210 215 220

Ile Ser Ile Phe Phe Arg Asn Gly Thr Gly Thr Ala Leu Arg Ile Leu
225 230 235 240

Ser Asn Gly Met Ser Val Pro Ile Gln Glu Gly Gln Ser Leu Phe Leu
245 250 255

Ala Cys Thr Val Asp Ser Asn Pro Pro Ala Ser Leu Ser Trp Phe Arg
260 265 270

Glu Gly Lys Ala Leu Asn Pro Ser Gln Thr Ser Met Ser Gly Thr Leu
275 280 285

Glu Leu Pro Asn Ile Gly Ala Arg Glu Gly Gly Glu Phe Thr Cys Arg
290 295 300

Val Gln His Pro Leu Gly Ser Gln His Leu Ser Phe Ile Leu Ser Val
305 310 315 320

Gln Arg Ser Ser Ser Ser Cys Ile Cys Val Thr Glu Lys Gln Gln Gly
325 330 335

Ser Trp Pro Leu Val Leu Asp Lys Thr His Thr Cys Pro Pro Cys Pro
340 345 350

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
355 360 365

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    370 375 380

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
385 390 395 400

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                405 410 415

Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            420 425 430

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        435 440 445

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    450 455 460

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
465 470 475 480

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                485 490 495

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            500 505 510

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        515 520 525

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
545 550 555 560

Lys Ser Leu Ser Leu Ser Pro Gly Lys
                565

<210> 152
<211> 19

<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(19)
<223> N-terminal signal sequence

<400> 152

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

Val His Ser

<210> 153
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(19)
<223> N-terminal signal sequence

<400> 153

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 154
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 3 Fragment (18-259) / hIgG1 Fc N297G

<400> 154

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

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

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

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

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

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

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    450 455 460

Leu Ser Pro Gly Lys
465

<210> 155
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 14 Fragment (17-358) / hIgG1 Fc N297G

<400> 155

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

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
            20 25 30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
        35 40 45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
    50 55 60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
65 70 75 80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
                85 90 95

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
            100 105 110

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
        115 120 125

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
    130 135 140

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
145 150 155 160

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
165 170 175

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
180 185 190

Thr Asn Leu Thr Cys Gln Val Lys Arg Gln Gly Ala Gln Val Thr Thr
195 200 205

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Asn Leu Ala
210 215 220

Ile Ser Ile Phe Phe Arg Asn Gly Thr Gly Thr Ala Leu Arg Ile Leu
225 230 235 240

Ser Asn Gly Met Ser Val Pro Ile Gln Glu Gly Gln Ser Leu Phe Leu
245 250 255

Ala Cys Thr Val Asp Ser Asn Pro Pro Ala Ser Leu Ser Trp Phe Arg
260 265 270

Glu Gly Lys Ala Leu Asn Pro Ser Gln Thr Ser Met Ser Gly Thr Leu
275 280 285

Glu Leu Pro Asn Ile Gly Ala Arg Glu Gly Gly Glu Phe Thr Cys Arg
290 295 300

Val Gln His Pro Leu Gly Ser Gln His Leu Ser Phe Ile Leu Ser Val
305 310 315 320

Gln Arg Ser Ser Ser Ser Cys Ile Cys Val Thr Glu Lys Gln Gln Gly
325 330 335

Ser Trp Pro Leu Val Leu Asp Lys Thr His Thr Cys Pro Pro Cys Pro
340 345 350

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
355 360 365

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
370 375 380

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
385 390 395 400

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
405 410 415

Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
420 425 430

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
435 440 445

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
450 455 460

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
465 470 475 480

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
485 490 495

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
500 505 510

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
515 520 525

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
545 550 555 560

Lys Ser Leu Ser Leu Ser Pro Gly Lys
565

<210> 156
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX

<400> 156

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg
50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Lys
85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser
100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile
260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val

<210> 157
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX

<400> 157
caagagcggc ggtttcagct ggaaggacct gagagcctga cagtgcaaga gggcctgtgt 60

gtgctggtgc cttgtagact gcctaccaca ctgcccgcca gctactacgg ctacggctat 120

tggtttctgg aaggcgccga tgtgcccgtg gccaccaatg atcctgacga ggaagtgcaa 180

gaagagacac ggggcagatt ccatctgctg tgggacccca gacggaagaa ctgcagcctg 240

agcatcagag atgccagaag gcgggataac gccgcctact tcttcaagct gaagtccaag 300

tggatgaagt acggctacac cagcagcaag ctgagcgtca gagtgatggc cctgacacac 360

agacccaaca tcagcatccc cggcacactg gaaagcggac accctagcaa tctgacctgc 420

agcgtgccat gggtttgcga gcagggaacc cctcctatct tctcctggat gtctgccgct 480

cctacctctc tgggccctag aacaacacag agcagcgtgc tgaccatcac acccagacct 540

caggaccaca gcaccaacct gacctgccaa gtgacctttc ctggcgctgg cgtgaccatg 600

gaaagaacca tccagctcaa cgtgtcctac gctccccaga aggtggccat cagcattttc 660

cagggcaaca gcgccgcctt caagatcctg cagaatacca gcagcctgcc tgtgctggaa 720

ggccaggctc tgagactgct gtgtgacgcc gatggcaatc ctcctgctca cctgagctgg 780

ttccagggct tcccagctct gaacgccaca cctatcagca acaccggcgt gctggaactg 840

cctcaagtgg gatctgccga ggaaggcgac ttcacctgta gagcccaaca tcctctgggc 900

agcctgcaga tctccctgag cctgtttgtg cactggaagc ccgaaggcag agctggcgga 960

gtg 963

<210> 158
<211> 553
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX / EPKSS / hIgG1 Fc N297G

<400> 158

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

Glu Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro
20 25 30

Ala Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val
35 40 45

Pro Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg

50 55 60

Gly Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu
65 70 75 80

Ser Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Lys
85 90 95

Leu Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser
100 105 110

Val Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly
115 120 125

Thr Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp
130 135 140

Val Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala
145 150 155 160

Pro Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile
165 170 175

Thr Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr
180 185 190

Phe Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val
195 200 205

Ser Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser
210 215 220

Ala Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu
225 230 235 240

Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala
245 250 255

His Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile
260 265 270

Ser Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu
275 280 285

Gly Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile
290 295 300

Ser Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly
305 310 315 320

Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
325 330 335

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
340 345 350

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
355 360 365

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
370 375 380

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
385 390 395 400

Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
405 410 415

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
420 425 430

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
435 440 445

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
450 455 460

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
465 470 475 480

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

485 490 495

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
500 505 510

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
515 520 525

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
530 535 540

Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550

<210> 159
<211> 1659
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: Siglec 6 Fragment (27-347) SAX / EPKSS / hIgG1 Fc N297G

<400> 159
caagagcggc ggtttcagct ggaaggacct gagagcctga cagtgcaaga gggcctgtgt 60

gtgctggtgc cttgtagact gcctaccaca ctgcccgcca gctactacgg ctacggctat 120

tggtttctgg aaggcgccga tgtgcccgtg gccaccaatg atcctgacga ggaagtgcaa 180

gaagagacac ggggcagatt ccatctgctg tgggacccca gacggaagaa ctgcagcctg 240

agcatcagag atgccagaag gcgggataac gccgcctact tcttcaagct gaagtccaag 300

tggatgaagt acggctacac cagcagcaag ctgagcgtca gagtgatggc cctgacacac 360

agacccaaca tcagcatccc cggcacactg gaaagcggac accctagcaa tctgacctgc 420

agcgtgccat gggtttgcga gcagggaacc cctcctatct tctcctggat gtctgccgct 480

cctacctctc tgggccctag aacaacacag agcagcgtgc tgaccatcac acccagacct 540

caggaccaca gcaccaacct gacctgccaa gtgacctttc ctggcgctgg cgtgaccatg 600

gaaagaacca tccagctcaa cgtgtcctac gctccccaga aggtggccat cagcattttc 660

cagggcaaca gcgccgcctt caagatcctg cagaatacca gcagcctgcc tgtgctggaa 720

ggccaggctc tgagactgct gtgtgacgcc gatggcaatc ctcctgctca cctgagctgg 780

ttccagggct tcccagctct gaacgccaca cctatcagca acaccggcgt gctggaactg 840

cctcaagtgg gatctgccga ggaaggcgac ttcacctgta gagcccaaca tcctctgggc 900

agcctgcaga tctccctgag cctgtttgtg cactggaagc ccgaaggcag agctggcgga 960

gtggagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaactc 1020

ctgggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 1080

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 1140

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1200

cagtacggta gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1260

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1320

accatctcca aagccaaagg gcagccccga gaaccacagg tctacaccct gcccccatcc 1380

cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1440

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1500

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1560

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1620

cactacacgc agaagagcct ctccctgtct ccgggtaaa 1659

<210> 160
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hIgG1 Fc N297G with N-terminal EPKSS included.

<400> 160

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

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

Lys Asp Thr Leu Met Ile Ser 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 Gly 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 Glu Glu Met Thr
    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
225 230

<210> 161
<211> 696
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic: hIgG1 Fc N297G with N-terminal EPKSS included.

<400> 161
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacggtagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 420

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 600

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660

tacacgcaga agagcctctc cctgtctccg ggtaaa 696