SEQUENCE LISTING

<110> Smith, Ernest S.
Zauderer, Maurice
Bowers, William J.
Jonason, Alan

<120> USE OF SEMAPHORIN-4D BINDING MOLECULES FOR TREATING NEURODEGENERATIVE DISORDERS

<130> 58008-137466

<140> To be assigned
<141> Herewith

<150> US 62/012805
<151> 2014-06-16

<150> US 61/979384
<151> 2014-04-14

<150> US 61/893814
<151> 2013-10-21

<160> 40

<170> PatentIn version 3.3

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<213> Homo sapiens

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Glu His Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr
35 40 45

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

Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
65 70 75 80

Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys
85 90 95

Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
100 105 110

Arg Val Leu Gln Pro Leu Ser Ala Thr Ser Leu Tyr Val Cys Gly Thr
115 120 125

Asn Ala Phe Gln Pro Ala Cys Asp His Leu Asn Leu Thr Ser Phe Lys

130 135 140

Phe Leu Gly Lys Asn Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
145 150 155 160

Ala His Ser Tyr Thr Ser Val Met Val Asp Gly Glu Leu Tyr Ser Gly
165 170 175

Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
180 185 190

Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
195 200 205

Pro Ser Phe Val Phe Ala Asp Val Ile Arg Lys Ser Pro Asp Ser Pro
210 215 220

Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val Ser Val
225 230 235 240

Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg Val
245 250 255

Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr
260 265 270

Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu
275 280 285

Val Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu
290 295 300

Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val
305 310 315 320

Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val
325 330 335

Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His
340 345 350

Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly
355 360 365

Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu
370 375 380

Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met
385 390 395 400

Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys

405 410 415

Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
420 425 430

Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu
435 440 445

His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr
450 455 460

Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser
465 470 475 480

Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
485 490 495

Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys
500 505 510

Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr
515 520 525

Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln
530 535 540

Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser
545 550 555 560

Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
565 570 575

Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly
580 585 590

Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn
595 600 605

Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys
610 615 620

Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala
625 630 635 640

Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro
645 650 655

Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val
660 665 670

Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln

675 680 685

Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr
690 695 700

Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu
705 710 715 720

His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu
725 730 735

Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu Phe Phe
740 745 750

Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg
755 760 765

Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp
770 775 780

Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser
785 790 795 800

Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu
805 810 815

Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp
820 825 830

Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val
835 840 845

Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
850 855 860

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35 40 45

Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp Thr Leu Tyr Val
50 55 60

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Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
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Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ser Lys
                85                  90                  95

Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
            100                 105                 110

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

Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu Thr Ser Phe Lys
    130                 135                 140

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

Ala His Ser Tyr Thr Ser Val Met Val Gly Gly Glu Leu Tyr Ser Gly
                165                 170                 175

Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
            180                 185                 190

Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
        195                 200                 205

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

Glu Gly Glu Asp Asp Lys Val Tyr Phe Phe Phe Thr Glu Val Ser Val
225                 230                 235                 240

Glu Tyr Glu Phe Val Phe Lys Leu Met Ile Pro Arg Val Ala Arg Val
                245                 250                 255

Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr
            260                 265                 270

Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Lys Pro Asp Ser Gly Leu
        275                 280                 285

Val Phe Asn Ile Leu Gln Asp Val Phe Val Leu Arg Ala Pro Gly Leu
    290                 295                 300

Lys Glu Pro Val Phe Tyr Ala Val Phe Thr Pro Gln Leu Asn Asn Val
305                 310                 315                 320

Gly Leu Ser Ala Val Cys Ala Tyr Thr Leu Ala Thr Val Glu Ala Val
                325                 330                 335
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Phe Ser Arg Gly Lys Tyr Met Gln Ser Ala Thr Val Glu Gln Ser His
            340                 345                 350

Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Thr Pro Arg Pro Gly
        355                 360                 365

Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu
    370                 375                 380

Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met
385                 390                 395                 400

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

Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
            420                 425                 430

Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp Arg Gly Ala Leu
        435                 440                 445

His Lys Ala Val Ile Leu Thr Lys Glu Val His Val Ile Glu Glu Thr
    450                 455                 460

Gln Leu Phe Arg Asp Ser Glu Pro Val Leu Thr Leu Leu Leu Ser Ser
465                 470                 475                 480

Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
                485                 490                 495

Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser Cys Glu Asp Cys
            500                 505                 510

Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Ala Ile Lys Ala
        515                 520                 525

Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg Gly Trp Ile Gln
    530                 535                 540

Asp Met Ser Gly Asp Thr Ser Ser Cys Leu Asp Lys Ser Lys Glu Ser
545                 550                 555                 560

Phe Asn Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
                565                 570                 575

Phe Gln Lys Ser Asn Leu Ala Arg Val Val Trp Lys Phe Gln Asn Gly
            580                 585                 590

Glu Leu Lys Ala Ala Ser Pro Lys Tyr Gly Phe Val Gly Arg Lys His
        595                 600                 605
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Leu Leu Ile Phe Asn Leu Ser Asp Gly Asp Ser Gly Val Tyr Gln Cys
    610                 615                 620

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625                 630                 635                 640

Lys His Val Leu Glu Val Lys Met Val Pro Arg Thr Pro Pro Ser Pro
                645                 650                 655

Thr Ser Glu Asp Ala Gln Thr Glu Gly Ser Lys Ile Thr Ser Lys Met
            660                 665                 670

Pro Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Leu Trp
        675                 680                 685

Ala Thr Ser Pro Arg Ala Ala Thr Leu Pro Pro Lys Ser Ser Ser Gly
    690                 695                 700

Thr Ser Cys Glu Pro Lys Met Val Ile Asn Thr Val Pro Gln Leu His
705                 710                 715                 720

Ser Glu Lys Thr Val Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu Met
                725                 730                 735

Ser Leu Leu Leu Phe Ile Phe Val Leu Phe Leu Cys Leu Phe Ser Tyr
            740                 745                 750

Asn Cys Tyr Lys Gly Tyr Leu Pro Gly Gln Cys Leu Lys Phe Arg Ser
        755                 760                 765

Ala Leu Leu Leu Gly Lys Lys Thr Pro Lys Ser Asp Phe Ser Asp Leu
    770                 775                 780

Glu Gln Ser Val Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser Gln
785                 790                 795                 800

Gln Asn Gly Asp His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr
                805                 810                 815

Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser
            820                 825                 830

Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys
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Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
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<220>
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<210> 5
<211> 27
<212> DNA
<213> Artificial

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<210> 6
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<212> PRT
<213> Artificial

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<400> 6

Gly Tyr Ser Phe Ser Asp Tyr Tyr Met His
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<210> 7
<211> 17
<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VH CDR2

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Gln Ile Asn Pro Thr Thr Gly Gly Ala Ser Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 8
<211> 9

<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VH CDR3

<400> 8

Tyr Tyr Tyr Gly Arg His Phe Asp Val
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<210> 9
<211> 118
<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VH 2503

<400> 9

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

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Tyr Tyr Tyr Gly Arg His Phe Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
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<210> 10
<211> 118
<212> PRT
<213> Artificial

<220>
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<400> 10

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser Asp Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Ser Pro Glu Asn Ser Leu Glu Trp Ile
35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Thr Arg Tyr Tyr Tyr Gly Arg His Phe Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
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<220>
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<210> 13
<211> 27
<212> DNA
<213> Artificial

<220>
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<400> 13
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<210> 14
<211> 15
<212> PRT
<213> Artificial

<220>
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<400> 14

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
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<210> 15
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VL CDR2

<400> 15

Ala Ala Ser Asn Leu Glu Ser
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<210> 16
<211> 9
<212> PRT
<213> Artificial

<220>
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<400> 16

Gln Gln Ser Asn Glu Asp Pro Tyr Thr
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<210> 17
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VL 2503

<400> 17

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

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

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

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

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

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

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

<210> 18
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Polypeptide anti-CD100 VL 67

<400> 18

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

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

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

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

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

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

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tcctgcaagg ctagcggcta cagcttcagc gactactaca tgcactgggt gagacaggcc 120

cctggccaag gcctggagtg gatgggccag attaatccta ccactggcgg cgctagctac 180

aaccagaagt tcaagggcaa ggccaccatt accgtggaca aaagcaccag cacagcctac 240

atggagctga gcagcctgag aagcgaggac accgccgtgt attactgtgc cagatattac 300

tacggcagac acttcgatgt ctggggccaa ggcaccacgg tcaccgtctc ttca 354

<210> 20
<211> 354
<212> DNA
<213> Artificial

<220>
<223> Polynucleotide anti-CD100 VH 67

<400> 20
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tcctgcaagg cttctggtta ctcattcagt gactactaca tgcactgggt gaagcaaagt 120

cctgaaaata gtcttgagtg gattggacag attaatccta ccactggggg tgctagctac 180

aaccagaagt tcaagggcaa ggccacatta actgtagata aatcctccag cacagcctac 240

atgcagctca agagcctgac atctgaagag tctgcagtct attactgtac aagatattac 300

tacggtagac acttcgatgt ctggggccaa gggaccacgg tcaccgtttc ctca 354

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<211> 333
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<220>
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atcaactgca aggccagcca aagcgtggat tatgatggcg atagctatat gaactggtac 120

cagcagaaac caggccagcc tcctaagctg ctgatttacg ctgcatccaa tctggaaagc 180

ggcgtgcctg acagattcag cggcagcggc agcggcacag atttcactct gaccatcagc 240

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accttcggcc aagggaccaa gctcgagatc aaa 333

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caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 180

gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240

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acgttcggag gggggaccaa gctcgagatc aaa 333

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<211> 118

<212> PRT
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<220>
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<400> 23

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

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

Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Ser Asp Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Leu Val Thr Val Ser Ser
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<213> Artificial

<220>
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<210> 25
<211> 17
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<220>
<223> Polypeptide anti-CD100 VH 76 CDR2

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Asp

<210> 26
<211> 9
<212> PRT
<213> Artificial

<220>
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Asp Pro Tyr Gly Trp Thr Met Asp Ser
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<210> 27
<211> 107
<212> PRT
<213> Artificial

<220>
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<400> 27

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Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

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

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

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

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

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

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<210> 29
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1 5

<210> 30
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Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 31
<211> 354
<212> DNA
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<220>
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tcctgcaagg cttctggcta cacctttact aggtactgga tgcactgggt aaaacagagg 120

cctggacagg gtctggaatg gattggatac attaatccta gcactggtta ttctgattac 180

aatcagaagt tcaaggacaa ggccacattg actgcagaca aatcctccag cacagcctac 240

atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagagacccc 300

tacggctgga ctatggactc ctggggccaa gggactctgg tcaccgtctc ctca 354

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<210> 33
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<210> 35
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atcacttgcc atgccagtca gaacattaat gtttggttaa gctggtacca gcagaaacca 120

ggaaatattc ctaaactatt gatctataag gcttccaact tgcacacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgcagcct 240

gaagacattg ccacttacta ctgtcaacag ggtcaaagtt atccgtacac gttcggaggg 300

gggaccaagc tcgagatcaa a 321

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<220>
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Glu Pro Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Phe Asn Ser
            20   25   30
Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Leu Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
                85   90   95
Asp His Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100   105   110
Lys

<210> 40
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> 2282 VH domain

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