SEQUENCE LISTING

<110> Dyax Corp.
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TenHoor, Christopher

<120> FC RECEPTOR BINDING PROTEINS

<130> D0617.70028WO00

<140> N/A
<141> 2012-06-01

<150> 61/492,617
<151> 2011-06-02

<150> 61/498,266
<151> 2011-06-17

<160> 26

<170> PatentIn version 3.5

<210> 1
<211> 365
<212> PRT
<213> H. sapiens

<400> 1

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Leu Gly Leu Leu Leu Phe
1 5 10 15

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
20 25 30

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
35 40 45

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Leu Ser Tyr Asn Ser Leu
50 55 60

Arg Gly Glu Ala Glu Pro Cys Gly Ala Trp Val Trp Glu Asn Gln Val
65 70 75 80

Ser Trp Tyr Trp Glu Lys Glu Thr Thr Asp Leu Arg Ile Lys Glu Lys
85 90 95

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

Leu Gln Gly Leu Leu Gly Cys Glu Leu Gly Pro Asp Asn Thr Ser Val
115 120 125

Pro Thr Ala Lys Phe Ala Leu Asn Gly Glu Glu Phe Met Asn Phe Asp

130 135 140

Leu Lys Gln Gly Thr Trp Gly Gly Asp Trp Pro Glu Ala Leu Ala Ile
145 150 155 160

Ser Gln Arg Trp Gln Gln Gln Asp Lys Ala Ala Asn Lys Glu Leu Thr
165 170 175

Phe Leu Leu Phe Ser Cys Pro His Arg Leu Arg Glu His Leu Glu Arg
180 185 190

Gly Arg Gly Asn Leu Glu Trp Lys Glu Pro Pro Ser Met Arg Leu Lys
195 200 205

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

Ser Phe Tyr Pro Pro Glu Leu Gln Leu Arg Phe Leu Arg Asn Gly Leu
225 230 235 240

Ala Ala Gly Thr Gly Gln Gly Asp Phe Gly Pro Asn Ser Asp Gly Ser
245 250 255

Phe His Ala Ser Ser Ser Leu Thr Val Lys Ser Gly Asp Glu His His
260 265 270

Tyr Cys Cys Ile Val Gln His Ala Gly Leu Ala Gln Pro Leu Arg Val
275 280 285

Glu Leu Glu Ser Pro Ala Lys Ser Ser Val Leu Val Val Gly Ile Val
290 295 300

Ile Gly Val Leu Leu Leu Thr Ala Ala Ala Val Gly Gly Ala Leu Leu
305 310 315 320

Trp Arg Arg Met Arg Ser Gly Leu Pro Ala Pro Trp Ile Ser Leu Arg
325 330 335

Gly Asp Asp Thr Gly Val Leu Leu Pro Thr Pro Gly Glu Ala Gln Asp
340 345 350

Ala Asp Leu Lys Asp Val Asn Val Ile Pro Ala Thr Ala
355 360 365

<210> 2
<211> 366
<212> PRT
<213> R. Rattus

<400> 2

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

Leu Pro Gln Thr Trp Gly Ala Glu Pro Arg Leu Pro Leu Met Tyr His
            20                  25                  30

Leu Ala Ala Val Ser Asp Leu Ser Thr Gly Leu Pro Ser Phe Trp Ala
        35                  40                  45

Thr Gly Trp Leu Gly Ala Gln Gln Tyr Leu Thr Tyr Asn Asn Leu Arg
    50                  55                  60

Gln Glu Ala Asp Pro Cys Gly Ala Trp Ile Trp Glu Asn Gln Val Ser
65                  70                  75                  80

Trp Tyr Trp Glu Lys Glu Thr Thr Asp Leu Lys Ser Lys Glu Gln Leu
                85                  90                  95

Phe Leu Glu Ala Ile Arg Thr Leu Glu Asn Gln Ile Asn Gly Thr Phe
            100                 105                 110

Thr Leu Gln Gly Leu Leu Gly Cys Glu Leu Ala Pro Asp Asn Ser Ser
        115                 120                 125

Leu Pro Thr Ala Val Phe Ala Leu Asn Gly Glu Glu Phe Met Arg Phe
    130                 135                 140

Asn Pro Arg Thr Gly Asn Trp Ser Gly Glu Trp Pro Glu Thr Asp Ile
145                 150                 155                 160

Val Gly Asn Leu Trp Met Lys Gln Pro Glu Ala Ala Arg Lys Glu Ser
                165                 170                 175

Glu Phe Leu Leu Thr Ser Cys Pro Glu Arg Leu Leu Gly His Leu Glu
            180                 185                 190

Arg Gly Arg Gln Asn Leu Glu Trp Lys Glu Pro Pro Ser Met Arg Leu
        195                 200                 205

Lys Ala Arg Pro Gly Asn Ser Gly Ser Ser Val Leu Thr Cys Ala Ala
    210                 215                 220

Phe Ser Phe Tyr Pro Pro Glu Leu Lys Phe Arg Phe Leu Arg Asn Gly
225                 230                 235                 240
```

```
Leu Ala Ser Gly Ser Gly Asn Cys Ser Thr Gly Pro Asn Gly Asp Gly
                245                 250                 255

Ser Phe His Ala Trp Ser Leu Leu Glu Val Lys Arg Gly Asp Glu His
            260                 265                 270

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

Val Asp Leu Asp Ser Pro Ala Arg Ser Ser Val Pro Val Val Gly Ile
    290                 295                 300

Ile Leu Gly Leu Leu Leu Val Val Val Ala Ile Ala Gly Gly Val Leu
305                 310                 315                 320

Leu Trp Asn Arg Met Arg Ser Gly Leu Pro Ala Pro Trp Leu Ser Leu
                325                 330                 335

Ser Gly Asp Asp Ser Gly Asp Leu Leu Pro Gly Gly Asn Leu Pro Pro
            340                 345                 350

Glu Ala Glu Pro Gln Gly Val Asn Ala Phe Pro Ala Thr Ser
        355                 360                 365
```

<210> 3
<211> 119
<212> PRT
<213> H. sapiens

<400> 3

```
Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
1               5                   10                  15

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

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
        35                  40                  45

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

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
65                  70                  75                  80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
                85                  90                  95
```

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
100 105 110

Val Lys Trp Asp Arg Asp Met
115

<210> 4
<211> 119
<212> PRT
<213> R. Rattus

<400> 4

Met Ala Arg Ser Val Thr Val Ile Phe Leu Val Leu Val Ser Leu Ala
1 5 10 15

Val Val Leu Ala Ile Gln Lys Thr Pro Gln Ile Gln Val Tyr Ser Arg
20 25 30

His Pro Pro Glu Asn Gly Lys Pro Asn Phe Leu Asn Cys Tyr Val Ser
35 40 45

Gln Phe His Pro Pro Gln Ile Glu Ile Glu Leu Leu Lys Asn Gly Lys
50 55 60

Lys Ile Pro Asn Ile Glu Met Ser Asp Leu Ser Phe Ser Lys Asp Trp
65 70 75 80

Ser Phe Tyr Ile Leu Ala His Thr Glu Phe Thr Pro Thr Glu Thr Asp
85 90 95

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

Val Thr Trp Asp Arg Asp Met
115

<210> 5
<211> 1510
<212> DNA
<213> H. sapiens

<400> 5
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cgggaggagt cacgtgcccc ctcccgcccc aggtcgtcct ctcagcatgg gggtcccgcg 180

gcctcagccc tgggcgctgg ggctcctgct ctttctcctt cctgggagcc tgggcgcaga 240

aagccacctc tccctcctgt accaccttac cgcggtgtcc tcgcctgccc cggggactcc 300

tgccttctgg gtgtccggct ggctgggccc gcagcagtac ctgagctaca atagcctgcg 360

gggcgaggcg gagccctgtg gagcttgggt ctgggaaaac caggtgtcct ggtattggga 420

gaaagagacc acagatctga ggatcaagga gaagctcttt ctggaagctt tcaaagcttt 480

gggggaaaa ggtccctaca ctctgcaggg cctgctgggc tgtgaactgg gccctgacaa 540

cacctcggtg cccaccgcca agttcgccct gaacggcgag gagttcatga atttcgacct 600

caagcagggc acctggggtg gggactggcc cgaggccctg gctatcagtc agcggtggca 660

gcagcaggac aaggcggcca acaaggagct caccttcctg ctattctcct gcccgcaccg 720

cctgcgggag cacctggaga ggggccgcgg aaacctggag tggaaggagc ccccctccat 780

gcgcctgaag gcccgaccca gcagccctgg cttttccgtg cttacctgca gcgccttctc 840

cttctaccct ccggagctgc aacttcggtt cctgcggaat gggctggccg ctggcaccgg 900

ccagggtgac ttcggcccca acagtgacgg atccttccac gcctcgtcgt cactaacagt 960

caaaagtggc gatgagcacc actactgctg cattgtgcag cacgcggggc tggcgcagcc 1020

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cggtgtcttg ctactcacgg cagcggctgt aggaggagct ctgttgtgga gaaggatgag 1140

gagtgggctg ccagcccctt ggatctccct tcgtggagac gacaccgggg tcctcctgcc 1200

caccccaggg gaggcccagg atgctgattt gaaggatgta aatgtgattc cagccaccgc 1260

ctgaccatcc gccattccga ctgctaaaag cgaatgtagt caggcccctt tcatgctgtg 1320

agacctcctg gaacactggc atctctgagc ctccagaagg ggttctgggc ctagttgtcc 1380

tccctctgga gccccgtcct gtggtctgcc tcagtttccc ctcctaatac atatggctgt 1440

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aaaaaaaaaa 1510

<210> 6
<211> 984
<212> DNA
<213> H. sapiens

<400> 6
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gccccgggga ctcctgcctt ctgggtgtcc ggctggctgg gcccgcagca gtacctgagc 180

tacaatagcc tgcggggcga ggcggagccc tgtggagctt gggtctggga aaaccaggtg 240

tcctggtatt gggagaaaga gaccacagat ctgaggatca aggagaagct ctttctggaa 300

gctttcaaag ctttgggggg aaaaggtccc tacactctgc agggcctgct gggctgtgaa 360

ctgggccctg acaacacctc ggtgcccacc gccaagttcg ccctgaacgg cgaggagttc 420

atgaatttcg acctcaagca gggcacctgg ggtggggact ggcccgaggc cctggctatc 480

agtcagcggt ggcagcagca ggacaaggcg gccaacaagg agctcacctt cctgctattc 540

tcctgcccgc accgcctgcg ggagcacctg gagaggggcc gcggaaacct ggagtggaag 600

gagcccccct ccatgcgcct gaaggcccga cccagcagcc ctggcttttc cgtgcttacc 660

tgcagcgcct tctccttcta ccctccggag ctgcaacttc ggttcctgcg gaatgggctg 720

gccgctggca ccggccaggg tgacttcggc cccaacagtg acggatcctt ccacgcctcg 780

tcgtcactaa cagtcaaaag tggcgatgag caccactact gctgcattgt gcagcacgcg 840

gggctggcgc agcccctcag ggtggagctg gaatctccag ccaagtcctc ccggccgctc 900

gacgggctac gagcatcagt aacactacta ggcgcaggcc tactactatc actactacca 960

gcactactac gatttgggcc ataa 984

<210> 7
<211> 987
<212> DNA
<213> H. sapiens

<400> 7
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atgtctcgct ccgtggcctt agctgtgctc gcgctactct ctctttctgg cctggaggct 120

atccagcgta ctccaaagat tcaggtttac tcacgtcatc cagcagagaa tggaaagtca 180

aatttcctga attgctatgt gtctgggttt catccatccg acattgaagt tgacttactg 240

aagaatggag agagaattga aaaagtggag cattcagact tgtctttcag caaggactgg 300

tctttctatc tcttgtacta cactgaattc acccccactg aaaaagatga gtatgcctgc 360

cgtgtgaacc atgtgacttt gtcacagccc aagatagtta agtgggatcg agacatgtaa 420

gcagcatcat ggaggtttga agatgccgca tttggattgg atgaattcca aattctgctt 480

gcttgctttt taatattgat atgcttatac acttacactt tatgcacaaa atgtagggtt 540

ataataatgt taacatggac atgatcttct ttataattct actttgagtg ctgtctccat 600

gtttgatgta tctgagcagg ttgctccaca ggtagctcta ggagggctgg caacttagag 660

gtggggagca gagaattctc ttatccaaca tcaacatctt ggtcagattt gaactcttca 720

atctcttgca ctcaaagctt gttaagatag ttaagcgtgc ataagttaac ttccaattta 780

catactctgc ttagaatttg ggggaaaatt tagaaatata attgacagga ttattggaaa 840

tttgttataa tgaatgaaac attttgtcat ataagattca tatttacttc ttatacattt 900

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tcataaaact tgatgtgtta tctctta 987

<210> 8

<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region for DX-2504

<400> 8

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

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

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

Met Ile Tyr Gly Asp Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
                85                  90                  95

Gly Ile Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110
```

<210> 9
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region for DX-2504

<400> 9

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

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

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

Ser Ser Ile Gly Ser Ser Gly Gly Gln Thr Lys Tyr Ala Asp Ser Val
    50                  55                  60
```

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

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

Ala Arg Leu Ala Ile Gly Asp Ser Tyr Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 10
<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain Variable region for 532A-X53-C02

<400> 10

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

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

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

Met Ile Tyr Gly Asp Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
85 90 95

Gly Ile Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 11
<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain Variable region for 532A-X54-B03

<400> 11

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

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

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

Met Ile Tyr Gly Asp Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Ala Gly Ser
                85                  90                  95

Gly Ile Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110
```

<210> 12
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3 of 532A-X53-C02

<400> 12

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Ser Ser Tyr Ala Gly Ser Gly Ile Tyr Val
1               5                   10
```

<210> 13
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3 of 532A-X54-B03

<400> 13

```
Ala Ser Tyr Ala Gly Ser Gly Ile Tyr Val
1               5                   10
```

<210> 14
<211> 14
<212> PRT
<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 14

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

<210> 15
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR2

<400> 15

Gly Asp Ser Gln Arg Pro Ser
1 5

<210> 16
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> Full length light chain for DX-2504

<400> 16

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

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

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

Met Ile Tyr Gly Asp Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
85 90 95

Gly Ile Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

```
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 17
<211> 446
<212> PRT
<213> Artificial sequence

<220>
<223> Full length heavy chain for DX-2504

<400> 17

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

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

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

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

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

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

Ala Arg Leu Ala Ile Gly Asp Ser Tyr Trp Gly Gln Gly Thr Met Val
            100                 105                 110
```

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 18
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> Full length light chain for DX-2507

<400> 18

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

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

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

Met Ile Tyr Gly Asp Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Ala Gly Ser
                85                  90                  95

Gly Ile Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125
```

```
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 19
<211> 445
<212> PRT
<213> Artificial sequence

<220>
<223> Full length heavy chain for DX-2507

<400> 19

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

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

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

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

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

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

Ala Arg Leu Ala Ile Gly Asp Ser Tyr Trp Gly Gln Gly Thr Met Val
            100                 105                 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
```

115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 20
<211> 48
<212> PRT
<213> Artificial sequence

<220>
<223> C-terminal fragment of DX-2504 heavy chain

<400> 20

```
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
1               5                   10                  15

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            20                  25                  30

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        35                  40                  45
```

<210> 21
<211> 47
<212> PRT
<213> Artificial sequence

<220>
<223> the C-terminal fragment of DX-2507 heavy chain

<400> 21

```
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
1               5                   10                  15

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            20                  25                  30

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        35                  40                  45
```

<210> 22
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR1

<400> 22

Glu Tyr Ala Met Gly
1 5

<210> 23
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR2

<400> 23

Ser Ile Gly Ser Ser Gly Gly Gln Thr Lys Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 24
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR3

<400> 24

Leu Ala Ile Gly Asp Ser Tyr
1 5

<210> 25
<211> 10
<212> PRT
<213> Artificial sequence

<220>
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<400> 25

Cys Ser Tyr Ala Gly Ser Gly Ile Tyr Val
1 5 10

<210> 26
<211> 329

<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain constant region of DX-2507

<400> 26

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                  10                  15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

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

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
```

```
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
                325
```