

SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Multi-specific binding proteins for cancer treatment

<130> 12-0431-WO-1

<160> 265

<170> BiSSAP 1.2

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<400> 1

Arg Ala Ser Gln Ser Val Ser Ser Asn Phe Leu Val

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<400> 2

Gly Ala Ser Thr Arg Ala Ser

1 5

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Gln Gln Tyr Gly Asp Ser Pro Tyr Thr

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<400> 4
Gly Asn Thr Phe Thr Asn Tyr Tyr Met His
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<400> 5
Ile Ile Asp Pro Ser Val Gly Ser Lys Ser Tyr Ala Gln Lys Phe Leu
1 5 10 15
Gly

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<400> 6
Ala Gly Lys Arg Phe Gly Glu Ser Tyr Phe Asp Tyr
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<400> 7
Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
1 5 10

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<400> 8
Ala Ala Ser Ser Leu Gln Ser
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<400> 9
Leu Gln His Asn Ser Ser Pro Tyr Thr
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<400> 10
Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5 10

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<400> 11
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15
Gly

<210> 12
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<400> 12
Gly Glu Ala Val Gly Gly Asn Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

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<400> 13

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Val
1 5 10

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<400> 14

Ala Val Ser Ser Leu Tyr Ser
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<223> DLL3#3 LCCDR3

<400> 15

Leu Gln His Asp Ser Tyr Pro Tyr Thr
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<400> 16

Gly Tyr Thr Phe Thr Ser Tyr Tyr Val His
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<210> 17

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<223> DLL3#3 HCCDR2

<400> 17

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

<210> 18
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<400> 18
Gly Glu Ala Val Thr Gly Asn Tyr Phe Tyr Tyr Gly Met Asp Val
1 5 10 15

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<400> 19
Arg Ala Ser Lys Ser Val Ser Ser Phe Gly Tyr Ser Phe Met His
1 5 10 15

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<220>
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<400> 20
Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 21
Gln His Ser Arg Glu Leu Pro Trp Thr
1 5

<210> 22
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<212> PRT
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<223> DLL3#4 HCCDR1

<400> 22

Val Tyr Thr Phe Thr Ser Tyr Phe Met Tyr
1 5 10

<210> 23

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<223> DLL3#4 HCCDR2

<400> 23

Glu Ile Ser Pro Thr Asn Gly Asn Ser Asn Leu Asn Glu Arg Phe Lys
1 5 10 15
Asn

<210> 24

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<220>

<223> DLL3#4 HCCDR3

<400> 24

Gly Gly Asp Gly Tyr Leu Asp Tyr
1 5

<210> 25

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<223> DLL3#5 LCCDR1

<400> 25

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 26

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<223> DLL3#5 LCCDR2

<400> 26

Asp Ala Ser Asn Leu Glu Thr

1 5

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<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#5 LCCDR3

<400> 27

Gln Gln Tyr Asp Asn Leu Pro Thr Trp Thr

1 5 10

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<223> DLL3#5 HCCDR1

<400> 28

Gly Phe Thr Phe Thr Gly Tyr Tyr Ile His

1 5 10

<210> 29

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#5 HCCDR2

<400> 29

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln

1 5 10 15

Gly

<210> 30

<211> 4

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<223> DLL3#5 HCCDR3

<400> 30

Gly Trp Asp Tyr

1

<210> 31

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 LCCDR1

<400> 31

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Phe Ala

1 5 10

<210> 32

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 LCCDR2

<400> 32

Ala Ala Ser Thr Leu Gln Ser

1 5

<210> 33

<211> 9

<212> PRT

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<220>

<223> DLL3#6 LCCDR3

<400> 33

Gln Gln Leu Asn Ser Tyr Pro Tyr Thr

1 5

<210> 34

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 HCCDR1

<400> 34

Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser

1 5 10

<210> 35

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 HCCDR2

<400> 35

Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn Ser

1 5 10 15

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#6 HCCDR3

<400> 36
Arg Gly Asp Trp Gly Gly Phe Asp Ile
1 5

<210> 37
<211> 108
<212> PRT
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<220>
<223> DLL3#1 VL

<400> 37
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30
Phe Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu
 35 40 45
Ile Tyr Gly Ala Ser Thr Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60
Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro
 85 90 95
Tyr Thr Phe Gly Gln Gly Thr Thr Leu Glu Ile Lys
 100 105

<210> 38
<211> 121
<212> PRT
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<220>
<223> DLL3#1 VH

<400> 38
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Asn Tyr
 20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Pro Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asp Pro Ser Val Gly Ser Lys Ser Tyr Ala Gln Lys Phe
 50 55 60
 Leu Gly Arg Val Thr Ile Ala Arg Asp Thr Ser Thr Ser Thr Val Phe
 65 70 75 80
 Leu Asp Leu Tyr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Ala Gly Lys Arg Phe Gly Glu Ser Tyr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 39

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#2 VL

<400> 39

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

<210> 40

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#2 VH

<400> 40

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

85 90 95
 Ala Arg Gly Glu Ala Val Gly Gly Asn Tyr Tyr Tyr Tyr Gly Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 41
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#3 VL

<400> 41
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Val Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
 35 40 45
 Tyr Ala Val Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asp Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 42
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#3 VH

<400> 42
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Val Ile Ile Asn Pro Gly Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Leu Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80
 Met Glu Leu Lys Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Glu Ala Val Thr Gly Asn Tyr Phe Tyr Tyr Gly Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 43
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#4 VL

<400> 43
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Ser Phe
20 25 30
Gly Tyr Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val 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 His Ser Arg
85 90 95
Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 44
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#4 VH

<400> 44
Gln Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Val Tyr Thr Phe Thr Ser Tyr
20 25 30
Phe Met Tyr Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45
Gly Glu Ile Ser Pro Thr Asn Gly Asn Ser Asn Leu Asn Glu Arg Phe
50 55 60
Lys Asn Lys Ala Thr Leu Thr Val 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
Thr Arg Gly Gly Asp Gly Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110
Leu Thr Val Ser Ser
115

<210> 45
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#5 VL

<400> 45

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

<210> 46

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#5 VH

<400> 46

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

<210> 47

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 VL

<400> 47

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

<210> 48

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 VH

<400> 48

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

<210> 49

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#1 scFab

<400> 49

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30
 Phe Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu

35 40 45
 Ile Tyr Gly Ala Ser Thr Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro
 85 90 95
 Tyr Thr Phe Gly Gln Gly Thr Thr Leu Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270
 Val Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Asn Tyr Tyr Met His
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Pro Gly Leu Glu Trp Met Gly Ile Ile
 290 295 300
 Asp Pro Ser Val Gly Ser Lys Ser Tyr Ala Gln Lys Phe Leu Gly Arg
 305 310 315 320
 Val Thr Ile Ala Arg Asp Thr Ser Thr Ser Thr Val Phe Leu Asp Leu
 325 330 335
 Tyr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ala
 340 345 350
 Gly Lys Arg Phe Gly Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 355 360 365
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 370 375 380
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 385 390 395 400
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 405 410 415
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 420 425 430
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 435 440 445
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 450 455 460
 Asn Thr Lys Lys Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475

<210> 50
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#2 scFab

<400> 50
Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Glu Pro Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Val Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Ser Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
210 215 220
Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
225 230 235 240
Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
245 250 255
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
260 265 270
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp
275 280 285
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
290 295 300
Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val
305 310 315 320
Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
325 330 335
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Glu
340 345 350
Ala Val Gly Gly Asn Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

355 360 365
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 370 375 380
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 385 390 395 400
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 405 410 415
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 420 425 430
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 435 440 445
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 450 455 460
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475

<210> 51

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#3 scFab

<400> 51

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

Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Val His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Val Ile Ile Asn
 290 295 300
 Pro Gly Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe Leu Gly Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr Met Glu Leu Lys
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Glu
 340 345 350
 Ala Val Thr Gly Asn Tyr Phe Tyr Tyr Gly Met Asp Val Trp Gly Gln
 355 360 365
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 370 375 380
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 385 390 395 400
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 405 410 415
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 420 425 430
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 435 440 445
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 450 455 460
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475

<210> 52

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#4 scFab

<400> 52

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

115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
 210 215 220
 Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys
 225 230 235 240
 Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser
 245 250 255
 Gln Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Val Lys Pro Gly Ala
 260 265 270
 Ser Val Lys Leu Ser Cys Lys Ala Ser Val Tyr Thr Phe Thr Ser Tyr
 275 280 285
 Phe Met Tyr Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
 290 295 300
 Gly Glu Ile Ser Pro Thr Asn Gly Asn Ser Asn Leu Asn Glu Arg Phe
 305 310 315 320
 Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 325 330 335
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 340 345 350
 Thr Arg Gly Gly Asp Gly Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365
 Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 370 375 380
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 385 390 395 400
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 405 410 415
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 420 425 430
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 435 440 445
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 450 455 460
 Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475

<210> 53

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#5 scFab

<400> 53

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Val Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Thr
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270
 Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Gly Tyr Tyr Ile His
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile
 290 295 300
 Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg
 305 310 315 320
 Val Thr Met Thr Arg Asp Ser Ser Ile Asn Thr Ala Phe Met Glu Leu
 325 330 335
 Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly
 340 345 350
 Trp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 355 360 365
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 370 375 380
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 385 390 395 400
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 405 410 415
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 420 425 430
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile

435 440 445
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
 450 455 460
 Glu Pro Lys Ser Cys
 465

<210> 54
 <211> 472
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#6 scFab

<400> 54
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Thr Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Phe Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Gly Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu
 260 265 270
 Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp
 275 280 285
 Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile Tyr
 290 295 300
 Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn Ser Arg Leu Thr
 305 310 315 320

Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser
 325 330 335
 Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Arg Gly Asp
 340 345 350
 Trp Gly Gly Phe Asp Ile Trp Gly Gln Gly Thr Val Val Thr Val Ser
 355 360 365
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 385 390 395 400
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
 Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 55

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 LCCDR1

<400> 55

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
 1 5 10

<210> 56

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 LCCDR2

<400> 56

Gly Thr Asn Lys Arg Ala Pro
 1 5

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 LCCDR3

<400> 57

Ala Leu Trp Tyr Ser Asn Leu Trp Val

1 5

<210> 58

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 HCCDR1

<400> 58

Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn

1 5 10

<210> 59

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 HCCDR2

<400> 59

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 60

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 HCCDR3

<400> 60

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr

1 5 10

<210> 61

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 LCCDR1

<400> 61

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn

1 5 10

<210> 62

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 LCCDR2

<400> 62

Gly Thr Asn Lys Arg Ala Pro

1 5

<210> 63

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 LCCDR3

<400> 63

Ala Leu Trp Tyr Ser Asn Leu Trp Val

1 5

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 HCCDR1

<400> 64

Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn

1 5 10

<210> 65

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 HCCDR2

<400> 65

Arg Ile Arg Ser Lys Tyr Ile Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 66

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 HCCDR3

<400> 66

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

<210> 67

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 VL

<400> 67

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

<210> 68

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 VH

<400> 68

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

<210> 69

<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#2 VL

<400> 69
Glu Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Leu Pro Arg Gly
35 40 45
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Val Pro Ala Arg Phe
50 55 60
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80
Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95
Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 70
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#2 VH

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

<210> 71
<211> 481
<212> PRT
<213> Artificial Sequence

<220>

<223> CD3#1 scFab

<400> 71

Glu Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Leu Pro Arg Gly
35 40 45
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Val Pro Ala Arg Phe
50 55 60
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80
Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95
Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140
Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro Val Asn Thr
145 150 155 160
Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205
Val Ala Pro Ala Glu Cys Ser Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Glu Val Gln
245 250 255
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
260 265 270
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
275 280 285
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
290 295 300
Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305 310 315 320
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
325 330 335
Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
340 345 350
Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
355 360 365
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
370 375 380
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
385 390 395 400
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
405 410 415

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
420 425 430
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
435 440 445
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
450 455 460
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
465 470 475 480
Cys

<210> 72
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#2 scFab

<400> 72
Glu Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Leu Pro Arg Gly
35 40 45
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Val Pro Ala Arg Phe
50 55 60
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80
Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95
Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140
Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro Val Asn Thr
145 150 155 160
Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205
Val Ala Pro Ala Glu Cys Ser Gly Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Glu Val Gln
245 250 255
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
260 265 270
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn

275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
 290 295 300
 Arg Ser Lys Tyr Ile Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
 305 310 315 320
 Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
 325 330 335
 Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
 340 345 350
 Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
 355 360 365
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
 370 375 380
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 385 390 395 400
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 405 410 415
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 420 425 430
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 435 440 445
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 450 455 460
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 465 470 475 480
 Cys

<210> 73

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#1 chain

<400> 73

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270
 Val Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Asn Tyr Tyr Met His
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Pro Gly Leu Glu Trp Met Gly Ile Ile
 290 295 300
 Asp Pro Ser Val Gly Ser Lys Ser Tyr Ala Gln Lys Phe Leu Gly Arg
 305 310 315 320
 Val Thr Ile Ala Arg Asp Thr Ser Thr Ser Thr Val Phe Leu Asp Leu
 325 330 335
 Tyr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ala
 340 345 350
 Gly Lys Arg Phe Gly Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 355 360 365
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 370 375 380
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 385 390 395 400
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 405 410 415
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 420 425 430
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 435 440 445
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 450 455 460
 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
 465 470 475 480
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 485 490 495
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 500 505 510
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 515 520 525
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 530 535 540
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 545 550 555 560
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 565 570 575
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

580 585 590
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 595 600 605
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys
 610 615 620
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 625 630 635 640
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 645 650 655
 Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 660 665 670
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 675 680 685
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695 700

<210> 74

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#2 chain

<400> 74

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

Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
 290 295 300
 Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Glu
 340 345 350
 Ala Val Gly Gly Asn Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
 355 360 365
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 370 375 380
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 385 390 395 400
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 405 410 415
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 420 425 430
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 435 440 445
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 450 455 460
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 465 470 475 480
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 485 490 495
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 500 505 510
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 515 520 525
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 530 535 540
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 545 550 555 560
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 565 570 575
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 580 585 590
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 595 600 605
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 610 615 620
 Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 625 630 635 640
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 645 650 655
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 660 665 670
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

675 680 685
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 690 695 700
 Gly
 705

<210> 75
 <211> 705
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#3 chain

<400> 75
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Val Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
 35 40 45
 Tyr Ala Val Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asp Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Val His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Val Ile Ile Asn
 290 295 300
 Pro Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe Leu Gly Arg Val
 305 310 315 320

Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr Met Glu Leu Lys
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Glu
 340 345 350
 Ala Val Thr Gly Asn Tyr Phe Tyr Tyr Gly Met Asp Val Trp Gly Gln
 355 360 365
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 370 375 380
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 385 390 395 400
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 405 410 415
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 420 425 430
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 435 440 445
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 450 455 460
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 465 470 475 480
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 485 490 495
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 500 505 510
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 515 520 525
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 530 535 540
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 545 550 555 560
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 565 570 575
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 580 585 590
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 595 600 605
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 610 615 620
 Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 625 630 635 640
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 645 650 655
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 660 665 670
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 675 680 685
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 690 695 700
 Gly
 705

<210> 76

<211> 702

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#4 chain

<400> 76

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Ser Phe
20 25 30
Gly Tyr Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val 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 His Ser Arg
85 90 95
Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
210 215 220
Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys
225 230 235 240
Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser
245 250 255
Gln Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Val Lys Pro Gly Ala
260 265 270
Ser Val Lys Leu Ser Cys Lys Ala Ser Val Tyr Thr Phe Thr Ser Tyr
275 280 285
Phe Met Tyr Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
290 295 300
Gly Glu Ile Ser Pro Thr Asn Gly Asn Ser Asn Leu Asn Glu Arg Phe
305 310 315 320
Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
325 330 335
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
340 345 350
Thr Arg Gly Gly Asp Gly Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365
Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
370 375 380
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
385 390 395 400

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 405 410 415
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 420 425 430
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 435 440 445
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 450 455 460
 Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
 465 470 475 480
 Thr Cys Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 485 490 495
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 500 505 510
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 515 520 525
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 530 535 540
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 545 550 555 560
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 565 570 575
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 580 585 590
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 595 600 605
 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
 610 615 620
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 625 630 635 640
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 645 650 655
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 660 665 670
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 675 680 685
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695 700

<210> 77

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#5 chain

<400> 77

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

50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Thr
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205
Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
245 250 255
Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270
Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Gly Tyr Tyr Ile His
275 280 285
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile
290 295 300
Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg
305 310 315 320
Val Thr Met Thr Arg Asp Ser Ser Ile Asn Thr Ala Phe Met Glu Leu
325 330 335
Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly
340 345 350
Trp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
355 360 365
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
370 375 380
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
385 390 395 400
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
405 410 415
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
420 425 430
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
435 440 445
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
450 455 460
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
465 470 475 480
Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
485 490 495

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

<210> 78

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#6 chain

<400> 78

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

145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
225 230 235 240
Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu
 260 265 270
Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp
 275 280 285
Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile Tyr
 290 295 300
Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn Ser Arg Leu Thr
305 310 315 320
Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser
 325 330 335
Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Arg Gly Asp
 340 345 350
Trp Gly Gly Phe Asp Ile Trp Gly Gln Gly Thr Val Val Thr Val Ser
 355 360 365
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
385 390 395 400
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
465 470 475 480
Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 485 490 495
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 500 505 510
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 515 520 525
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 530 535 540
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
545 550 555 560
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 565 570 575
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 580 585 590

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 595 600 605
 Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
 610 615 620
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 625 630 635 640
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 645 650 655
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 660 665 670
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 675 680 685
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695

<210> 79

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#1 chain

<400> 79

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

245 250 255
 Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
 260 265 270
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
 290 295 300
 Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
 305 310 315 320
 Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
 325 330 335
 Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
 340 345 350
 Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
 355 360 365
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
 370 375 380
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 385 390 395 400
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 405 410 415
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 420 425 430
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 435 440 445
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 450 455 460
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 465 470 475 480
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 485 490 495
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 500 505 510
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 515 520 525
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 530 535 540
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 545 550 555 560
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 565 570 575
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 580 585 590
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 595 600 605
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 610 615 620
 Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 625 630 635 640
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 645 650 655
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 660 665 670
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 675 680 685

Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu
690 695 700
Ser Pro Gly
705

<210> 80

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#2 chain

<400> 80

Glu Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Leu Pro Arg Gly
35 40 45
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Val Pro Ala Arg Phe
50 55 60
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80
Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95
Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140
Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro Val Asn Thr
145 150 155 160
Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205
Val Ala Pro Ala Glu Cys Ser Gly Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Glu Val Gln
245 250 255
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
260 265 270
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
275 280 285
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
290 295 300
Arg Ser Lys Tyr Ile Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305 310 315 320
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335
 Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
 340 345 350
 Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
 355 360 365
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
 370 375 380
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 385 390 395 400
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 405 410 415
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 420 425 430
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 435 440 445
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 450 455 460
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 465 470 475 480
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 485 490 495
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 500 505 510
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 515 520 525
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 530 535 540
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 545 550 555 560
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 565 570 575
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 580 585 590
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 595 600 605
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 610 615 620
 Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 625 630 635 640
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 645 650 655
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 660 665 670
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 675 680 685
 Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu
 690 695 700
 Ser Pro Gly
 705

<210> 81

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Fcdomain* (IgG1)

<400> 81

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
225

<210> 82

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Fcknobdomain (IgG1,LALA)

<400> 82

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Trp 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
 225

<210> 83

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Fcholedomain (IgG1,RF/LALA)

<400> 83

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Ser Cys Ala 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 Val 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 Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly
225

<210> 84
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Fcdomain (IgG4Pro)

<400> 84
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45
Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110
Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190
Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220
Leu Ser Leu Gly
225

<210> 85
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Fcknobdomain(IgG4Pro)

<400> 85
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe

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

<210> 86

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Fcholedomain(IgG4Pro,RF)

<400> 86

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

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

<210> 87

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> constantregionofakappalightchain

<400> 87

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

<210> 88

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> constantregionofalambdalightchain

<400> 88

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1 5 10 15
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 20 25 30
 Phe Tyr Pro Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro
 35 40 45
 Val Asn Thr Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn

50 55 60
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 65 70 75 80
 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 85 90 95
 Glu Lys Thr Val Ala Pro Ala Glu Cys Ser
 100 105

<210> 89
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 89
 Gly Gly Gly Gly Ser Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser
 1 5 10 15
 Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
 20 25 30
 Thr Gly Gly Gly Gly Ser
 35

<210> 90
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 90
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser
 1 5 10 15
 Gly Gly Gly Gly Gly Ser
 20

<210> 91
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 91
 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 Gly Ser
 20 25

<210> 92
 <211> 30
 <212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 92

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
20 25 30

<210> 93

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 93

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
20 25 30
Gly Ser

<210> 94

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 94

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30
Gly Gly Gly Gly Gly Ser
35

<210> 95

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly
20 25 30

20 25 30
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40

<210> 96
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#3 LCCDR1

<400> 96
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#3 LCCDR2

<400> 97
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#3 LCCDR3

<400> 98
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 99
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3#3 HCCDR1

<400> 99
Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5 10

<210> 100
<211> 19
<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 HCCDR2

<400> 100

Arg Ile Arg Ser Lys Tyr Ala Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15
Val Lys Asp

<210> 101

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 HCCDR3

<400> 101

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

<210> 102

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 VL

<400> 102

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

<210> 103

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 HL

<400> 103

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

<210> 104

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 scFab

<400> 104

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

Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Glu Val Gln
 245 250 255
 Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
 260 265 270
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
 290 295 300
 Arg Ser Lys Tyr Ala Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
 305 310 315 320
 Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
 325 330 335
 Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
 340 345 350
 Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
 355 360 365
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
 370 375 380
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 385 390 395 400
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 405 410 415
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 420 425 430
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 435 440 445
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 450 455 460
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 465 470 475 480
 Cys

<210> 105

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3#3 chain

<400> 105

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

85 90 95
 Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro Val Asn Thr
 145 150 155 160
 Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
 165 170 175
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
 180 185 190
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Ala Glu Cys Ser Gly Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Glu Val Gln
 245 250 255
 Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
 260 265 270
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
 290 295 300
 Arg Ser Lys Tyr Ala Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
 305 310 315 320
 Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
 325 330 335
 Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
 340 345 350
 Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
 355 360 365
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
 370 375 380
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 385 390 395 400
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 405 410 415
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 420 425 430
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 435 440 445
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 450 455 460
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 465 470 475 480
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 485 490 495
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 500 505 510
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 515 520 525

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 530 535 540
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 545 550 555 560
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 565 570 575
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 580 585 590
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 595 600 605
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 610 615 620
 Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 625 630 635 640
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 645 650 655
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 660 665 670
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 675 680 685
 Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu
 690 695 700
 Ser Pro Gly
 705

<210> 106

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> HuDLL3(ECD)-His

<400> 106

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

165 170 175
 Gly Leu Arg Pro Cys Ala Pro Leu Glu Asp Glu Cys Glu Ala Pro Leu
 180 185 190
 Val Cys Arg Ala Gly Cys Ser Pro Glu His Gly Phe Cys Glu Gln Pro
 195 200 205
 Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu Cys Thr Val
 210 215 220
 Pro Val Ser Thr Ser Ser Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala
 225 230 235 240
 Thr Thr Gly Cys Leu Val Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro
 245 250 255
 Cys Ala Asn Gly Gly Ser Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys
 260 265 270
 Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser Gly Val
 275 280 285
 Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys Val Gly Gly
 290 295 300
 Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro Gly Phe Gln
 305 310 315 320
 Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu Gln Pro Cys
 325 330 335
 Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg Cys Arg
 340 345 350
 Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu Asp Asp
 355 360 365
 Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu Gly Gly
 370 375 380
 Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys
 385 390 395 400
 Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly
 405 410 415
 Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly
 420 425 430
 Tyr Met Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Ala Ser
 435 440 445
 Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg
 450 455 460
 Tyr Leu Ala Gly Ser Ala His His His His His His
 465 470 475

<210> 107

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> CynoDLL3(ECD)-His

<400> 107

Ala Gly Val Phe Glu Leu Gln Ile His Ser Phe Gly Pro Gly Pro Gly
 1 5 10 15
 Pro Gly Ala Pro Arg Ser Pro Cys Ser Ala Arg Gly Pro Cys Arg Leu
 20 25 30
 Phe Phe Arg Val Cys Leu Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu
 35 40 45

Ser Pro Cys Ala Leu Gly Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr
 50 55 60
 Thr Glu Gln Pro Glu Ala Pro Ala Pro Asp Leu Pro Leu Pro Asn Gly
 65 70 75 80
 Leu Leu Gln Val Pro Phe Arg Asp Ala Trp Pro Gly Thr Phe Ser Leu
 85 90 95
 Ile Ile Glu Thr Trp Arg Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro
 100 105 110
 Ala Trp Ser Leu Leu Ala Arg Val Thr Arg Arg Arg Arg Leu Ala Ala
 115 120 125
 Gly Gly Pro Trp Ala Arg Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu
 130 135 140
 Arg Phe Ser Tyr Arg Ala Arg Cys Glu Leu Pro Ala Val Gly Thr Ala
 145 150 155 160
 Cys Thr Arg Leu Cys Arg Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro
 165 170 175
 Gly Leu Arg Pro Cys Ala Pro Leu Glu Asp Glu Cys Glu Ala Pro Pro
 180 185 190
 Val Cys Arg Ala Gly Cys Ser Leu Glu His Gly Phe Cys Glu Gln Pro
 195 200 205
 Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu Cys Met Val
 210 215 220
 Pro Val Ser Thr Ser Ser Cys Leu Gly Leu Arg Gly Pro Ser Ser Thr
 225 230 235 240
 Thr Thr Gly Cys Leu Val Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro
 245 250 255
 Cys Ala Asn Gly Gly Ser Cys Ser Glu Thr Pro Gly Ser Phe Glu Cys
 260 265 270
 Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser Gly Val
 275 280 285
 Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys Val Gly Gly
 290 295 300
 Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro Gly Phe Gln
 305 310 315 320
 Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu Gln Pro Cys
 325 330 335
 Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg Cys Arg
 340 345 350
 Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu Asp Asp
 355 360 365
 Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu Gly Gly
 370 375 380
 Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg Asn Cys
 385 390 395 400
 Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly
 405 410 415
 Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly
 420 425 430
 Tyr Met Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Val Ser
 435 440 445
 Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg
 450 455 460
 Tyr Leu Ala Gly Ser Ala His His His His His His
 465 470 475

<210> 108
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCD3E+G-HuFc-His

<400> 108
Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys
1 5 10 15
Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
20 25 30
Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp
35 40 45
Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys
50 55 60
Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg
65 70 75 80
Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg
85 90 95
Val Cys Glu Asn Cys Met Glu Met Asp Gly Gly Gly Ser Gly Gly Gly
100 105 110
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125
Ser Gly Gly Gln Ser Ile Lys Gly Asn His Leu Val Lys Val Tyr Asp
130 135 140
Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala Glu Ala Lys
145 150 155 160
Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe Leu Thr Glu
165 170 175
Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp Pro Arg Gly
180 185 190
Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro Leu Gln Val
195 200 205
Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala Ala Thr Ile
210 215 220
Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
225 230 235 240
Gly Gly Ser Gly Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 370 375 380
 Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 385 390 395 400
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 405 410 415
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 420 425 430
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 435 440 445
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 450 455 460
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Gly Ser
 465 470 475 480
 Ala His His His His His His
 485

<210> 109

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> CynoCD3E+G-Fc-His

<400> 109

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

225 230 235 240
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys Ala Gly Ser Ala His His His His His His
 465 470 475

<210> 110

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG-tagged human DLL3 full length

<400> 110

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

Asp Gly Leu Leu Gln Val Pro Phe Arg Asp Ala Trp Pro Gly Thr Phe
 115 120 125
 Ser Phe Ile Ile Glu Thr Trp Arg Glu Glu Leu Gly Asp Gln Ile Gly
 130 135 140
 Gly Pro Ala Trp Ser Leu Leu Ala Arg Val Ala Gly Arg Arg Arg Leu
 145 150 155 160
 Ala Ala Gly Gly Pro Trp Ala Arg Asp Ile Gln Arg Ala Gly Ala Trp
 165 170 175
 Glu Leu Arg Phe Ser Tyr Arg Ala Arg Cys Glu Pro Pro Ala Val Gly
 180 185 190
 Thr Ala Cys Thr Arg Leu Cys Arg Pro Arg Ser Ala Pro Ser Arg Cys
 195 200 205
 Gly Pro Gly Leu Arg Pro Cys Ala Pro Leu Glu Asp Glu Cys Glu Ala
 210 215 220
 Pro Leu Val Cys Arg Ala Gly Cys Ser Pro Glu His Gly Phe Cys Glu
 225 230 235 240
 Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu Cys
 245 250 255
 Thr Val Pro Val Ser Thr Ser Ser Cys Leu Ser Pro Arg Gly Pro Ser
 260 265 270
 Ser Ala Thr Thr Gly Cys Leu Val Pro Gly Pro Gly Pro Cys Asp Gly
 275 280 285
 Asn Pro Cys Ala Asn Gly Gly Ser Cys Ser Glu Thr Pro Arg Ser Phe
 290 295 300
 Glu Cys Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser
 305 310 315 320
 Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys Val
 325 330 335
 Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro Gly
 340 345 350
 Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu Gln
 355 360 365
 Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg
 370 375 380
 Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu
 385 390 395 400
 Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu
 405 410 415
 Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg
 420 425 430
 Asp Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His
 435 440 445
 Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala
 450 455 460
 Pro Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly
 465 470 475 480
 Ala Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro
 485 490 495
 Gln Arg Tyr Leu Leu Pro Pro Ala Leu Gly Leu Leu Val Ala Ala Gly
 500 505 510
 Val Ala Gly Ala Ala Leu Leu Leu Val His Val Arg Arg Arg Gly His
 515 520 525
 Ser Gln Asp Ala Gly Ser Arg Leu Leu Ala Gly Thr Pro Glu Pro Ser
 530 535 540
 Val His Ala Leu Pro Asp Ala Leu Asn Asn Leu Arg Thr Gln Glu Gly

545 550 555 560
 Ser Gly Asp Gly Pro Ser Ser Ser Val Asp Trp Asn Arg Pro Glu Asp
 565 570 575
 Val Asp Pro Gln Gly Ile Tyr Val Ile Ser Ala Pro Ser Ile Tyr Ala
 580 585 590
 Arg Glu Val Ala Thr Pro Leu Phe Pro Pro Leu His Thr Gly Arg Ala
 595 600 605
 Gly Gln Arg Gln His Leu Leu Phe Pro Tyr Pro Ser Ser Ile Leu Ser
 610 615 620
 Val Lys
 625

<210> 111

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG-tagged cyno DLL3 full length

<400> 111

Met Val Ser Pro Arg Met Ser Arg Leu Leu Ser Gln Thr Val Ile Leu
 1 5 10 15
 Ala Leu Ile Phe Ile Pro Gln Ala Arg Pro Asp Tyr Lys Asp Asp Asp
 20 25 30
 Asp Lys Ala Gly Val Phe Glu Leu Gln Ile His Ser Phe Gly Pro Gly
 35 40 45
 Pro Gly Pro Gly Ala Pro Arg Ser Pro Cys Ser Ala Arg Gly Pro Cys
 50 55 60
 Arg Leu Phe Phe Arg Val Cys Leu Lys Pro Gly Leu Ser Glu Glu Ala
 65 70 75 80
 Ala Glu Ser Pro Cys Ala Leu Gly Ala Ala Leu Ser Ala Arg Gly Pro
 85 90 95
 Val Tyr Thr Glu Gln Pro Glu Ala Pro Ala Pro Asp Leu Pro Leu Pro
 100 105 110
 Asn Gly Leu Leu Gln Val Pro Phe Arg Asp Ala Trp Pro Gly Thr Phe
 115 120 125
 Ser Leu Ile Ile Glu Thr Trp Arg Glu Glu Leu Gly Asp Gln Ile Gly
 130 135 140
 Gly Pro Ala Trp Ser Leu Leu Ala Arg Val Thr Arg Arg Arg Arg Leu
 145 150 155 160
 Ala Ala Gly Gly Pro Trp Ala Arg Asp Ile Gln Arg Ala Gly Ala Trp
 165 170 175
 Glu Leu Arg Phe Ser Tyr Arg Ala Arg Cys Glu Leu Pro Ala Val Gly
 180 185 190
 Thr Ala Cys Thr Arg Leu Cys Arg Pro Arg Ser Ala Pro Ser Arg Cys
 195 200 205
 Gly Pro Gly Leu Arg Pro Cys Ala Pro Leu Glu Asp Glu Cys Glu Ala
 210 215 220
 Pro Pro Val Cys Arg Ala Gly Cys Ser Leu Glu His Gly Phe Cys Glu
 225 230 235 240
 Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu Cys
 245 250 255
 Met Val Pro Val Ser Thr Ser Ser Cys Leu Gly Leu Arg Gly Pro Ser
 260 265 270

Ser Thr Thr Thr Gly Cys Leu Val Pro Gly Pro Gly Pro Cys Asp Gly
 275 280 285
 Asn Pro Cys Ala Asn Gly Gly Ser Cys Ser Glu Thr Pro Gly Ser Phe
 290 295 300
 Glu Cys Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser
 305 310 315 320
 Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys Val
 325 330 335
 Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro Gly
 340 345 350
 Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu Gln
 355 360 365
 Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg
 370 375 380
 Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu
 385 390 395 400
 Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu
 405 410 415
 Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg
 420 425 430
 Asn Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His
 435 440 445
 Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala
 450 455 460
 Pro Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly
 465 470 475 480
 Val Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro
 485 490 495
 Gln Arg Tyr Leu Leu Pro Pro Ala Leu Gly Leu Leu Val Ala Ala Gly
 500 505 510
 Val Ala Gly Ala Ala Leu Leu Leu Val His Val Arg Arg Arg Gly His
 515 520 525
 Ala Gln Asp Ala Gly Ser Arg Leu Leu Ala Gly Thr Pro Glu Pro Ser
 530 535 540
 Val His Ala Leu Pro Asp Ala Leu Asn Asn Leu Arg Thr Gln Glu Gly
 545 550 555 560
 Pro Gly Asp Val Pro Ser Ser Ser Val Asp Trp Asn Arg Pro Glu Asp
 565 570 575
 Val Asp Ser Arg Gly Ile Tyr Val Ile Ser Ala Pro Ser Ile Tyr Ala
 580 585 590
 Arg Glu Val Ala Met Pro Leu Phe Pro Pro Leu His Thr Gly Arg Ala
 595 600 605
 Gly Gln Arg Gln Asn Leu Leu Phe Pro Phe Pro Ser Ser Ile Leu Ser
 610 615 620
 Val Lys
 625

<210> 112

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG-tagged human DLL1 full length

<400> 112

Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
1 5 10 15
Cys Asp Tyr Lys Asp Asp Asp Asp Lys Gln Val Trp Ser Ser Gly Val
20 25 30
Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly Leu Leu Gly
35 40 45
Asn Arg Asn Cys Cys Arg Gly Gly Ala Gly Pro Pro Pro Cys Ala Cys
50 55 60
Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser
65 70 75 80
Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro Val Leu Gly
85 90 95
Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp Ser Ala Phe
100 105 110
Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe
115 120 125
Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala
130 135 140
Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His
145 150 155 160
Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg
165 170 175
Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr
180 185 190
Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly
195 200 205
His Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp
210 215 220
Lys Gly Pro Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu
225 230 235 240
Gln His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly
245 250 255
Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu
260 265 270
His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp
275 280 285
Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys
290 295 300
Pro Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr
305 310 315 320
Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Thr Cys Glu Leu Gly
325 330 335
Ile Asp Glu Cys Asp Pro Ser Pro Cys Lys Asn Gly Gly Ser Cys Thr
340 345 350
Asp Leu Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly
355 360 365
Lys Ile Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe
370 375 380
Asn Gly Gly Arg Cys Ser Asp Ser Pro Asp Gly Gly Tyr Ser Cys Arg
385 390 395 400
Cys Pro Val Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr
405 410 415
Cys Ser Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly
420 425 430

Asp Ala Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg His Cys
 435 440 445
 Asp Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly
 450 455 460
 Thr Cys Arg Asp Gly Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly
 465 470 475 480
 Tyr Thr Gly Arg Asn Cys Ser Ala Pro Val Ser Arg Cys Glu His Ala
 485 490 495
 Pro Cys His Asn Gly Ala Thr Cys His Glu Arg Gly His Arg Tyr Val
 500 505 510
 Cys Glu Cys Ala Arg Gly Tyr Gly Gly Pro Asn Cys Gln Phe Leu Leu
 515 520 525
 Pro Glu Leu Pro Pro Gly Pro Ala Val Val Asp Leu Thr Glu Lys Leu
 530 535 540
 Glu Gly Gln Gly Gly Pro Phe Pro Trp Val Ala Val Cys Ala Gly Val
 545 550 555 560
 Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Val Val Val Cys
 565 570 575
 Val Arg Leu Arg Leu Gln Lys His Arg Pro Pro Ala Asp Pro Cys Arg
 580 585 590
 Gly Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys
 595 600 605
 Asp Ile Ser Val Ser Ile Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn
 610 615 620
 Lys Lys Ala Asp Phe His Gly Asp His Ser Ala Asp Lys Asn Gly Phe
 625 630 635 640
 Lys Ala Arg Tyr Pro Ala Val Asp Tyr Asn Leu Val Gln Asp Leu Lys
 645 650 655
 Gly Asp Asp Thr Ala Val Arg Asp Ala His Ser Lys Arg Asp Thr Lys
 660 665 670
 Cys Gln Pro Gln Gly Ser Ser Gly Glu Glu Lys Gly Thr Pro Thr Thr
 675 680 685
 Leu Arg Gly Gly Glu Ala Ser Glu Arg Lys Arg Pro Asp Ser Gly Cys
 690 695 700
 Ser Thr Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Ile Ser Glu
 705 710 715 720
 Glu Lys Asp Glu Cys Val Ile Ala Thr Glu Val
 725 730

<210> 113

<211> 693

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG-tagged human DLL4 full length

<400> 113

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

50 55 60
 Phe Phe Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly
 65 70 75 80
 Pro Cys Thr Phe Gly Thr Val Ser Thr Pro Val Leu Gly Thr Asn Ser
 85 90 95
 Phe Ala Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln
 100 105 110
 Leu Pro Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu
 115 120 125
 Ala Trp His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro
 130 135 140
 Asp Ala Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly
 145 150 155 160
 Gln Asn Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg
 165 170 175
 Tyr Ser Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys
 180 185 190
 Ser Arg Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys
 195 200 205
 Gln Pro Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr
 210 215 220
 Cys Gln Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr
 225 230 235 240
 Cys Ser Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg
 245 250 255
 Leu Cys Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys
 260 265 270
 Ser Thr Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe
 275 280 285
 Cys Asp Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn
 290 295 300
 Gly Ala Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys
 305 310 315 320
 Arg Pro Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys
 325 330 335
 Asp Ser Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp
 340 345 350
 Gly Tyr His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu
 355 360 365
 His Ser Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser
 370 375 380
 Cys Arg Glu Arg Asn Gln Gly Ala Asn Tyr Ala Cys Glu Cys Pro Pro
 385 390 395 400
 Asn Phe Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser
 405 410 415
 Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg
 420 425 430
 Met Cys Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Leu His
 435 440 445
 Val Ser Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His
 450 455 460
 Asp Leu Glu Asn Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly
 465 470 475 480
 Arg Arg Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro
 485 490 495

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

<210> 114
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG tag

<400> 114
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 115
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vk leader

<400> 115
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp
 20

<210> 116
 <211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> 6His-myc tag

<400> 116
His His His His His His Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10 15

<210> 117
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Ser/Gly linker

<400> 117
Ser Gly Gly Gly Gly Ser
1 5

<210> 118
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> EpCAM transmembrane domain

<400> 118
Ala Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala Val Val Ala
1 5 10 15
Gly Ile Val Val Leu Val Ile
20

<210> 119
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> EpCAM intracellular domain

<400> 119
Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
1 5 10 15
Met Gly Glu Met His Arg Glu Leu Asn Ala
20 25

<210> 120
<211> 34
<212> PRT

<213> Artificial Sequence

<220>

<223> EGF1

<400> 120

Ala Pro Leu Val Cys Arg Ala Gly Cys Ser Pro Glu His Gly Phe Cys
1 5 10 15
Glu Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu
 20 25 30
Cys Thr

<210> 121

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF 1+2

<400> 121

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

<210> 122

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> EGF2

<400> 122

Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser Cys
1 5 10 15
Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr
 20 25 30
Gly Leu Arg Cys Glu
 35

<210> 123

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF 2+3

<400> 123

Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser Cys
1 5 10 15
Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr
20 25 30
Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro Cys
35 40 45
Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr
50 55 60
Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu
65 70 75

<210> 124

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> EGF3

<400> 124

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
1 5 10 15
Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
20 25 30
Gly Phe Gln Gly Ser Asn Cys Glu
35 40

<210> 125

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF 3+4

<400> 125

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
1 5 10 15
Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
20 25 30
Gly Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu
35 40 45
Gln Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu
50 55 60
Arg Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu
65 70 75

<210> 126

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> EGF4

<400> 126

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
1 5 10 15
Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 20 25 30
Gly Pro Arg Cys Glu
 35

<210> 127

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF 4+5

<400> 127

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
1 5 10 15
Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 20 25 30
Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys
 35 40 45
Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
 50 55 60
Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg
65 70 75

<210> 128

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> EGF5

<400> 128

Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys
1 5 10 15
Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly
 20 25 30
Gly Arg Asp Cys Arg
 35

<210> 129

<211> 73

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF 5+6

<400> 129

Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu
1 5 10 15
Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg
 20 25 30
Asp Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His
 35 40 45
Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala
 50 55 60
Pro Gly Tyr Met Gly Ala Arg Cys Glu
65 70

<210> 130

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> EGF6

<400> 130

Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys
1 5 10 15
Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met
 20 25 30
Gly Ala Arg Cys Glu
 35

<210> 131

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu DLL3 EGF6-membrane proximal peptide

<400> 131

Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys
1 5 10 15
Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met
 20 25 30
Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu
 35 40 45
Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu
 50 55 60

<210> 132

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Membrane proximal peptide

<400> 132

Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro Pro

1 5 10 15

Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu

20 25

<210> 133

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 LCCDR1

<400> 133

Arg Ala Ser Gln Ser Val Asn Ser Asn Phe Leu Ala

1 5 10

<210> 134

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 LCCDR2

<400> 134

Gly Thr Ser Ser Arg Ala Thr

1 5

<210> 135

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 LCCDR3

<400> 135

Gln Gln Tyr Gly Ser Ser Pro Trp Thr

1 5

<210> 136

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 HCCDR1

<400> 136

Gly Phe Thr Phe Ser Ser Tyr Gly Met Phe

1 5 10

<210> 137

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 HCCDR2

<400> 137

Val Ile Trp Leu Asp Gly Asp Asp Glu Asp Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 138

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 HCCDR3

<400> 138

Val Leu Asp Tyr

1

<210> 139

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#8 LCCDR1

<400> 139

Lys Ser Ser Gln Ser Val Leu Asp Thr Ser Asn Asn Lys Asn Tyr Leu

1 5 10 15

Val

<210> 140

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#8 LCCDR2

<400> 140

Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 141

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

<220>
<223> DLL3#8 LCCDR3

<400> 141
Gln His Tyr Tyr Asn Ser Pro Tyr Thr
1 5

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#8 HCCDR1

<400> 142
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His
1 5 10

<210> 143
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#8 HCCDR2

<400> 143
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Glu Gln Lys Phe Gln
1 5 10 15
Gly

<210> 144
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#8 HCCDR3

<400> 144
Asp Ala Val Val Ile Pro Met Asp Tyr
1 5

<210> 145
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#9 LCCDR1

<400> 145

Arg Ala Ser Gln Ser Ile Ser Arg Ser Tyr Leu Ala
1 5 10

<210> 146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 LCCDR2

<400> 146

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 147

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 LCCDR3

<400> 147

Gln Gln Tyr Gly Thr Ser Pro Ile Thr
1 5

<210> 148

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 HCCDR1

<400> 148

Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser
1 5 10

<210> 149

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 HCCDR2

<400> 149

Tyr Arg Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#9 HCCDR3

<400> 150
Ile Gly Val Ala Gly Phe Tyr Phe Asp Tyr
1 5 10

<210> 151
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#10 LCCDR1

<400> 151
Arg Ala Ser Gln Ser Leu Asn Ser Ile Phe Leu Ala
1 5 10

<210> 152
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#10 LCCDR2

<400> 152
Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#10 LCCDR3

<400> 153
Gln Gln Tyr Gly Gly Ser Met Asn Thr
1 5

<210> 154
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#10 HCCDR1

<400> 154

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5 10

<210> 155

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 HCCDR2

<400> 155

Trp Ile Asn Pro Asn Ser Gly Gly Thr Ile Phe Ala Gln Arg Phe Gln
1 5 10 15
Gly

<210> 156

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 HCCDR3

<400> 156

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

<210> 157

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 LCCDR1

<400> 157

Ser Ala Ser Ser Ser Val Thr Tyr Ile His
1 5 10

<210> 158

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 LCCDR2

<400> 158

Arg Thr Ser Tyr Leu Ala Ser
1 5

<210> 159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#11 LCCDR3

<400> 159
Gln Gln Arg Ser Ser Tyr Pro Arg Thr
1 5

<210> 160
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#11 HCCDR1

<400> 160
Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr
1 5 10

<210> 161
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#11 HCCDR2

<400> 161
Asp Ile Tyr Pro Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys
1 5 10 15
Asn

<210> 162
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#11 HCCDR3

<400> 162
Leu Tyr Tyr Tyr Gly Ser His Tyr Leu Asp Thr
1 5 10

<210> 163
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#12 LCCDR1

<400> 163

Ser Ala Ser Ser Ser Val Thr Tyr Ile His

1 5 10

<210> 164

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 LCCDR2

<400> 164

Arg Thr Ser Tyr Leu Ala Ser

1 5

<210> 165

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 LCCDR3

<400> 165

Gln Gln Arg Ser Ser Tyr Pro Arg Thr

1 5

<210> 166

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 HCCDR1

<400> 166

Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr

1 5 10

<210> 167

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 HCCDR2

<400> 167

Asp Ile Tyr Pro Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys

1 5 10 15

Asn

<210> 168

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 HCCDR3

<400> 168

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

<210> 169

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 LCCDR1

<400> 169

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 170

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 LCCDR2

<400> 170

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 171

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 LCCDR3

<400> 171

Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 172

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 HCCDR1

<400> 172

Gly Tyr Thr Phe Thr Asn Tyr Gly Val Thr
1 5 10

<210> 173

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 HCCDR2

<400> 173

Trp Ile Asn Thr Tyr Ser Gly Ala Pro Thr Tyr Ala Asp Asp Phe Asn
1 5 10 15
Gly

<210> 174

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 HCCDR3

<400> 174

Leu Asp Asp Tyr Asp Leu Tyr Tyr Phe Asp Tyr
1 5 10

<210> 175

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#14 LCCDR1

<400> 175

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

<210> 176

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#14 LCCDR2

<400> 176
Ala Ala Ser Thr Leu Glu Ser
1 5

<210> 177
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#14 LCCDR3

<400> 177
Gln Gln Ser Asp Glu Asp Pro Trp Thr
1 5

<210> 178
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#14 HCCDR1

<400> 178
Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile His
1 5 10

<210> 179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#14 HCCDR2

<400> 179
Tyr Ile Tyr Pro Gly Asn Ser Tyr Thr Ala Tyr Asn Gln Lys Phe Lys
1 5 10 15
Asp

<210> 180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#14 HCCDR3

<400> 180
Ser Gly Gly Ser Ala Met Asp Tyr
1 5

<210> 181
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#15 LCCDR1

<400> 181
Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn
1 5 10 15

<210> 182
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#15 LCCDR2

<400> 182
Ala Ala Ser Asn Leu Glu Ser
1 5

<210> 183
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#15 LCCDR3

<400> 183
Gln Gln Ser Ser Glu Asp Pro Arg Thr
1 5

<210> 184
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#15 HCCDR1

<400> 184
Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 185
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#15 HCCDR2

<400> 185

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys

1 5 10 15

Gly

<210> 186

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#15 HCCDR3

<400> 186

Phe His Phe Ser Ser Asn Gly Asp Ala Met Asp Asn

1 5 10

<210> 187

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 LCCDR1

<400> 187

Arg Ala Ser Gln Ser Val Ser Asp Trp Leu Ala

1 5 10

<210> 188

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 LCCDR2

<400> 188

Arg Ala Ser Ser Leu Glu Ser

1 5

<210> 189

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 LCCDR3

<400> 189

Gln Leu Tyr Asn Ser Tyr Ser Pro Thr

1 5

<210> 190
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#16 HCCDR1

<400> 190
Gly Phe Thr Phe Ser Ser Tyr Trp Met Thr
1 5 10

<210> 191
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#16 HCCDR2

<400> 191
Asn Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15
Gly

<210> 192
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#16 HCCDR3

<400> 192
Asp Trp Gly Tyr Phe Asp Tyr
1 5

<210> 193
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#17 LCCDR1

<400> 193
Arg Ala Ser Glu Asn Ile Tyr Tyr Ser Leu Ala
1 5 10

<210> 194
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#17 LCCDR2

<400> 194

Asn Thr Asn Ser Leu Glu Asp

1 5

<210> 195

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 LCCDR3

<400> 195

Lys Gln Ala Tyr Asp Phe Pro Leu Thr

1 5

<210> 196

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 HCCDR1

<400> 196

Gly Tyr Thr Phe Ile Ser Tyr Tyr Ile His

1 5 10

<210> 197

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 HCCDR2

<400> 197

Trp Ile Tyr Pro Gly Asp Gly Ser Thr Asn Asn Asn Glu Lys Phe Lys

1 5 10 15

Gly

<210> 198

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 HCCDR3

<400> 198

Gly Glu Gly Asn Ala Met Asp Asp

1 5

<210> 199

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 LCCDR1

<400> 199

Arg Ala Ser Glu Asn Ile Tyr Tyr Ser Leu Ala

1 5 10

<210> 200

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 LCCDR2

<400> 200

Asn Ala Asn Ser Leu Glu Asp

1 5

<210> 201

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 LCCDR3

<400> 201

Lys Gln Ala Tyr Asp Val Pro Leu Thr

1 5

<210> 202

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 HCCDR1

<400> 202

Gly Tyr Thr Phe Thr Ala Tyr Phe Ile His

1 5 10

<210> 203

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 HCCDR2

<400> 203

Tyr Ile Asp Pro Phe Asn Asp Asp Thr Asn Tyr Asn Val Lys Phe Lys
1 5 10 15
Gly

<210> 204

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 HCCDR3

<400> 204

Gly Thr Ser Ala Thr Leu Asp Tyr
1 5

<210> 205

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 VL

<400> 205

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

<210> 206

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 VH

<400> 206

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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

<210> 207
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#8 VL

<400> 207
 Asp Ile Val Met Ala Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Thr
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp 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 His
 85 90 95
 Tyr Tyr Asn Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 100 105 110
 Lys

<210> 208
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#8 VH

<400> 208
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr 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 Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Glu Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Thr Arg Asp Ala Val Val Ile Pro Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 209

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 VL

<400> 209

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

<210> 210

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 VH

<400> 210

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

65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys Ala
 85 90 95
 Ser Ile Gly Val Ala Gly Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 211

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 VL

<400> 211

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

<210> 212

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 VH

<400> 212

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

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 213

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 VL

<400> 213

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

<210> 214

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 VH

<400> 214

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

<210> 215

<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#12 VL

<400> 215
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Ile
20 25 30
His Trp Phe Gln Gln Asn Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Arg Thr Ser Tyr Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Arg Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 216
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#12 VH

<400> 216
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Phe Val Gln Pro Gly Ser
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr
20 25 30
Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Asp Ile Tyr Pro Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe
50 55 60
Lys Asn Arg Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Ile Gln Phe Ser Ser Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Val Ser Leu Tyr Tyr Tyr Gly Ser Tyr Tyr Leu Asp Thr Trp Gly Gln
100 105 110
Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 217
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#13 VL

<400> 217

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

<210> 218

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 VH

<400> 218

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

<210> 219

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#14 VL

<400> 219

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

1 5 10 15
 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 Thr 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 Asp
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 220

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#14 VH

<400> 220

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

<210> 221

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#15 VL

<400> 221

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu 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 Ser
85 90 95
Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 222

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#15 VH

<400> 222

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

<210> 223

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 VL

<400> 223

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

85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 224
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#16 VH

<400> 224
 Glu Val His Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Asn Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Trp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 225
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#17 VL

<400> 225
 Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ala Ala Ser Val Gly
 1 5 10 15
 Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Tyr Ser
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
 35 40 45
 Tyr Asn Thr Asn Ser Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Gln Tyr Ser Met Lys Ile Asn Ser Met Gln Pro
 65 70 75 80
 Glu Asp Thr Ala Thr Tyr Phe Cys Lys Gln Ala Tyr Asp Phe Pro Leu
 85 90 95
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 226

<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#17 VH

<400> 226
Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Val Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr
20 25 30
Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Asn Asn Asn Glu Lys Phe
50 55 60
Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Gly Glu Gly Asn Ala Met Asp Asp Trp Gly Gln Gly Thr Ser
100 105 110
Val Thr Val Ser Ser
115

<210> 227
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#18 VL

<400> 227
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ala Ala Ser Val Gly
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Tyr Ser
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Asn Ala Asn Ser Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Gln Tyr Ser Met Lys Ile Asn Asn Met Gln Pro
65 70 75 80
Glu Asp Thr Ala Thr Tyr Phe Cys Lys Gln Ala Tyr Asp Val Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 228
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> DLL3#18 VH

<400> 228

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

<210> 229

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 scFab

<400> 229

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

Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
 260 265 270
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met Phe
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
 290 295 300
 Trp Leu Asp Gly Asp Asp Glu Asp Tyr Val Asp Ser Val Lys Gly Arg
 305 310 315 320
 Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
 325 330 335
 Asn Ser Leu Arg Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val
 340 345 350
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 355 360 365
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 370 375 380
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 385 390 395 400
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 405 410 415
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 420 425 430
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 435 440 445
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
 450 455 460
 Glu Pro Lys Ser Cys
 465

<210> 230

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#8 scFab

<400> 230

Asp Ile Val Met Ala Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Thr
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp 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 His

85	90	95	
Tyr Tyr Asn Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile			
100	105	110	
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp			
115	120	125	
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn			
130	135	140	
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu			
145	150	155	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp			
165	170	175	
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr			
180	185	190	
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser			
195	200	205	
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly			
210	215	220	
Ser Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu			
225	230	235	240
Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly			
245	250	255	
Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro			
260	265	270	
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr			
275	280	285	
Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu			
290	295	300	
Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Glu Gln			
305	310	315	320
Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr			
325	330	335	
Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr			
340	345	350	
Tyr Cys Thr Arg Asp Ala Val Val Ile Pro Met Asp Tyr Trp Gly Gln			
355	360	365	
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val			
370	375	380	
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala			
385	390	395	400
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser			
405	410	415	
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val			
420	425	430	
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro			
435	440	445	
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys			
450	455	460	
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys			
465	470	475	

<210> 231

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#9 scFab

<400> 231

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
100 105 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205
Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val His
245 250 255
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser
260 265 270
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser
275 280 285
Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Asp Trp Ile Gly Tyr Arg
290 295 300
Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val
305 310 315 320
Thr Ile Ser Leu Asp Met Ser Asn Asn Gln Phe Ser Leu Lys Leu Ser
325 330 335
Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys Ala Ser Ile Gly
340 345 350
Val Ala Gly Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
355 360 365
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
370 375 380
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
385 390 395 400
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala

405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 232

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 scFab

<400> 232

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Asn Ser Ile
 20 25 30
 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Trp Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Gly Ser Met
 85 90 95
 Asn Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270
 Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His
 275 280 285

Trp Val Arg Leu Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile
 290 295 300
 Asn Pro Asn Ser Gly Gly Thr Ile Phe Ala Gln Arg Phe Gln Gly Arg
 305 310 315 320
 Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Asp Leu
 325 330 335
 Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
 340 345 350
 Phe Gly Asp Thr Val Gly Asn Ala Phe Asp Ile Trp Gly Gln Gly Thr
 355 360 365
 Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 370 375 380
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 385 390 395 400
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 405 410 415
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 420 425 430
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 435 440 445
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 450 455 460
 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475

<210> 233

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 scFab

<400> 233

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

165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser Ser Gly
 210 215 220
 Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly
 225 230 235 240
 Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 245 250 255
 Gln Pro Gly Ala Glu Leu Val Gln Pro Gly Ser Ser Val Lys Met Ser
 260 265 270
 Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr Trp Val
 275 280 285
 Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro
 290 295 300
 Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys Asn Lys Ala Thr
 305 310 315 320
 Leu Thr Ala Asp Thr Ser Ser Ser Lys Ala Tyr Ile Gln Phe Ser Ser
 325 330 335
 Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Leu Tyr Tyr
 340 345 350
 Tyr Gly Ser His Tyr Leu Asp Thr Trp Gly Gln Gly Thr Thr Leu Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 234

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 scFab

<400> 234

Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15
 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Ile
 20 25 30
 His Trp Phe Gln Gln Asn Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
 35 40 45

Arg Thr Ser Tyr Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Arg Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser Ser Gly
 210 215 220
 Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly
 225 230 235 240
 Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 245 250 255
 Gln Pro Gly Ala Glu Phe Val Gln Pro Gly Ser Ser Val Lys Met Ser
 260 265 270
 Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr Trp Val
 275 280 285
 Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro
 290 295 300
 Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys Asn Arg Ala Thr
 305 310 315 320
 Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Ile Gln Phe Ser Ser
 325 330 335
 Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Leu Tyr Tyr
 340 345 350
 Tyr Gly Ser Tyr Tyr Leu Asp Thr Trp Gly Gln Gly Thr Thr Leu Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 235
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3#13 scFab

<400> 235
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ala Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95
Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser
210 215 220
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly
225 230 235 240
Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly
245 250 255
Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly
260 265 270
Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
275 280 285
Tyr Gly Val Thr Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp
290 295 300
Met Gly Trp Ile Asn Thr Tyr Ser Gly Ala Pro Thr Tyr Ala Asp Asp
305 310 315 320
Phe Asn Gly Arg Phe Ala Leu Ser Leu Glu Thr Ser Ala Ser Thr Ala
325 330 335
Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe
340 345 350
Cys Ala Arg Leu Asp Asp Tyr Asp Leu Tyr Tyr Phe Asp Tyr Trp Gly
355 360 365

Gln Gly Thr Ala Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 370 375 380
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 385 390 395 400
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 405 410 415
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 420 425 430
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 435 440 445
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 450 455 460
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475 480

<210> 236
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#14 scFab

<400> 236
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Leu Gly
 1 5 10 15
 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 Thr 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 Asp
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
 210 215 220
 Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys

225 230 235 240
 Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser
 245 250 255
 Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Val
 260 265 270
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile
 275 280 285
 His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 290 295 300
 Ile Tyr Pro Gly Asn Ser Tyr Thr Ala Tyr Asn Gln Lys Phe Lys Asp
 305 310 315 320
 Lys Ala Thr Leu Thr Ala Asp Asn Pro Ser Ser Thr Ala Tyr Met Gln
 325 330 335
 Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 340 345 350
 Ser Gly Gly Ser Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 237

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#15 scFab

<400> 237

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu 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 Ser
 85 90 95
 Glu Asp Pro Arg Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
 210 215 220
 Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys
 225 230 235 240
 Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser
 245 250 255
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 260 265 270
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 275 280 285
 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 290 295 300
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 305 310 315 320
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 325 330 335
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
 340 345 350
 Thr Lys Phe His Phe Ser Ser Asn Gly Asp Ala Met Asp Asn Trp Gly
 355 360 365
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 370 375 380
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 385 390 395 400
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 405 410 415
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 420 425 430
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 435 440 445
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 450 455 460
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475 480

<210> 238

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 scFab

<400> 238

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Asp Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45
Tyr Arg Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Ala Asp Phe Ala Thr Tyr Tyr Cys Gln Leu Tyr Asn Ser Tyr Ser Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
210 215 220
Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
225 230 235 240
Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Glu Val His Leu
245 250 255
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Thr Trp
275 280 285
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys
290 295 300
Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe
305 310 315 320
Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
325 330 335
Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asp Trp
340 345 350
Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
355 360 365
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
370 375 380
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
385 390 395 400
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
405 410 415

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 420 425 430
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 435 440 445
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 450 455 460
 Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 239

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 scFab

<400> 239

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ala Ala Ser Val Gly
 1 5 10 15
 Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Tyr Ser
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
 35 40 45
 Tyr Asn Thr Asn Ser Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Gln Tyr Ser Met Lys Ile Asn Ser Met Gln Pro
 65 70 75 80
 Glu Asp Thr Ala Thr Tyr Phe Cys Lys Gln Ala Tyr Asp Phe Pro Leu
 85 90 95
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Ile Gln Leu
 245 250 255
 Gln Gln Ser Gly Pro Glu Val Val Lys Pro Gly Ala Ser Val Lys Ile
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr Tyr Ile His Trp
 275 280 285
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr

290 295 300
 Pro Gly Asp Gly Ser Thr Asn Asn Asn Glu Lys Phe Lys Gly Lys Thr
 305 310 315 320
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Leu Leu Ser
 325 330 335
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Gly Glu
 340 345 350
 Gly Asn Ala Met Asp Asp Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 355 360 365
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 385 390 395 400
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
 Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 240

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 scFab

<400> 240

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala Ser Val Lys Met
 260 265 270
 Ser Cys Glu Ala Ser Gly Tyr Thr Phe Thr Ala Tyr Phe Ile His Trp
 275 280 285
 Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asp
 290 295 300
 Pro Phe Asn Asp Asp Thr Asn Tyr Asn Val Lys Phe Lys Gly Lys Ala
 305 310 315 320
 Thr Leu Thr Ser Asp Thr Ser Ser Ser Ile Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Thr Ser Glu Asp Ser Ser Phe Tyr Tyr Cys Ala Arg Gly Thr
 340 345 350
 Ser Ala Thr Leu Asp Tyr Trp Gly His Gly Thr Thr Leu Thr Val Ser
 355 360 365
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 385 390 395 400
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
 Lys Arg Val Glu Pro Lys Ser Cys
 465 470

<210> 241

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#7 chain

<400> 241

Glu Ile Val Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn
 20 25 30
 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Leu Leu
 35 40 45
 Ile Phe Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
 245 250 255
 Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
 260 265 270
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met Phe
 275 280 285
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
 290 295 300
 Trp Leu Asp Gly Asp Asp Glu Asp Tyr Val Asp Ser Val Lys Gly Arg
 305 310 315 320
 Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
 325 330 335
 Asn Ser Leu Arg Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val
 340 345 350
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 355 360 365
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 370 375 380
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 385 390 395 400
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 405 410 415
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 420 425 430
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 435 440 445
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
 450 455 460
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 465 470 475 480
 Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 485 490 495

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

<210> 242

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#8 chain

<400> 242

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

145 150 155 160
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 165 170 175
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 180 185 190
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 195 200 205
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly
 210 215 220
 Ser Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu
 225 230 235 240
 Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly
 245 250 255
 Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 260 265 270
 Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 275 280 285
 Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 290 295 300
 Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Glu Gln
 305 310 315 320
 Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr
 325 330 335
 Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr
 340 345 350
 Tyr Cys Thr Arg Asp Ala Val Val Ile Pro Met Asp Tyr Trp Gly Gln
 355 360 365
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 370 375 380
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 385 390 395 400
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 405 410 415
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 420 425 430
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 435 440 445
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 450 455 460
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 465 470 475 480
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 485 490 495
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 500 505 510
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 515 520 525
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 530 535 540
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 545 550 555 560
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 565 570 575
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 580 585 590

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 595 600 605
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 610 615 620
 Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 625 630 635 640
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 645 650 655
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 660 665 670
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 675 680 685
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 690 695 700
 Gly
 705

<210> 243
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLL3#9 chain

<400> 243
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Ser Pro
 85 90 95
 Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser
 210 215 220
 Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly

225 230 235 240
 Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Gln Val His
 245 250 255
 Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser
 260 265 270
 Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser
 275 280 285
 Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Asp Trp Ile Gly Tyr Arg
 290 295 300
 Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val
 305 310 315 320
 Thr Ile Ser Leu Asp Met Ser Asn Asn Gln Phe Ser Leu Lys Leu Ser
 325 330 335
 Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys Ala Ser Ile Gly
 340 345 350
 Val Ala Gly Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 465 470 475 480
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 485 490 495
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 500 505 510
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 515 520 525
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 530 535 540
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 545 550 555 560
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 565 570 575
 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 580 585 590
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 595 600 605
 Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
 610 615 620
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 625 630 635 640
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 645 650 655
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 660 665 670

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
675 680 685
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
690 695 700

<210> 244

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#10 chain

<400> 244

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Asn Ser Ile
20 25 30
Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Trp Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Gly Ser Met
85 90 95
Asn Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205
Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser
210 215 220
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
225 230 235 240
Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln
245 250 255
Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270
Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His
275 280 285
Trp Val Arg Leu Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile
290 295 300
Asn Pro Asn Ser Gly Gly Thr Ile Phe Ala Gln Arg Phe Gln Gly Arg
305 310 315 320
Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Asp Leu

325	330	335	
Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp			
340	345	350	
Phe Gly Asp Thr Val Gly Asn Ala Phe Asp Ile Trp Gly Gln Gly Thr			
355	360	365	
Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro			
370	375	380	
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly			
385	390	395	400
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn			
405	410	415	
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln			
420	425	430	
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser			
435	440	445	
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser			
450	455	460	
Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr			
465	470	475	480
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser			
485	490	495	
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg			
500	505	510	
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro			
515	520	525	
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala			
530	535	540	
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val			
545	550	555	560
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr			
565	570	575	
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr			
580	585	590	
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu			
595	600	605	
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys			
610	615	620	
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser			
625	630	635	640
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
645	650	655	
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
660	665	670	
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
675	680	685	
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly			
690	695	700	

<210> 245

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#11 chain

<400> 245

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Ile
20 25 30
His Trp Phe Gln Gln Asn Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Arg Thr Ser Tyr Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Arg Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser Gly
210 215 220
Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly
225 230 235 240
Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Gln Val Gln Leu Gln
245 250 255
Gln Pro Gly Ala Glu Leu Val Gln Pro Gly Ser Ser Val Lys Met Ser
260 265 270
Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr Trp Val
275 280 285
Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro
290 295 300
Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys Asn Lys Ala Thr
305 310 315 320
Leu Thr Ala Asp Thr Ser Ser Ser Lys Ala Tyr Ile Gln Phe Ser Ser
325 330 335
Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Leu Tyr Tyr
340 345 350
Tyr Gly Ser His Tyr Leu Asp Thr Trp Gly Gln Gly Thr Thr Leu Thr
355 360 365
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
370 375 380
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
385 390 395 400
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
405 410 415
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly

420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 465 470 475 480
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 485 490 495
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 500 505 510
 Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 515 520 525
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 530 535 540
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 545 550 555 560
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 565 570 575
 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 580 585 590
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 595 600 605
 Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
 610 615 620
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 625 630 635 640
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 645 650 655
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 660 665 670
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 675 680 685
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695 700

<210> 246

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#12 chain

<400> 246

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Arg Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Glu Gly Lys Ser Ser Gly
 210 215 220
 Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly
 225 230 235 240
 Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 245 250 255
 Gln Pro Gly Ala Glu Phe Val Gln Pro Gly Ser Ser Val Lys Met Ser
 260 265 270
 Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Thr Trp Val
 275 280 285
 Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro
 290 295 300
 Gly Ser Gly Ser Thr Lys Ser Ser Glu Lys Phe Lys Asn Arg Ala Thr
 305 310 315 320
 Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Ile Gln Phe Ser Ser
 325 330 335
 Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Leu Tyr Tyr
 340 345 350
 Tyr Gly Ser Tyr Tyr Leu Asp Thr Trp Gly Gln Gly Thr Thr Leu Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 465 470 475 480
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 485 490 495
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 500 505 510
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

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

<210> 247

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#13 chain

<400> 247

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

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser
 210 215 220
 Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly
 225 230 235 240
 Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly
 245 250 255
 Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly
 260 265 270
 Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
 275 280 285
 Tyr Gly Val Thr Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp
 290 295 300
 Met Gly Trp Ile Asn Thr Tyr Ser Gly Ala Pro Thr Tyr Ala Asp Asp
 305 310 315 320
 Phe Asn Gly Arg Phe Ala Leu Ser Leu Glu Thr Ser Ala Ser Thr Ala
 325 330 335
 Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe
 340 345 350
 Cys Ala Arg Leu Asp Asp Tyr Asp Leu Tyr Tyr Phe Asp Tyr Trp Gly
 355 360 365
 Gln Gly Thr Ala Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 370 375 380
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 385 390 395 400
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 405 410 415
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 420 425 430
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 435 440 445
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 450 455 460
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475 480
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 485 490 495
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 500 505 510
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 515 520 525
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 530 535 540
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 545 550 555 560
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 565 570 575
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 580 585 590
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 595 600 605
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

610 615 620
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 625 630 635 640
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 645 650 655
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 660 665 670
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 675 680 685
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 690 695 700
 Pro Gly
 705

<210> 248

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#14 chain

<400> 248

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Leu Gly
 1 5 10 15
 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 Thr 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 Asp
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
 210 215 220
 Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys
 225 230 235 240
 Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser
 245 250 255

Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Val
 260 265 270
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile
 275 280 285
 His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 290 295 300
 Ile Tyr Pro Gly Asn Ser Tyr Thr Ala Tyr Asn Gln Lys Phe Lys Asp
 305 310 315 320
 Lys Ala Thr Leu Thr Ala Asp Asn Pro Ser Ser Thr Ala Tyr Met Gln
 325 330 335
 Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 340 345 350
 Ser Gly Gly Ser Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 355 360 365
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 370 375 380
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 385 390 395 400
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 405 410 415
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 420 425 430
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 435 440 445
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 450 455 460
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 465 470 475 480
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 485 490 495
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 500 505 510
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 515 520 525
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 530 535 540
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 545 550 555 560
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 565 570 575
 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 580 585 590
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 595 600 605
 Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
 610 615 620
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 625 630 635 640
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 645 650 655
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 660 665 670
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 675 680 685
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

690 695 700

<210> 249

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#15 chain

<400> 249

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Leu 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 Ser
85 90 95
Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu
210 215 220
Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys
225 230 235 240
Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser
245 250 255
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
260 265 270
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
275 280 285
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
290 295 300
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
305 310 315 320
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
325 330 335
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
340 345 350

Thr Lys Phe His Phe Ser Ser Asn Gly Asp Ala Met Asp Asn Trp Gly
 355 360 365
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 370 375 380
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 385 390 395 400
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 405 410 415
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 420 425 430
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 435 440 445
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 450 455 460
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 465 470 475 480
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 485 490 495
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 500 505 510
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 515 520 525
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 530 535 540
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 545 550 555 560
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 565 570 575
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 580 585 590
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 595 600 605
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 610 615 620
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 625 630 635 640
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 645 650 655
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 660 665 670
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 675 680 685
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 690 695 700
 Pro Gly
 705

<210> 250

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#16 chain

<400> 250

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Asp Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45
Tyr Arg Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Ala Asp Phe Ala Thr Tyr Cys Gln Leu Tyr Asn Ser Tyr Ser Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
210 215 220
Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
225 230 235 240
Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Ser Glu Val His Leu
245 250 255
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Thr Trp
275 280 285
Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys
290 295 300
Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe
305 310 315 320
Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
325 330 335
Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asp Trp
340 345 350
Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
355 360 365
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
370 375 380
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
385 390 395 400
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
405 410 415
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
420 425 430

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 435 440 445
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 450 455 460
 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 465 470 475 480
 Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 485 490 495
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 500 505 510
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 515 520 525
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 530 535 540
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 545 550 555 560
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 565 570 575
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 580 585 590
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 595 600 605
 Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
 610 615 620
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 625 630 635 640
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 645 650 655
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 660 665 670
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 675 680 685
 Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695

<210> 251

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#17 chain

<400> 251

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

85 90 95
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Ile Gln Leu
 245 250 255
 Gln Gln Ser Gly Pro Glu Val Val Lys Pro Gly Ala Ser Val Lys Ile
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr Tyr Ile His Trp
 275 280 285
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr
 290 295 300
 Pro Gly Asp Gly Ser Thr Asn Asn Asn Glu Lys Phe Lys Gly Lys Thr
 305 310 315 320
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Leu Leu Ser
 325 330 335
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Gly Glu
 340 345 350
 Gly Asn Ala Met Asp Asp Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 355 360 365
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 385 390 395 400
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
 Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 465 470 475 480
 Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 485 490 495
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 500 505 510
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 515 520 525

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 530 535 540
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 545 550 555 560
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 565 570 575
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 580 585 590
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 595 600 605
 Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
 610 615 620
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 625 630 635 640
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 645 650 655
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 660 665 670
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 675 680 685
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695

<210> 252

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> DLL3#18 chain

<400> 252

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

180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Glu Gly Lys Ser Ser
 210 215 220
 Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser
 225 230 235 240
 Gly Ser Glu Ser Lys Ser Thr Gly Gly Gly Gly Ser Gln Val Gln Leu
 245 250 255
 Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala Ser Val Lys Met
 260 265 270
 Ser Cys Glu Ala Ser Gly Tyr Thr Phe Thr Ala Tyr Phe Ile His Trp
 275 280 285
 Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asp
 290 295 300
 Pro Phe Asn Asp Asp Thr Asn Tyr Asn Val Lys Phe Lys Gly Lys Ala
 305 310 315 320
 Thr Leu Thr Ser Asp Thr Ser Ser Ser Ile Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Thr Ser Glu Asp Ser Ser Phe Tyr Tyr Cys Ala Arg Gly Thr
 340 345 350
 Ser Ala Thr Leu Asp Tyr Trp Gly His Gly Thr Thr Leu Thr Val Ser
 355 360 365
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 370 375 380
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 385 390 395 400
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 405 410 415
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 420 425 430
 Ser Leu Ser Ser Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 435 440 445
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 450 455 460
 Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 465 470 475 480
 Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 485 490 495
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 500 505 510
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 515 520 525
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 530 535 540
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 545 550 555 560
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 565 570 575
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 580 585 590
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 595 600 605
 Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
 610 615 620

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 625 630 635 640
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 645 650 655
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 660 665 670
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 675 680 685
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 690 695

<210> 253

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> region of heavy chain

<400> 253

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 1 5 10 15
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 20 25 30
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 35 40 45
 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 50 55 60

<210> 254

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse

<400> 254

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

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

<210> 255

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse

<400> 255

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

<210> 256

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-1 HC

<400> 256

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ala Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Tyr Ile Ser Gly Gly Gly Asp Thr Tyr Tyr Ser Ser Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg His Ser Asn Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg

405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

<210> 257
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PD1-1 LC

<400> 257
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Met Ser Cys Arg Ala Ser Glu Asn Ile Asp Thr Ser
 20 25 30
 Gly Ile Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 35 40 45
 Lys Leu Leu Ile Tyr Val Ala Ser Asn Gln Gly Ser Gly Ile Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Lys
 85 90 95
 Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 258
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PD1-2 HC

<400> 258
 Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ala Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Tyr Ile Ser Gly Gly Gly Gly Asp Thr Tyr Tyr Ser Ser Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg His Ser Asn Pro Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445

<210> 259
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> PD1-2 LC

<400> 259
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Met Ser Cys Arg Ala Ser Glu Asn Ile Asp Thr Ser
20 25 30
Gly Ile Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Gln Gly Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Lys
85 90 95
Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 260
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> PD1-3 HC

<400> 260
Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Lys Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Tyr Ile Ser Gly Gly Gly Asp Thr Tyr Tyr Ser Ser Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg His Ser Asn Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

<210> 261

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-3 LC

<400> 261

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

<210> 262

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-4 HC

<400> 262

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

<210> 263

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-4 LC

<400> 263

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

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

<210> 264

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-5 HC

<400> 264

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

<210> 265

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1-5 LC

<400> 265

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

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