

Page 1
SEQUENCE LISTING

<110> RemeGen Co., Ltd.

<120> BISPECIFIC FUSION PROTEIN AND APPLICATION THEREOF

<130> OP0021-EP-KR-SG-0084

<160> 137

<170> PatentIn version 3.3

<210> 1

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 1

Gly Phe Ser Leu Ser Arg Tyr
1 5

<210> 2

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 2

Gly Phe Ser Leu Ser Arg Tyr Ser Val His
1 5 10

<210> 3

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 3

Arg Tyr Ser Val His
1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR1

<400> 4

Ser Arg Tyr Ser Val His
1 5

<210> 5
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR1

<400> 5

Gly Phe Ser Leu Ser Arg Tyr Ser
1 5

<210> 6
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR2

<400> 6

Trp Gly Val Gly Thr
1 5

<210> 7
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR2

<400> 7

Met Ile Trp Gly Val Gly Thr Thr Asp
 1 5

<210> 8
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR2

<400> 8

Met Ile Trp Gly Val Gly Thr Thr Asp Tyr Asn Ser Ala Leu Lys Ser
 1 5 10 15

<210> 9
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR2

<400> 9

Trp Leu Gly Met Ile Trp Gly Val Gly Thr Thr Asp
 1 5 10

<210> 10
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR2

<400> 10

Ile Trp Gly Val Gly Thr Thr
 1 5

<210> 11
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR3

<400> 11

Asn	Trp	Gly	Thr	Ala	Asp	Tyr	Phe	Asp	Tyr
1				5					10

<210> 12

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR3

<400> 12

Asn	Trp	Gly	Thr	Ala	Asp	Tyr	Phe	Asp	Tyr
1				5					10

<210> 13

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR3

<400> 13

Asn	Trp	Gly	Thr	Ala	Asp	Tyr	Phe	Asp	Tyr
1				5					10

<210> 14

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR3

<400> 14

Ala	Arg	Asn	Trp	Gly	Thr	Ala	Asp	Tyr	Phe	Asp
1				5						10

<210> 15

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR3

<400> 15

Ala	Arg	Asn	Trp	Gly	Thr	Ala	Asp	Tyr	Phe	Asp	Tyr
1				5					10		

<210> 16

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 16

Arg	Ala	Ser	Lys	Ser	Val	His	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His
1				5					10					15

<210> 17

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 17

Arg	Ala	Ser	Lys	Ser	Val	His	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His
1				5					10					15

<210> 18

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 18

Arg	Ala	Ser	Lys	Ser	Val	His	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His
1				5					10					15

<210> 19

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

<220>
 <223> Light chain variable region CDR1

<400> 19

His	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His	Trp	Tyr
1				5					10	

<210> 20
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR1

<400> 20

Lys	Ser	Val	His	Thr	Ser	Gly	Tyr	Ser	Tyr
1				5					10

<210> 21
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 21

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 22
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 22

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 23
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 23

Leu Ala Ser Asn Leu Glu Ser
 1 5

<210> 24
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 24

Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1 5 10

<210> 25
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 25

Leu Ala Ser
 1

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

<220>
 <223> Light chain variable region CDR3

<400> 26

Gln His Ser Gly Glu Leu Pro Tyr Thr
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3

<400> 27

Gln His Ser Gly Glu Leu Pro Tyr Thr
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3

<400> 28

Gln His Ser Gly Glu Leu Pro Tyr Thr
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3

<400> 29

Gln His Ser Gly Glu Leu Pro Tyr
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial sequence

<220>

<223> Light chain variable region CDR3

<400> 30

Gln His Ser Gly Glu Leu Pro Tyr Thr
1 5

<210> 31

<211> 137

<212> PRT

<213> Artificial sequence

<220>

<223> Human TGF- β RII

<400> 31

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

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

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
115 120 125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp
130 135

<210> 32
 <211> 198
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CD80 ECD

<400> 32

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
 1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
 20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
 35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
 50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
 85 90 95

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

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
 115 120 125

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

Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
 145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
 165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
 180 185 190

Gln Thr Phe Asn Trp Asn
 195

<210> 33
 <211> 202
 <212> PRT
 <213> Artificial sequence

<220>
 <223> VEGFR

<400> 33

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
 1 5 10 15

Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro
 20 25 30

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro
 35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser
 50 55 60

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val
 65 70 75 80

Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn
 85 90 95

Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser
 100 105 110

Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn
 115 120 125

Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His

130

135

140

Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met
 145 150 155 160

Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp
 165 170 175

Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys
 180 185 190

Asn Ser Thr Phe Val Arg Val His Glu Pro
 195 200

<210> 34
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR1

<400> 34

Gly Ile Thr Phe Ser Asn Ser
 1 5

<210> 35
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region CDR1

<400> 35

Gly Ile Thr Phe Ser Asn Ser Gly Met His
 1 5 10

<210> 36
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 36

Asn Ser Gly Met His
1 5

<210> 37

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 37

Ser Asn Ser Gly Met His
1 5

<210> 38

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR1

<400> 38

Gly Ile Thr Phe Ser Asn Ser Gly
1 5

<210> 39

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR2

<400> 39

Trp Tyr Asp Gly Ser Lys
1 5

<210> 40

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR2

<400> 40

Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr
1				5				10	

<210> 41

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR2

<400> 41

Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 42

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR2

<400> 42

Trp	Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr
1				5				10				

<210> 43

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR2

<400> 43

Ile Trp Tyr Asp Gly Ser Lys Arg
1 5

<210> 44
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR3

<400> 44

Asn Asp Asp Tyr
1

<210> 45
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR3

<400> 45

Asn Asp Asp Tyr
1

<210> 46
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR3

<400> 46

Asn Asp Asp Tyr
1

<210> 47
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region CDR3

<400> 47

Ala Thr Asn Asp Asp
1 5

<210> 48

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain variable region CDR3

<400> 48

Ala Thr Asn Asp Asp Tyr
1 5

<210> 49

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 49

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

<210> 50

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 50

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

<210> 51

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 51

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

<210> 52

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 52

Ser	Ser	Tyr	Leu	Ala	Trp	Tyr
1				5		

<210> 53

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR1

<400> 53

Gln	Ser	Val	Ser	Ser	Tyr
1				5	

<210> 54

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region CDR2

<400> 54

Asp	Ala	Ser	Asn	Arg	Ala	Thr
1				5		

<210> 55

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

<220>
 <223> Light chain variable region CDR2

<400> 55

Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 56
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 56

Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 57
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 57

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

<210> 58
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR2

<400> 58

Asp Ala Ser
 1

<210> 59
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR3

<400> 59

Gln Gln Ser Ser Asn Trp Pro Arg Thr
 1 5

<210> 60
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR3

<400> 60

Gln Gln Ser Ser Asn Trp Pro Arg Thr
 1 5

<210> 61
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR3

<400> 61

Gln Gln Ser Ser Asn Trp Pro Arg Thr
 1 5

<210> 62
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region CDR3

<400> 62

Gln Gln Ser Ser Asn Trp Pro Arg
1 5

<210> 63
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region CDR3

<400> 63

Gln Gln Ser Ser Asn Trp Pro Arg Thr
1 5

<210> 64
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region amino acid sequence

<400> 64

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

Ser

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain variable region amino acid sequence

<400> 65

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 66
 <211> 120
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain variable region amino acid sequence

<400> 66

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 Phe Ser Leu Ser Arg Tyr
20 25 30

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

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

Ser Arg Leu Thr Ile Ser Lys 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 Asn Trp Gly Thr Ala Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser
115 120

<210> 67

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region amino acid sequence

<400> 67

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

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

Gly Tyr Ser Tyr 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 Thr Ile Asn
 65 70 75 80

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

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

Thr

<210> 68

<211> 668

<212> PRT

<213> Artificial sequence

<220>

<223> Hib-PDC heavy chain amino acid sequence

<400> 68

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

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

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

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Arg Val Glu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
210 215 220

Gly Gly Gly Ser Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala
225 230 235 240

Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr
245 250 255

Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser
260 265 270

Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp
275 280 285

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

Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe
 305 310 315 320

Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe
 325 330 335

Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg
 340 345 350

Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser
 355 360 365

Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser
 370 375 380

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

Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His
 405 410 415

Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Gly Gly Gly Gly Ser Gly
 420 425 430

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Tyr Gly Pro Pro Cys Pro
 435 440 445

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
 450 455 460

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

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

500

505

510

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 530 535 540

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 545 550 555 560

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 595 600 605

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

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 660 665

<210> 69

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Hib-PDC light chain amino acid sequence

<400> 69

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
 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

210

<210> 70
 <211> 672
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Hib-PDV heavy chain amino acid sequence

<400> 70

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 145 150 155 160

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

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

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
 195 200 205

Lys Arg Val Glu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 210 215 220

Gly Gly Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro
 225 230 235 240

Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg
 245 250 255

Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp
 260 265 270

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

Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys
 290 295 300

Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His
 305 310 315 320

Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly
 325 330 335

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

Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser
 355 360 365

Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser

370

375

380

Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val
 385 390 395 400

Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu
 405 410 415

Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Pro Gly Gly
 420 425 430

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Tyr Gly
 435 440 445

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 450 455 460

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 485 490 495

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 500 505 510

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

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

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 545 550 555 560

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

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 580 585 590

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

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

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

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
660 665 670

<210> 71
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Hib-PDV light chain amino acid sequence

<400> 71

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg

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
210

<210> 72
<211> 615
<212> PRT
<213> Artificial sequence

<220>
<223> Hib-PLT heavy chain amino acid sequence

<400> 72

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 Phe Ser Leu Ser Arg Tyr
20 25 30

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

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

Ser Arg Leu Thr Ile Ser Lys 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 Asn Trp Gly Thr Ala Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

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

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

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

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

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

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Gly
 210 215 220

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Thr Ile
 225 230 235 240

Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr Asp

245

250

255

Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val
 260 265 270

Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser
 275 280 285

Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp
 290 295 300

Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro
 305 310 315 320

Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys
 325 330 335

Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met Cys
 340 345 350

Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu
 355 360 365

Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 385 390 395 400

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 405 410 415

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 420 425 430

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 435 440 445

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 450 455 460

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
465 470 475 480

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
485 490 495

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
500 505 510

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
515 520 525

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
530 535 540

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
545 550 555 560

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
565 570 575

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
595 600 605

Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 73

<211> 218

<212> PRT

<213> Artificial sequence

<220>

<223> Hib-PLT light chain amino acid sequence

<400> 73

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

1	5	10	15
Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val His Thr Ser	20	25	30
Gly Tyr Ser Tyr 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 Thr Ile Asn	65	70	75
Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Gly	85	90	95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val 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
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> 74
 <211> 2007
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Hib-PDC heavy chain nucleic acid sequence

<400> 74
 caggtgcagc tcgtggagag cgggggaggc gtcgtccagc ctggccgtag cctgcggctg 60
 gactgtaagg ctagcggaat cacgttcagc aacagcggaa tgcactgggt cagacaggct 120
 cctggcaaag gcctcgaatg ggtcgccgtg atctggtacg acgggagcaa gagatactac 180
 gcagattcag tgaagggccg tttcacaatc agccgtgaca actcgaagaa cacactgttc 240
 ctgcagatga acagcctgag ggcagaagac acagcagtct actactgcgc taaaaatgac 300
 gactactggg gccagggaac actggtcacc gtgagctcag cttccaccaa gggcccatcc 360
 gtcttcccc tggcgccctg ctccaggagc acctccgaga gcacagccgc cctgggctgc 420
 ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480
 agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540
 gtggtgaccg tgccctccag cagcttgggc acgaagacct acacctgcaa cgtagatcac 600
 aagcccagca acaccaaggt ggacaagaga gttgagtccg gtggcggcgg aagcggcggc 660
 ggaggcagcg gcggaggcgg cagcgtgatc catgtcacga aggaggtcaa agaagtggcc 720
 accctcagct gcggtcacia cgtcagcgtg gaagagttgg ccagaccag aatctactgg 780
 cagaaggaga agaagatggt cttgaccatg atgagcggcg acatgaacat ctggccagag 840
 tacaagaata gaactatctt cgacatcacc aataacctga gcatcgtgat cctcgctttg 900
 cgtccgagcg acgaaggcac ctacgagtgc gtagtgctaa agtacgagaa agacgccttc 960
 aagcgggagc acctggcaga agtaaccctg agcgtgaagg cagacttccc aacgcctagc 1020
 atctccgact tcgagatccc cacaagcaac atccggcgga tcactctgtag cacctccggg 1080
 ggtttcccc agcctcacct gtcctggctc gagaacggcg aggagctgaa cgccatcaac 1140
 accaccgtga gccaggaccc cgagacagaa ctgtacgccg tgagctcaa gctcgacttc 1200
 aacatgacca caaatcacag cttcatgtgc ctcacaaagt acggacacct gcgggtgaat 1260

cagacgttca actggaacgg cgggggggggt agcggcggcg ggggctcagg tggggggggc 1320
 tcaaaatatg gtcccccattg cccaccatgc ccagcacctg agttcctggg gggaccatca 1380
 gtcttcctgt tcccccaaa acccaaggac actctcatga tctcccggac ccctgaggtc 1440
 acgtgcgtgg tgggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg 1500
 gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg 1560
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac 1620
 aagtgcagg tctccaacaa aggcctcccg tcctccatcg agaaaacat ctcaaagcc 1680
 aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc 1740
 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1800
 gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1860
 tccgacggct ctttcttct ctacagcagg ctaaccgtgg acaagagcag gtggcaggag 1920
 gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1980
 agcctctccc tgtctctggg taaatag 2007

<210> 75

<211> 645

<212> DNA

<213> Artificial sequence

<220>

<223> Hib-PDC light chain nucleic acid sequence

<400> 75

gagatcgtgc tgacacagag cccagccact ctgtcactgt cccagaggaga aagggtact 60
 ctgtcttgcc gggcaagcca gtctgtctcc agctacctgg cctggtatca gcagaagccc 120
 ggacaggctc ctagactgct gatctacgac gcaagtaaca gagccaccgg catccccgca 180
 cgcttcagtg gctcaggctc cggaacagac tttactctga ccatctctag tctggagcct 240
 gaagatttcg ccgtgtacta ttgtcagcag agctctaatt ggcctagaac cttcggccag 300
 ggacaccaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtttag 645

<210> 76
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Hib-PDV heavy chain nucleic acid sequence

<400> 76
 caggtgcagc tcgtggagag cgggggaggc gtcgtccagc ctggccgtag cctgicggctg 60
 gactgtaagg ctagcggaat cacgttcagc aacagcggaa tgcactgggt cagacaggct 120
 cctggcaaag gcctcgaatg ggtcgccgtg atctggtacg acgggagcaa gagatactac 180
 gcagattcag tgaagggccg tttcacaatc agccgtgaca actcgaagaa cacactgttc 240
 ctgcagatga acagcctgag ggcagaagac acagcagtct actactgcgc taaaaatgac 300
 gactactggg gccagggaa actgggtcacc gtgagctcag cttccaccaa gggcccatcc 360
 gtcttcccc tggcgccctg ctccaggagc acctccgaga gcacagccgc cctgggctgc 420
 ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480
 agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540
 gtggtgaccg tgccctccag cagcttgggc acgaagacct acacctgcaa cgtagatcac 600
 aagcccagca acaccaaggt ggacaagaga gttgagtccg gtggcggcgg aagcggcggc 660
 ggaggcagcg gcggaggcgg cagcggtaga ccattcgtag agatgtacag cgaaatcccc 720
 gaaatcatcc acatgactga aggaaggag ctcgtcatcc cctgccgggt tacgtcacct 780
 aacatcactg ttactctgaa gaagttcca ctcgacactt tgatccctga tggaaaacgc 840
 atcatctggg acagcagaaa gggcttcac atctcaa atg caacgtacaa agaaatcgga 900
 ctctgacct gtgaagcaac agtcaatgga catttgtata agacaaacta tctcacacat 960
 cgacagacca atacaatcat cgatgtgggt ctgagcccgt ccatggaat cgaactatct 1020
 gttggagaaa agctcgtcct gaattgtaca gcaagaactg aactgaatgt gggaatcgac 1080
 ttcaactggg aatacccttc ttcgaagcat cagcataaga aactcgtaaa ccgagaccta 1140

aagacccagt ctgggagcga gatgaagaaa ttcttgagca ccctgactat cgatggtgta 1200
acccggagcg accagggatt gtacacctgt gcagcatcca gcgggctgat gaccaagaag 1260
aacagcacat tcgtcagggt ccatgaaccc ggcggggggg gtagcggcgg cgggggctca 1320
ggtggggggg gctcaaaata tgggtcccca tgcccaccat gccagcacc tgagttcctg 1380
gggggacct cagtcttcct gttccccca aaaccaagg acacttcat gatctcccg 1440
acccctgagg tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc 1500
aactggtacg tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1560
ttcaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaac 1620
ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc 1680
atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag 1740
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1800
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1860
cccgtgctgg actccgacgg ctcttcttc ctctacagca ggctaaccgt ggacaagagc 1920
aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1980
tacacacaga agagcctctc cctgtctctg ggtaaatag 2019

<210> 77
<211> 645
<212> DNA
<213> Artificial sequence

<220>
<223> Hib-PDV light chain nucleic acid sequence

<400> 77
gagatcgtgc tgacacagag cccagccact ctgtcactgt ccccaggaga aagggtact 60
ctgtcttgcc gggcaagcca gtctgtctcc agctacctgg cctggtatca gcagaagccc 120
ggacaggctc ctagactgct gatctacgac gcaagtaaca gagccaccgg catccccgca 180
cgcttcagtg gctcaggctc cggaacagac tttactctga ccatctctag tctggagcct 240
gaagatttcg ccgtgtacta ttgtcagcag agctctaatt ggcctagaac cttcgccag 300
ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg	540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc	600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag	645

<210> 78
 <211> 1848
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Hib-PLT heavy chain nucleic acid sequence

<400> 78	
caggtgcagc tgcaggagtc cggaccagga ctggtgaagc catccgagac cctgagcctg	60
acctgtacag tgtccggctt cagcctgtct aggtacagcg tgcactggat cagacagcca	120
cctggcaagg gactggagtg gctgggcatg atctggggcg tgggcaccac agactacaac	180
tctgctctga agtccagact gaccatcagc aaggatacat ctaagaatca gttcagcctg	240
aagctgtcca gcgtgaccgc cgctgacaca gccgtgtact attgcgctcg caactggggc	300
accgccgact acttcgacta ttggggccag ggcaccacag tgacagtgtc ttccgctagc	360
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gccc aaatct	660
tgtgacaaag gcgggggagg cagcggcggc ggaggaagcg ggggcggagg tagcaccatc	720
cctccacacg tgcagaagag cgtgaacaat gacatgatcg tcaccgacaa caacggcgcc	780
gtcaagttcc cccagctgtg caaattctgc gacgtgaggt tctccacgtg cgacaaccag	840
aagagctgta tgagcaactg cagcatcaca tccatctgcg aaaaaccca ggaagtgtgc	900
gtcgccgtct ggcggaagaa cgacgagaac atcacactgg agaccgtgtg ccacgacccc	960
aaactgccct accacgactt catcctggag gacgccgcca gcccaaagtg catcatgaaa	1020

gagaagaaga agccgggcga gacttttcttc atgtgctcct gcagctccga cgagtgcac 1080
 gataatatca tcttcagcga agaatacaac acatctaacc cagacggagg gggcggatcc 1140
 gggggcggcg gaagcggcgg ggggggcagc actcacacat gccaccgtg cccagcacct 1200
 gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 1260
 atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 1320
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1380
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1440
 tggctgaatg gcaaggagta caagtgcag gtctccaaca aagccctccc agccccatc 1500
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1560
 ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1620
 tatcccgagc acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1680
 accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1740
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1800
 cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga 1848

<210> 79

<211> 657

<212> DNA

<213> Artificial sequence

<220>

<223> Hib-PLT light chain nucleic acid sequence

<400> 79

gatatcgtgc tgaccagtc tccagcttcc ctggccgtgt cccaggaca gagggccacc 60
 atcacatgtc gggcttccaa gagcgtgcac acaagcggct actcttatat gcattggtac 120
 cagcagaagc ccggccagcc ccctaagctg ctgatctatc tggcttccaa cctggagagc 180
 ggagtgccag ctaggttctc tggctccggc agcggcaccg actttaccct gacaatcaat 240
 cctgtggagg ccaacgatac agctaattac tattgccagc actccggaga gctgccatac 300
 accttcggcg gaggcacaaa ggtggagatc aagcgtacgg tggctgcacc atctgtcttc 360
 atcttccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttag 657

<210> 80
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 80

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

<210> 81
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 81

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

Val

<210> 82
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 82

Ala Lys Thr Thr Pro Lys Leu Gly Gly
 1 5

<210> 83
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 83

Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly
 1 5 10

<210> 84
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 84

Ser Ala Lys Thr Thr Pro
 1 5

<210> 85
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 85

Arg Ala Asp Ala Ala Pro
 1 5

<210> 86
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 86

Arg Ala Asp Ala Ala Pro Thr Val Ser
1 5

<210> 87
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 87

Arg Ala Asp Ala Ala Ala Ala Gly Gly Pro Gly Ser
1 5 10

<210> 88
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 88

Arg Ala Asp Ala Ala Ala Ala
1 5

<210> 89
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 89

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

Arg Val

<210> 90
<211> 5
<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 90

Ala Asp Ala Ala Pro
1 5

<210> 91

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 91

Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
1 5 10

<210> 92

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 92

Thr Val Ala Ala Pro
1 5

<210> 93

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 93

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
1 5 10

<210> 94
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 94

Gln Pro Lys Ala Ala Pro
 1 5

<210> 95
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 95

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
 1 5 10

<210> 96
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 96

Ala Lys Thr Thr Pro Pro
 1 5

<210> 97
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 97

Ala Lys Thr Thr Pro Pro Ser Val Thr Pro Leu Ala Pro

1 5

<210> 98
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 98

Ala Lys Thr Thr Ala Pro
1 5

<210> 99
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 99

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
1 5 10

<210> 100
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 100

Ala Ser Thr Lys Gly Pro
1 5

<210> 101
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 101

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

<210> 102

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 102

Gly	Glu	Asn	Lys	Val	Glu	Tyr	Ala	Pro	Ala	Leu	Met	Ala	Leu	Ser
1				5					10					15

<210> 103

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 103

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

<210> 104

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 104

Gly	His	Glu	Ala	Ala	Ala	Val	Met	Gln	Val	Gln	Tyr	Pro	Ala	Ser
1				5					10					15

<210> 105

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 105

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

<210> 106

<211> 448

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain amino acid sequence of Atezolizumab

<400> 106

Glu Val Gln 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 Asp Ser
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala 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 Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

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

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

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

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 107
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain amino acid sequence of Atezolizumab

<400> 107

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
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
210

<210> 108
<211> 450
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain amino acid sequence of Avelumab

<400> 108

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

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

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

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

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

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

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 109
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain amino acid sequence of Avelumab

<400> 109

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

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

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

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

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

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

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 110
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain amino acid sequence of Durvalumab

<400> 110

Glu Val Gln 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 Arg Tyr
20 25 30

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

Ala Asn Ile Lys Gln 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 111
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Light chain amino acid sequence of Durvalumab

<400> 111

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 Arg Val Ser Ser 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 Asp 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 Ser Leu Pro
 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
 210 215

<210> 112

<211> 440

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain amino acid sequence of Nivolumab

<400> 112

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 145 150 155 160

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

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys

180

185

190

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
 195 200 205

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
 210 215 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 225 230 235 240

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

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 275 280 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 305 310 315 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
 340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 370 375 380

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

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 113
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain amino acid sequence of Nivolumab

<400> 113

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
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
 210

<210> 114
 <211> 447
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Pembrolizumab heavy chain amino acid sequence

<400> 114

Gln Val Gln Leu Val Gln Ser Gly Val 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 Asn Tyr
 20 25 30

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

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
 50 55 60

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

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

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr 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 Lys
 435 440 445

<210> 115

<211> 218

<212> PRT

<213> Artificial sequence

<220>

<223> Pembrolizumab light chain amino acid sequence

<400> 115

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
 20 25 30

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

Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val 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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
 85 90 95

Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val 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> 116
 <211> 448
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Ipilimumab heavy chain amino acid sequence

<400> 116

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

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

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

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

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

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

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

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

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

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

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

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

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

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

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

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

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

370

375

380

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

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

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

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

<210> 117
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Ipilimumab light chain amino acid sequence

<400> 117

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 Gly Ser 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 Phe 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 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
 210 215

<210> 118
 <211> 444
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Cemiplimab heavy chain amino acid sequence

<400> 118

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
 20 25 30

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

Ser Gly Ile Ser Gly Gly Gly Arg Asp Thr Tyr Phe Ala Asp Ser Val
50 55 60

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

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

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

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

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

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

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

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

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

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

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

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

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

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

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

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 119
<211> 214
<212> PRT
<213> Artificial sequence

<220>

<223> Cemiplimab light chain amino acid sequence

<400> 119

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

Asp Ser Ile Thr Ile Thr Cys Arg Ala Ser Leu Ser Ile Asn Thr Phe
 20 25 30

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

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

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

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

Thr Phe Gly Pro Gly Thr Val Val Asp Phe Arg 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
 210

<210> 120
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 120

Gly Gly Gly Gly Ser
 1 5

<210> 121
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 121

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

<210> 122
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 122

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

<210> 123
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 123

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

Gly Gly Gly Ser
 20

<210> 124
 <211> 600
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain amino acid sequence of Control protein 1

<400> 124

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 Phe Ser Leu Ser Arg Tyr
 20 25 30

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

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

Ser Arg Leu Thr Ile Ser Lys 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 Asn Trp Gly Thr Ala Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

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

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

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

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

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

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

305		310		315		320
Lys	Cys	Lys	Val	Ser	Asn	Lys
				325		
					Ala	Leu
					330	
					Pro	Ala
						Pro
						Ile
						Glu
						Lys
						Thr
						335
Ile	Ser	Lys	Ala	Lys	Gly	Gln
			340			
					Pro	Arg
					345	
					Glu	Pro
						Gln
						Val
						Tyr
						Thr
						Leu
						350
Pro	Pro	Ser	Arg	Glu	Glu	Met
		355				
					Thr	Lys
					360	
					Asn	Gln
						Val
						Ser
						Leu
						Thr
						Cys
						365
Leu	Val	Lys	Gly	Phe	Tyr	Pro
	370					
					Pro	Ser
					375	
					Asp	Ile
						Ala
						Val
						Glu
						Trp
						Glu
						Ser
						380
Asn	Gly	Gln	Pro	Glu	Asn	Asn
385					390	
					Tyr	Lys
						Thr
						Thr
						Pro
						Pro
						Val
						Leu
						Asp
						400
Ser	Asp	Gly	Ser	Phe	Phe	Leu
				405		
					Tyr	Ser
						Lys
						Leu
						Thr
						Val
						Asp
						Lys
						Ser
						415
Arg	Trp	Gln	Gln	Gly	Asn	Val
						Phe
						Ser
						Cys
						Ser
						Val
						Met
						His
						Glu
						Ala
						420
Leu	His	Asn	His	Tyr	Thr	Gln
		435				
						Lys
						Ser
						Leu
						Ser
						Leu
						Ser
						Pro
						Gly
						Lys
						440
Gly	Gly	Gly	Gly	Ser	Gly	Gly
	450					
						Gly
						Gly
						Ser
						Gly
						Gly
						Gly
						Gly
						Ser
						Thr
						455
						460
Ile	Pro	Pro	His	Val	Gln	Lys
465					470	
						Ser
						Val
						Asn
						Asn
						Asp
						Met
						Ile
						Val
						Thr
						480
Asp	Asn	Asn	Gly	Ala	Val	Lys
				485		
						Phe
						Pro
						Gln
						Leu
						Cys
						Lys
						Phe
						Cys
						Asp
						490
Val	Arg	Phe	Ser	Thr	Cys	Asp
			500			
						Asn
						Gln
						Lys
						Ser
						Cys
						Met
						Ser
						Asn
						Cys
						510
Ser	Ile	Thr	Ser	Ile	Cys	Glu
						Lys
						Pro
						Gln
						Glu
						Val
						Cys
						Val
						Ala
						Val
						515
						520
						525

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
530 535 540

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
545 550 555 560

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
565 570 575

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
580 585 590

Glu Tyr Asn Thr Ser Asn Pro Asp
595 600

<210> 125

<211> 218

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain amino acid sequence of Control protein 1

<400> 125

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

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

Gly Tyr Ser Tyr 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 Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Gly

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 145 150 155 160

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

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

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
 195 200 205

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
 210 215 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 225 230 235 240

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

245

250

255

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 275 280 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 305 310 315 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
 340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 370 375 380

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

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
 405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Val Ile His Val Thr Lys Glu Val Lys
 450 455 460

Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu
465 470 475 480

Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr
485 490 495

Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr
500 505 510

Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg
515 520 525

Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys
530 535 540

Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys
545 550 555 560

Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser
565 570 575

Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro
580 585 590

His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr
595 600 605

Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys
610 615 620

Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys
625 630 635 640

Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn
645 650

<210> 127

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain amino acid sequence of Control protein 2

<400> 127

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
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
210

<210> 128
<211> 657
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain amino acid sequence of Control protein 3

<400> 128

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

130

135

140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 145 150 155 160

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

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

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
 195 200 205

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
 210 215 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 225 230 235 240

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

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 275 280 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 305 310 315 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
 340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
370 375 380

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

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
450 455 460

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
465 470 475 480

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
485 490 495

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
500 505 510

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
515 520 525

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
530 535 540

Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro
545 550 555 560

Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys
565 570 575

Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr
580 585 590

Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys
595 600 605

Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile
610 615 620

Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser
625 630 635 640

Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu
645 650 655

Pro

<210> 129
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain amino acid sequence of Control protein 3

<400> 129

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
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
210

<210> 130
<211> 202
<212> PRT
<213> Artificial sequence

<220>
<223> VEGF-R fragment

<400> 130

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
 1 5 10 15

Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro
 20 25 30

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro
 35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser
 50 55 60

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val
 65 70 75 80

Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn
 85 90 95

Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser
 100 105 110

Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn
 115 120 125

Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His
 130 135 140

Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met
 145 150 155 160

Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp
 165 170 175

Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys
 180 185 190

Asn Ser Thr Phe Val Arg Val His Glu Pro
 195 200

<210> 131
 <211> 117
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Human TGF- β RII

<400> 131

Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe
 1 5 10 15

Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr
 20 25 30

Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys
 35 40 45

Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu
 50 55 60

Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile
 65 70 75 80

Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys
 85 90 95

Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn
 100 105 110

Thr Ser Asn Pro Asp
 115

<210> 132
 <211> 115
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Human TGF- β RII

<400> 132

Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr

1 5 10 15

Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile
20 25 30

Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp
35 40 45

Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr
50 55 60

His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys
65 70 75 80

Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser
85 90 95

Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser
100 105 110

Asn Pro Asp
115

<210> 133
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> CD80 ECD

<400> 133

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
 50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
 85 90 95

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

<210> 134
 <211> 288
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CD80

<400> 134

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

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

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

<210> 135
<211> 256
<212> PRT
<213> Artificial sequence

<220>
<223> CD80

<400> 135

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140

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

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Ser Phe Ala Pro Arg Cys Arg
225 230 235 240

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
245 250 255

<210> 136
<211> 162
<212> PRT
<213> Artificial sequence

<220>
<223> CD80

<400> 136

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Gly Phe Ala Pro Arg
130 135 140

Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg
145 150 155 160

Pro Val

<210> 137
<211> 137
<212> PRT
<213> Artificial sequence

<220>
<223> TGF-βRII extracellular region fragment

<400> 137

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

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

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser

115

120

125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp
 130 135