

# SEQUENCE LISTING

<110> ImmunoBrain Checkpoint Inc.  
Yeda Research and Development Co. Ltd.  
Yoles, Ester  
Olsen Krogh, Berit  
Jensen , Allan  
Egebjerg , Jan  
David, Carol  
Baruch, Kuti  
Esienbach-Schwartz, Michal

<120> Modified anti-PD-L1 Antibody and Methods and Uses for Treating a  
Neurodegenerative Disease

<130> UEIBC1-0011W0

<150> US 62/836,247  
<151> 2019-04-19

<150> EP 19170438.6  
<151> 2019-04-19

<160> 108

<170> PatentIn version 3.5

<210> 1  
<211> 290  
<212> PRT  
<213> Homo sapiens

<400> 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ile | Phe | Ala | Val | Phe | Ile | Phe | Met | Thr | Tyr | Trp | His | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Phe | Thr | Val | Thr | Val | Pro | Lys | Asp | Leu | Tyr | Val | Val | Glu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Asn | Met | Thr | Ile | Glu | Cys | Lys | Phe | Pro | Val | Glu | Lys | Gln | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Ala | Ala | Leu | Ile | Val | Tyr | Trp | Glu | Met | Glu | Asp | Lys | Asn | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Phe | Val | His | Gly | Glu | Glu | Asp | Leu | Lys | Val | Gln | His | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn  
85 90 95

Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
100 105 110

Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val  
115 120 125

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val  
130 135 140

Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr  
145 150 155 160

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser  
165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn  
180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr  
195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu  
210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His  
225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr  
245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys  
260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu  
275 280 285

Glu Thr  
290

<210> 2  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 2

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

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

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

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 3  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

<400> 3

Gly Phe Thr Phe Asp Asp Tyr Ala  
 1 5

<210> 4  
 <211> 5

<212> PRT  
<213> Homo sapiens

<400> 4

Asp Tyr Ala Met His  
1 5

<210> 5  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 5

Ile Ser Trp Lys Ser Asn Ile Ile  
1 5

<210> 6  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 6

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

Gly

<210> 7  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 7

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

<210> 8  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 8

Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe Asp Pro

1 5 10

<210> 9  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 9

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

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

<210> 10  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 10

Gln Ser Ile Ser Ser Tyr  
1 5

<210> 11  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 11

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

<210> 12

<211> 3

<212> PRT

<213> Homo sapiens

<400> 12

Val Ala Ser  
1

<210> 13

<211> 7

<212> PRT

<213> Homo sapiens

<400> 13

Val Ala Ser Ser Leu Gln Ser  
1 5

<210> 14

<211> 9

<212> PRT

<213> Homo Sapiens

<400> 14

Gln Gln Ser Tyr Ser Asn Pro Ile Thr  
1 5

<210> 15

<211> 9

<212> PRT

<213> Homo sapiens

<400> 15

Gln Gln Ser Tyr Ser Asn Pro Ile Thr  
1 5

<210> 16

<211> 107

<212> PRT

<213> Homo sapiens

<400> 16

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> 17

<211> 97

<212> PRT

<213> Homo sapiens

<400> 17

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 Glu 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 Gly Glu Val Thr His Gln Gly Leu Ser Ser  
85 90 95

Pro

<210> 18  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 18

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 Arg Lys Val Asp Asn Ala Leu Gln  
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Glu 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> 19  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 19

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 Leu 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> 20  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 20

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 Asn 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> 21  
<211> 214  
<212> PRT  
<213> Homo sapiens

<400> 21

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg 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  
210

<210> 22  
<211> 204  
<212> PRT  
<213> Homo sapiens

<400> 22

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

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

<210> 23  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 23

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 Ser Ile Ser Ser Tyr  
 20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg 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 Arg Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Glu 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> 24  
<211> 214  
<212> PRT  
<213> Homo sapiens

<400> 24

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg 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 Leu 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> 25  
<211> 214  
<212> PRT  
<213> Homo sapiens

<400> 25

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg 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

Asn 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> 26  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 26

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
20 25 30

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys  
35 40 45

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
50 55 60

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
65 70 75 80

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
85 90 95

Thr Val Ala Pro Thr Glu Cys Ser  
100

<210> 27

<211> 106

<212> PRT

<213> Homo sapiens

<400> 27

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 Thr Val Ala Trp Lys Ala Asp Ser Ser Pro  
35 40 45

Val Lys Ala 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 Thr Glu Cys Ser  
100 105

<210> 28  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 28

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 Pro Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro  
35 40 45

Val Lys Ala 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 Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val  
85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
100 105

<210> 29  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 29

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> 30  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 30

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 Val Ser Asp  
 20 25 30

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

Val Lys Val Gly Val Glu Thr Thr Lys 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 Arg Val Thr His Glu Gly Ser Thr Val  
85 90 95

Glu Lys Thr Val Ala Pro Ala Glu Cys Ser  
100 105

<210> 31  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 31

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 Val Ser Asp  
20 25 30

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

Val Lys Val Gly Val Glu Thr Thr Lys 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 Arg Val Thr His Glu Gly Ser Thr Val  
85 90 95

Glu Lys Thr Val Ala Pro Ala Glu Cys Ser  
100 105

<210> 32  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 32

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

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

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

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr  
130 135 140

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

Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr  
165 170 175

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

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr  
195 200 205

Glu Cys Ser  
210

<210> 33

<211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 33

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 Ser Ile Ser Ser Tyr  
 20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
 85 90 95

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

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
 115 120 125

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

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

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

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

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

Pro Thr Glu Cys Ser  
 210

<210> 34  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 34

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 Ser Ile Ser Ser Tyr  
 20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
 85 90 95

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

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
 115 120 125

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

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

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

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

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

Pro Thr Glu Cys Ser  
210

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

<400> 35

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 Ser Ile Ser Ser Tyr  
20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

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

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
115 120 125

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

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

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

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

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

Pro Ala Glu Cys Ser  
 210

<210> 36  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 36

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 Ser Ile Ser Ser Tyr  
 20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile

85

90

95

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

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
 115 120 125

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

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

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

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

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

Pro Ala Glu Cys Ser  
 210

<210> 37  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 37

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 Ser Ile Ser Ser Tyr  
 20 25 30

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

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser 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 Ser Tyr Ser Asn Pro Ile  
85 90 95

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

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
115 120 125

Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp Phe Tyr Pro Gly Ala  
130 135 140

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

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

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

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

Pro Ala Glu Cys Ser  
210

<210> 38  
<211> 451  
<212> PRT  
<213> Homo sapiens

<400> 38

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

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

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

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

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

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

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

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

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

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

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

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

Ser Pro Gly  
450

<210> 39  
<211> 452  
<212> PRT  
<213> Homo sapiens

<400> 39

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys  
 450

<210> 40  
 <211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 40

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

325                      330                      335  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
                                  340                      345                      350

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

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

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

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

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

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

Ser Pro Gly Lys  
 450

<210> 41  
 <211> 451  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-PD-L1 antibody heavy chain with L239A, L240A, and K327A  
 variants

<400> 41

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly  
450

<210> 42  
 <211> 451  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and K327A variants

<400> 42

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp Trp Leu Asn  
305 310 315 320

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

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

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

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro



Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe Asp Pro Trp  
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly  
450

<210> 44

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A  
and H440Q variants

<400> 44

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

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

30

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

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

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp Trp Leu Asn  
305 310 315 320

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

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

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

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

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

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

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

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

Ser Pro Gly

450

<210> 45  
<211> 448  
<212> PRT  
<213> Homo sapiens

<400> 45

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
130 135 140

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

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

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

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
195 200 205

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

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

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

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

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

Ile Ser Lys Thr 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 Met 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> 46  
<211> 448  
<212> PRT  
<213> Homo sapiens

<400> 46

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr

140

Ile Ser Lys Thr 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 Met 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> 47  
 <211> 448  
 <212> PRT  
 <213> Homo sapiens

<400> 47

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
130 135 140

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

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

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

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

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

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

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

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

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

Ile Ser Lys Thr 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 Met 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> 48  
 <211> 448  
 <212> PRT  
 <213> Homo sapiens

<400> 48

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
130 135 140

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

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

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

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
195 200 205

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

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala |     |     |
| 275                                                             | 280 | 285 |
| Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val |     |     |
| 290                                                             | 295 | 300 |
| Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr |     |     |
| 305                                                             | 310 | 315 |
| Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr |     |     |
| 325                                                             | 330 | 335 |
| Ile Ser Lys Thr 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 Ser Val Glu Trp Glu Ser |     |     |
| 370                                                             | 375 | 380 |
| Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp |     |     |
| 385                                                             | 390 | 395 |
| 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> 49  
 <211> 451  
 <212> PRT  
 <213> Homo sapiens

<400> 49

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
 130 135 140

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro  
 225 230 235 240

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

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

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp  
 405 410 415

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

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

Leu Gly Lys  
450

<210> 50  
<211> 449  
<212> PRT  
<213> Homo sapiens

<400> 50

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

370

375

380

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

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

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

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

Lys

<210> 51  
 <211> 449  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 51

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 52  
<211> 449  
<212> PRT  
<213> Hono sapiens

<400> 52

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

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

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

35

40

45

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
 130 135 140

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro  
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 53

<211> 449  
 <212> PRT  
 <213> Homo sapiens

<400> 53

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
 130 135 140

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Gly Pro  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 54

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 heavy chain constant region with L239A, L240A, and K327A variants

<400> 54

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

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

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

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

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

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

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

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 115 |     | 120 |     | 125 |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro | Arg | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Thr | Val | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Ala | Val | Ser | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Phe | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln | Gly | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

<210> 55  
 <211> 329  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> anti-PD-L1 heacy chain constant region with L239A, L240A, H315A,  
 and K327A variants  
  
 <400> 55

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
325

<210> 56

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 heavy chain constant region with L239A, L240A, K327A,  
and H440Q variants

<400> 56

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 325

<210> 57

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 heavy chain constant region with L239A, L240A, H315A, K327A, and H440Q variants

<400> 57

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 325

<210> 58  
 <211> 1356  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1  
 antibody heavy chain with L239A, L240A and K327A variants

<400> 58  
 gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc ctgggaggtc cctgagactc 60  
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgccagact 120  
 ccagggaagg gcctggagtg ggtctcagga attagttgga aaagtaacat cattggatac 180  
 gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240  
 cttcaaatga acagcctgag agccgaggac acggctttgt attactgtgc aagagatatt 300  
 accggatccg gctcttacgg ctggttcgac ccctggggcc agggaaccct ggtcaccgtc 360  
 tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctag caagagcacc 420  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480  
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 540  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600  
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagcggggtt 660  
 gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcc 720  
 gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 780  
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgag agaggagcag  | 900  |
| tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 960  |
| ggcaaggagt acaagtgcgc cgtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1020 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1080 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1140 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1200 |
| cccgctgctgg actccgacgg ctccttcttc ctctattcta agctcaccgt ggacaagagc | 1260 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1320 |
| tacacgcaga agagcctctc cctgtctccc gggatga                           | 1356 |

<210> 59  
 <211> 1356  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1  
 antibody heavy chain with L239A, L240A, H315A and K327A variants

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 59                                                           |     |
| gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc  | 60  |
| tcctgtgcag cctctggatt cacctttgat gattatgcc a tgcactgggt ccgccagact | 120 |
| ccagggaagg gcctggagtg ggtctcagga attagtggga aaagtaacat cattggatac  | 180 |
| gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat  | 240 |
| cttcaaatga acagcctgag agccgaggac acggctttgt attactgtgc aagagatatt  | 300 |
| accggatccg gctcttacgg ctggttcgac ccctggggcc agggaaacct ggtcaccgtc  | 360 |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctag caagagcacc  | 420 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 480 |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag   | 540 |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 600 |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagcgggtt  | 660 |
| gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcc  | 720 |
| gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccg     | 780 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc | 840  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgag agaggagcag | 900  |
| tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tggctcagga ctggctgaat | 960  |
| ggcaaggagt acaagtgcgc cgtctccaac aaagccctcc cagcccccat cgagaaaacc | 1020 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg | 1080 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc | 1140 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct | 1200 |
| cccgtgctgg actccgacgg ctctttcttc ctctattcta agctcaccgt ggacaagagc | 1260 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac | 1320 |
| tacacgcaga agagcctctc cctgtctccc gggatga                          | 1356 |

<210> 60

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, K327A and H440Q variants

<400> 60

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc | 60  |
| tcctgtgcag cctctggatt cacctttgat gattatgcc a tgactgggt ccgccagact  | 120 |
| ccagggaagg gcctggagtg ggtctcagga attagttgga aaagtaacat cattggatac  | 180 |
| gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat  | 240 |
| cttcaaatga acagcctgag agccgaggac acggctttgt attactgtgc aagagatatt  | 300 |
| accggatccg gctcttacgg ctggttcgac ccctggggcc agggaaccct ggtcaccgtc  | 360 |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctag caagagcacc  | 420 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 480 |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag  | 540 |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 600 |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagcgggtt  | 660 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gagcccaa   | attgtgacaa | aactcacaca | tgcccaccgt | gccagcacc  | tgaagccgcc | 720  |
| gggggaccgt | cagtcttcct | cttccccca  | aaaccaagg  | acaccctcat | gatctcccgg | 780  |
| accctgagg  | tcacatgcgt | ggtggtggac | gtgagccacg | aagaccctga | ggtcaagttc | 840  |
| aactggtacg | tggacggcgt | ggaggtgcat | aatgccaaga | caaagccgag | agaggagcag | 900  |
| tacaacagca | cgtaccgtgt | ggtcagcgtc | ctcaccgtcc | tgcaccagga | ctggctgaat | 960  |
| ggcaaggagt | acaagtgcgc | cgtctccaac | aaagccctcc | cagcccccat | cgagaaaacc | 1020 |
| atctccaaag | caaaggga   | gccccgagaa | ccacaggtgt | acaccctgcc | cccatcccgg | 1080 |
| gaggagatga | ccaagaacca | ggtcagcctg | acctgcctgg | tcaaaggctt | ctatcccagc | 1140 |
| gacatcgccg | tggagtggga | gagcaatggg | cagccggaga | acaactacaa | gaccacgcct | 1200 |
| cccgtgctgg | actccgacgg | ctccttcttc | ctctattcta | agctcaccgt | ggacaagagc | 1260 |
| aggtggcagc | agggaacgt  | cttctcatgc | tccgtgatgc | atgaggctct | gcacaaccag | 1320 |
| tacacgcaga | agagcctctc | cctgtctccc | gggtga     |            |            | 1356 |

<210> 61

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A and H440 variants

<400> 61

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gaggtgcagc | tggtggagtc | tgggggaggc | ttggtccagc | ctgggaggtc | cctgagactc | 60  |
| tcctgtgcag | cctctggatt | cacctttgat | gattatgcc  | tgcactgggt | ccgccagact | 120 |
| ccagggaagg | gcctggagtg | ggtctcagga | attagttgga | aaagtaacat | cattggatac | 180 |
| gcggactccg | tgaagggccg | attcaccatc | tccagagaca | acgccaagaa | ctccctgtat | 240 |
| cttcaaatga | acagcctgag | agccgaggac | acggctttgt | attactgtgc | aagagatatt | 300 |
| accggatccg | gctcttacgg | ctggttcgac | ccctggggcc | agggaaccct | ggtcaccgtc | 360 |
| tcctcagcct | ccaccaaggg | cccatcggtc | ttccccctgg | caccctctag | caagagcacc | 420 |
| tctgggggca | cagcggccct | gggctgcctg | gtcaaggact | acttccccga | accggtgacg | 480 |
| gtgtcgtgga | actcaggcgc | cctgaccagc | ggcgtgcaca | ccttcccggc | tgtcctacag | 540 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 600  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagcgggtt  | 660  |
| gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcc | 720  |
| gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg   | 780  |
| acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc  | 840  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgag agaggagcag | 900  |
| tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tggctcagga ctggctgaat  | 960  |
| ggcaaggagt acaagtgcgc cgtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1020 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1080 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1140 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1200 |
| cccgtgctgg actccgacgg ctctttcttc ctctattcta agctcaccgt ggacaagagc  | 1260 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1320 |
| tacacgcaga agagcctctc cctgtctccc gggatga                           | 1356 |

<210> 62

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A and K327A variants

<400> 62

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaagtgcagc tgggtggaatc tggcggcgga ttggttcagc ctggcagatc cctgagactg | 60  |
| tcttgtgccg cctctggctt caccttcgac gactacgcta tgcaactgggt ccgacagacc | 120 |
| cctggcaaag gactggaatg ggtgtccggc atctcctgga agtccaacat catcggttac  | 180 |
| gccgactccg tgaagggcag attcaccatc tccagagaca acgccaagaa ctccctgtac  | 240 |
| ctgcagatga acagcctgag agccgaggac accgctctgt actactgcgc cagagacatc  | 300 |
| accggctccg gctcttacgg atgggttcgat ccttggggcc agggcacact ggtcacagtg | 360 |
| tcctctgctt ccaccaaggg acccagcgtt ttccctctgg ctccatcctc caagtctacc  | 420 |
| tctggcggaa cagctgctct gggctgcctg gtcaaggact actttcctga gcctgtgacc  | 480 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gtgtcctgga actctggcgc tctgacatct ggcgtgcaca cttttccagc tgtgctgcag | 540  |
| tcctccggcc tgtactctct gtcctctgtc gtgaccgtgc cttccagctc tctgggaacc | 600  |
| cagacctaca tctgcaatgt gaaccacaag cttccaaca ccaaggtgga caagagagt   | 660  |
| gaacccaagt cctgcgacaa gaccacacc tgtcctccat gtcctgctcc agaagctgct  | 720  |
| ggcggccctt ccgtgtttct gttccctcca aagcctaagg acaccctgat gatctctcgg | 780  |
| acccctgaag tgacctgcgt ggtggtggat gtgtctcacg aggaccaga agtgaagttc  | 840  |
| aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggacag  | 900  |
| tacaactcca cctatagagt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac | 960  |
| ggcaaagagt acaagtgcgc cgtgtccaac aaggccctgc ctgctcctat cgaaaagacc | 1020 |
| atcagcaagg ccaagggcca gcctagggaa cccaggttt acaccctgcc tccaagccgg  | 1080 |
| gaagagatga ccaagaacca ggtgtccctg acctgcctcg tgaagggtt ctaccctcc   | 1140 |
| gatatcgccg tggaatggga gtctaattggc cagccagaga acaactacaa gacaaccct | 1200 |
| cctgtgctgg actccgacgg ctcatcttc ctgtactcca agctgacagt ggacaagtcc  | 1260 |
| agatggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaatcac | 1320 |
| tacacacaga agtccctgtc tctgtcccct ggctga                           | 1356 |

<210> 63

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and K327A variants

<400> 63

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaagtgcagc tgggtggaatc tggcggcgga ttggttcagc ctggcagatc cctgagactg | 60  |
| tcttgtgccg cctctggctt caccttcgac gactacgcta tgcactgggt ccgacagacc  | 120 |
| cctggcaaag gactggaatg ggtgtccggc atctcctgga agtccaacat catcggtac   | 180 |
| gccgactccg tgaagggcag attcaccatc tccagagaca acgccaagaa ctccctgtac  | 240 |
| ctgcagatga acagcctgag agccgaggac accgctctgt actactgcgc cagagacatc  | 300 |
| accggctccg gctcttacgg atggttcgat ccttggggcc agggcacact ggtcacagt   | 360 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tcctctgctt ccaccaaggg acccagcgtt ttccctctgg ctccatcctc caagtctacc | 420  |
| tctggcggaa cagctgctct gggctgcctg gtcaaggact actttcctga gcctgtgacc | 480  |
| gtgtcctgga actctggcgc tctgacatct ggcgtgcaca cctttccagc tgtgtgcag  | 540  |
| tcctccggcc tgtactctct gtcctctgtc gtgaccgtgc cttccagctc tctgggaacc | 600  |
| cagacctaca tctgcaatgt gaaccacaag cttccaaca ccaaggtgga caagagagt   | 660  |
| gaacccaagt cctgcgacaa gaccacacc tgtcctccat gtcctgctcc agaagctgct  | 720  |
| ggcggccctt ccgtgtttct gttccctcca aagcctaagg acaccctgat gatctctcgg | 780  |
| accctgaag tgacctgcgt ggtggtggat gtgtctcacg aggaccaga agtgaagttc   | 840  |
| aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggaacag | 900  |
| tacaactcca cctatagagt ggtgtccgtg ctgaccgtgc tggcccagga ttggctgaac | 960  |
| ggcaaagagt acaagtgcgc cgtgtccaac aaggccctgc ctgctcctat cgaaaagacc | 1020 |
| atcagcaagg ccaagggcca gcctagggaa cccaggttt acaccctgcc tccaagccgg  | 1080 |
| gaagagatga ccaagaacca ggtgtccctg acctgcctcg tgaagggtt ctaccctcc   | 1140 |
| gatatcgccg tggaatggga gtctaattggc cagccagaga acaactacaa gacaaccct | 1200 |
| cctgtgctgg actccgacgg ctcatcttc ctgtactcca agctgacagt ggacaagtcc  | 1260 |
| agatggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaatcac | 1320 |
| tacacacaga agtccctgtc tctgtcccct ggctga                           | 1356 |

<210> 64

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, K327A and H440Q variants

<400> 64

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gaagtgcagc tggtggaatc tggcggcgga ttggttcagc ctggcagatc cctgagactg | 60  |
| tcttgtgccg cctctggctt caccttcgac gactacgcta tgcactgggt ccgacagacc | 120 |
| cctggcaaag gactggaatg ggtgtccggc atctcctgga agtccaacat catcggtac  | 180 |
| gccgactccg tgaagggcag attcaccatc tccagagaca acgccaagaa ctccctgtac | 240 |
| ctgcagatga acagcctgag agccgaggac accgctctgt actactgcgc cagagacatc | 300 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| accggctccg gctcttacgg atggttcgat ccttggggcc agggcacact ggtcacagtg | 360  |
| tcctctgctt ccaccaaggg acccagcgtt ttccctctgg ctccatcctc caagtctacc | 420  |
| tctggcggaa cagctgctct gggctgcctg gtcaaggact actttcctga gcctgtgacc | 480  |
| gtgtcctgga actctggcgc tctgacatct ggcgtgcaca cttttccagc tgtgtgcag  | 540  |
| tcctccggcc tgtactctct gtcctctgtc gtgaccgtgc cttccagctc tctgggaacc | 600  |
| cagacctaca tctgcaatgt gaaccacaag cttccaaca ccaaggtgga caagagagtg  | 660  |
| gaaccaagt cctgcgaaa gaccacacc tgtcctccat gtcctgctcc agaagctgct    | 720  |
| ggcggccctt ccgtgtttct gttccctcca aagcctaagg acaccctgat gatctctcgg | 780  |
| acccctgaag tgacctgcgt ggtggtggat gtgtctcacg aggaccaga agtgaagttc  | 840  |
| aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggaacag | 900  |
| tacaactcca cctatagagt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac | 960  |
| ggcaaagagt acaagtgcgc cgtgtccaac aaggccctgc ctgctcctat cgaaaagacc | 1020 |
| atcagcaagg ccaagggcca gcctagggaa cccaggttt acaccctgcc tccaagccgg  | 1080 |
| gaagagatga ccaagaacca ggtgtccctg acctgcctcg tgaagggatt ctaccctcc  | 1140 |
| gatatcgccg tggaatggga gtctaattggc cagccagaga acaactacaa gacaaccct | 1200 |
| cctgtgctgg actccgacgg ctcatcttc ctgtactcca agctgacagt ggacaagtcc  | 1260 |
| agatggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaatcag | 1320 |
| tacacacaga agtccctgtc tctgtcccct ggctga                           | 1356 |

<210> 65

<211> 1356

<212> DNA

<213> artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A and H440 variants

<400> 65

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaagtgcagc tgggtggaatc tggcggcgga ttggttcagc ctggcagatc cctgagactg | 60  |
| tcttgtgccg cctctggctt caccttcgac gactacgcta tgcactgggt ccgacagacc  | 120 |
| cctggcaaag gactggaatg ggtgtccggc atctcctgga agtccaacat catcggctac  | 180 |

gccgactccg tgaagggcag attcaccatc tccagagaca acgccaagaa ctccctgtac 240  
 ctgcagatga acagcctgag agccgaggac accgctctgt actactgcgc cagagacatc 300  
 accggctccg gctcttacgg atggttcgat ccttggggcc agggcacact ggtcacagtg 360  
 tcctctgctt ccaccaaggg acccagcgtt ttccctctgg ctccatcctc caagtctacc 420  
 tctggcggaa cagctgctct gggctgcctg gtcaaggact actttcctga gcctgtgacc 480  
 gtgtcctgga actctggcgc tctgacatct ggcgtgcaca cctttccagc tgtgtctgcag 540  
 tcctccggcc tgtactctct gtcctctgtc gtgaccgtgc cttccagctc tctgggaacc 600  
 cagacctaca tctgcaatgt gaaccacaag cttccaaca ccaaggtgga caagagagtg 660  
 gaacccaagt cctgcgacaa gaccacacc tgtcctccat gtcctgctcc agaagctgct 720  
 ggcgggccctt ccgtgtttct gttccctcca aagcctaagg acaccctgat gatctctcgg 780  
 acccctgaag tgacctgcgt ggtggtggat gtgtctcacg aggaccaga agtgaagttc 840  
 aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggaacag 900  
 tacaactcca cctatagagt ggtgtccgtg ctgaccgtgc tggcccagga ttggctgaac 960  
 ggcaaagagt acaagtgcgc cgtgtccaac aaggccctgc ctgctcctat cgaaaagacc 1020  
 atcagcaagg ccaagggcca gcctagggaa cccaggttt acaccctgcc tccaagccgg 1080  
 gaagagatga ccaagaacca ggtgtccctg acctgcctcg tgaagggatt ctaccctcc 1140  
 gatatcgccg tggaatggga gtctaattggc cagccagaga acaactacaa gacaaccct 1200  
 cctgtgctgg actccgacgg ctcatcttc ctgtactcca agctgacagt ggacaagtcc 1260  
 agatggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaatcag 1320  
 tacacacaga agtccctgtc tctgtcccct ggctga 1356

<210> 66

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A and K327A variants and signal peptide C

<400> 66

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
 225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 275 280 285

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

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

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

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

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

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

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

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

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

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

435

440

445

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

Leu Ser Leu Ser Pro Gly  
 465 470

&lt;210&gt; 67

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and  
 K327A variants and signal peptide C

&lt;400&gt; 67

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala  
 1 5 10 15

Thr Gln Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
 100 105 110

Tyr Tyr Cys Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe  
 115 120 125

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
275 280 285

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

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp  
325 330 335

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
 465 470

<210> 68  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-PD-L1 antibody heavy chain with L239A, L240A, K327A and  
 H440Q variants and signal peptide C

<400> 68

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala  
 1 5 10 15

Thr Gln Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

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

35

40

45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
 100 105 110

Tyr Tyr Cys Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe  
 115 120 125

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
 130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
 195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
 210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
 225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
275 280 285

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly

465

470

<210> 69

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A and H440 variants and signal peptide C

<400> 69

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala  
1 5 10 15

Thr Gln Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
100 105 110

Tyr Tyr Cys Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe  
115 120 125

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
275 280 285

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

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp  
325 330 335

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
 465 470

<210> 70  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-PD-L1 antibody heavy chain with L239A, L240A and K327A  
 variants and signal peptide LHC

<400> 70

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 1 5 10 15

Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
 465 470

<210> 71  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and K327A variants and signal peptide LHC

<400> 71

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
100 105 110

Tyr Tyr Cys Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe  
115 120 125

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
275 280 285

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

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp  
325 330 335

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
465 470

<210> 72

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 antibody heavy chain with L239A, L240A, K327A and H440Q variants and signal peptide LHC

<400> 72

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 100 | 105 | 110 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Tyr | Tyr | Cys | Ala | Arg | Asp | Ile | Thr | Gly | Ser | Gly | Ser | Tyr | Gly | Trp | Phe |  |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Asp | Pro | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Asn | Val | Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Arg | Val | Glu |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Pro | Lys | Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Glu | Ala | Ala | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
465 470

<210> 73  
<211> 470  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A  
and H440 variants and signal peptide LHC

<400> 73

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Gly Ile Ser Trp Lys Ser Asn Ile Ile Gly Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
100 105 110

Tyr Tyr Cys Ala Arg Asp Ile Thr Gly Ser Gly Ser Tyr Gly Trp Phe  
115 120 125

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
 225 230 235 240

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 275 280 285

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

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp  
 325 330 335

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly  
 465 470

<210> 74  
 <211> 1413  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1  
 antibody heavy chain with L239A, L240A and K327A variants and  
 signal peptide C

<400> 74  
 atgatgtcct ttgtctctct gtcctgggtt ggcatacctat tccatgccac ccaggccgag 60  
 gtgcagctgg tggagtctgg gggaggcttg gtccagcctg ggaggtccct gagactctcc 120  
 tgtgcagcct ctggattcac ctttgatgat tatgccatgc actgggtccg ccagactcca 180  
 gggaagggcc tggagtgggt ctgaggaatt agttggaaaa gtaacatcat tggatacgcg 240  
 gactccgtga agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatctt 300  
 caaatgaaca gcctgagagc cgaggacacg gctttgtatt actgtgcaag agatattacc 360  
 ggatccggct cttacggctg gttcgacccc tggggccagg gaaccctggt caccgtctcc 420  
 tcagcctcca ccaagggccc atcggctctt cccctggcac cctctagcaa gagcacctct 480  
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 540  
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600  
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 660  
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gcgggttgag 720  
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgccggg 780  
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 840  
 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900  
 tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgagaga ggagcagtac 960  
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaggagtaca agtgcgccgt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1080 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1140 |
| gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  | 1200 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1260 |
| gtgctggact ccgacggctc cttcttcctc tattctaagc tcaccgtgga caagagcagg  | 1320 |
| tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac | 1380 |
| acgcagaaga gcctctccct gtctcccggg tga                               | 1413 |

<210> 75

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and K327A variants and signal peptide C

<400> 75

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgatgtcct ttgtctctct gctcctggtt ggcattcctat tccatgccac ccaggccgag | 60  |
| gtgcagctgg tggagtctgg gggaggcttg gtccagcctg ggaggtccct gagactctcc  | 120 |
| tgtgcagcct ctggattcac ctttgatgat tatgccatgc actgggtccg ccagactcca  | 180 |
| gggaagggcc tggagtgggt ctcaggaatt agttggaaaa gtaacatcat tggatacgcg  | 240 |
| gactccgtga agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatctt  | 300 |
| caaatgaaca gcctgagagc cgaggacacg gctttgtatt actgtgcaag agatattacc  | 360 |
| ggatccggct cttacggctg gttcgacccc tggggccagg gaaccctggt caccgtctcc  | 420 |
| tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctctagcaa gagcacctct | 480 |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg  | 540 |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 600 |
| tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag  | 660 |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gcgggttgag  | 720 |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgccggg | 780 |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc   | 840 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 900  |
| tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgagaga ggagcagtag | 960  |
| aacagcacgt accgtgtggt cagcgtcctc accgtcctgg ctgaggactg gctgaatggc | 1020 |
| aaggagtaca agtgcgccgt ctccaacaaa gccctcccag ccccatcga gaaaaccatc  | 1080 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag  | 1140 |
| gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac | 1200 |
| atgccctgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1260 |
| gtgctggact ccgacggctc cttcttcctc tattctaagc tcaccgtgga caagagcagg | 1320 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac | 1380 |
| acgcagaaga gcctctccct gtctcccggg tga                              | 1413 |

<210> 76  
 <211> 1413  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1  
 antibody heavy chain with L239A, L240A, K327A and H440Q variants  
 and signal peptide C

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 76                                                           |     |
| atgatgtcct ttgtctctct gtcctggtt ggcacacctat tccatgccac ccaggccgag  | 60  |
| gtgcagctgg tggagtctgg gggaggcttg gtccagcctg ggaggtccct gagactctcc  | 120 |
| tgtgcagcct ctggattcac ctttgatgat tatgccatgc actgggtccg ccagactcca  | 180 |
| gggaagggcc tggagtgggt ctgaggaatt agttggaaaa gtaacatcat tggatacgcg  | 240 |
| gactccgtga agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatctt  | 300 |
| caaatgaaca gcctgagagc cgaggacacg gctttgtatt actgtgcaag agatattacc  | 360 |
| ggatccggct cttacggctg gttcgacccc tggggccagg gaaccctggt caccgtctcc  | 420 |
| tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctctagcaa gagcacctct | 480 |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg | 540 |
| tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 600 |
| tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag  | 660 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gcgggttgag  | 720  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgccggg | 780  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc   | 840  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 900  |
| tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgagaga ggagcagtac  | 960  |
| aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 1020 |
| aaggagtaca agtgcgccgt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1080 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1140 |
| gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  | 1200 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1260 |
| gtgctggact ccgacggctc cttcttcctc tattctaagc tcaccgtgga caagagcagg  | 1320 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccagtac  | 1380 |
| acgcagaaga gcctctccct gtctcccggtg tga                              | 1413 |

<210> 77

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A and H440 variants and signal peptide C

<400> 77

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atgatgtcct ttgtctctct gtcctggtt ggcctcctat tccatgccac ccaggccgag  | 60  |
| gtgcagctgg tggagtctgg gggaggcttg gtccagcctg ggaggtccct gagactctcc | 120 |
| tgtgcagcct ctggattcac ctttgatgat tatgccatgc actgggtccg ccagactcca | 180 |
| gggaagggcc tggagtgggt ctcaggaatt agttggaaaa gtaacatcat tggatacgcg | 240 |
| gactccgtga agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatctt | 300 |
| caaatgaaca gcctgagagc cgaggacacg gctttgtatt actgtgcaag agatattacc | 360 |
| ggatccggct cttacggctg gttcgacccc tggggccagg gaaccctggt caccgtctcc | 420 |
| tcagcctcca ccaagggcc atcggctctt cccctggcac cctctagcaa gagcacctct  | 480 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg  | 540  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgtg cctacagtcc  | 600  |
| tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag | 660  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gcgggttgag  | 720  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgccggg | 780  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc   | 840  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac | 900  |
| tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgagaga ggagcagtac  | 960  |
| aacagcacgt accgtgtggg cagcgtcctc accgtcctgg ctccaggactg gctgaatggc | 1020 |
| aaggagtaca agtgcgccgt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1080 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1140 |
| gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  | 1200 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1260 |
| gtgctggact ccgacggctc cttcttcctc tattctaagc tcaccgtgga caagagcagg  | 1320 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccagtac  | 1380 |
| acgcagaaga gcctctccct gtctcccggg tga                               | 1413 |

<210> 78  
 <211> 1413  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A and K327A variants and signal peptide LHC

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 78                                                          |     |
| atggactgga cttggagaat cctgttcctg gtggccgctg ctaccggcgc tcattctgaa | 60  |
| gtgcagctgg tggaatctgg cggcggattg gttcagcctg gcagatccct gagactgtct | 120 |
| tgtgccgcct ctggcttcac cttcagcagc tacgctatgc actgggtccg acagaccctt | 180 |
| ggcaaaggac tggaatgggt gtccggcatc tcctggaagt ccaacatcat cggctacgcc | 240 |
| gactccgtga agggcagatt caccatctcc agagacaacg ccaagaactc cctgtacctg | 300 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagatgaaca gcctgagagc cgaggacacc gctctgtact actgcgccag agacatcacc  | 360  |
| ggctccggct cttacggatg gttcgatcct tggggccagg gcacactggc cacagtgtcc  | 420  |
| tctgcttcca ccaagggacc cagcgttttc cctctggctc catcctcaa gtctacctct   | 480  |
| ggcggaacag ctgctctggg ctgcctggtc aaggactact ttcctgagcc tgtgaccgtg  | 540  |
| tcctggaact ctggcgctct gacatctggc gtgcacacct ttccagctgt gctgcagtcc  | 600  |
| tccggcctgt actctctgtc ctctgtcgtg accgtgcctt ccagctctct gggaaccag   | 660  |
| acctacatct gcaatgtgaa ccacaagcct tccaacacca aggtggacaa gagagtggaa  | 720  |
| cccaagtcct gcgacaagac ccacacctgt cctccatgtc ctgctccaga agctgctggc  | 780  |
| ggcccttccg tgtttctggt ccctccaaag cctaaggaca ccctgatgat ctctcgacc   | 840  |
| cctgaagtga cctgcgtggg ggtggatgtg tctcacgagg acccagaagt gaagttcaat  | 900  |
| tggtagctgg acggcgtgga agtgcacaat gccaaagacca agcctagaga ggaacagtac | 960  |
| aactccacct atagagtggg gtccgtgctg accgtgctgc accaggattg gctgaacggc  | 1020 |
| aaagagtaca agtgcgccgt gtccaacaag gccctgcctg ctcctatcga aaagaccatc  | 1080 |
| agcaaggcca agggccagcc tagggaaccc caggtttaca ccctgcctcc aagccgggaa  | 1140 |
| gagatgacca agaaccagggt gtccctgacc tgcctcgtga agggattcta cccctccgat | 1200 |
| atcgccgtgg aatgggagtc taatggccag ccagagaaca actacaagac aaccctctct  | 1260 |
| gtgctggact ccgacggctc attcttcctg tactccaagc tgacagtgga caagtccaga  | 1320 |
| tggcagcagg gcaacgtggt ctctgtctcc gtgatgcacg aggccctgca caatcactac  | 1380 |
| acacagaagt ccctgtctct gtcccctggc tga                               | 1413 |

<210> 79

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A and K327A variants and signal peptide LHC

<400> 79

|                                                                   |    |
|-------------------------------------------------------------------|----|
| atggactgga cttggagaat cctgttcctg gtggccgctg ctaccggcgc tcattctgaa | 60 |
|-------------------------------------------------------------------|----|

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gtgcagctgg tggaatctgg cggcggattg gttcagcctg gcagatccct gagactgtct | 120 |
|-------------------------------------------------------------------|-----|

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tgtgccgcct ctggcttcac cttcgacgac tacgctatgc actgggtccg acagaccct  | 180  |
| ggcaaaggac tggaatgggt gtccggcatc tcctggaagt ccaacatcat cggctacgcc | 240  |
| gactccgtga agggcagatt caccatctcc agagacaacg ccaagaactc cctgtacctg | 300  |
| cagatgaaca gcctgagagc cgaggacacc gctctgtact actgcgccag agacatcacc | 360  |
| ggctccggct cttacggatg gttcgatcct tggggccagg gcacactggc cacagtgtcc | 420  |
| tctgcttcca ccaagggacc cagcgttttc cctctggctc catcctcaa gtctacctct  | 480  |
| ggcggaacag ctgctctggg ctgcctggc aaggactact ttcctgagcc tgtgaccgtg  | 540  |
| tcctggaact ctggcgctct gacatctggc gtgcacacct ttccagctgt gctgcagtcc | 600  |
| tccggcctgt actctctgtc ctctgtcgtg accgtgcctt ccagctctct gggaaccag  | 660  |
| acctacatct gcaatgtgaa ccacaagcct tccaacacca aggtggacaa gagagtggaa | 720  |
| cccaagtcct gcgacaagac ccacacctgt cctccatgtc ctgctccaga agctgctggc | 780  |
| ggcccttccg tgtttctgtt ccctccaaag cctaaggaca ccctgatgat ctctcggacc | 840  |
| cctgaagtga cctgcgtggg ggtggatgtg tctcacgagg acccagaagt gaagttcaat | 900  |
| tggtacgtgg acggcgtgga agtgcacaat gccaaagaca agcctagaga ggaacagtac | 960  |
| aactccacct atagagtggg gtccgtgctg accgtgctgg ccaggattg gctgaacggc  | 1020 |
| aaagagtaca agtgcgccgt gtccaacaag gccctgcctg ctcttatcga aaagaccatc | 1080 |
| agcaaggcca agggccagcc tagggaaccc caggtttaca ccctgcctcc aagccgggaa | 1140 |
| gagatgacca agaaccaggt gtccctgacc tgcctcgtga agggattcta cccctccgat | 1200 |
| atgccgtgg aatgggagtc taatggccag ccagagaaca actacaagac aaccctctct  | 1260 |
| gtgctggact ccgacggctc attcttctg tactccaagc tgacagtgga caagtccaga  | 1320 |
| tggcagcagg gcaacgtgtt ctctgctcc gtgatgcacg aggccctgca caatcactac  | 1380 |
| acacagaagt ccctgtctct gtcccctggc tga                              | 1413 |

<210> 80

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, K327A and H440Q variants

and signal peptide LHC

<400> 80

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atggactgga cttggagaat cctgttcctg gtggccgctg ctaccggcgc tcattctgaa   | 60   |
| gtgcagctgg tggaatctgg cggcggattg gttcagcctg gcagatccct gagactgtct   | 120  |
| tgtgccgcct ctggcttcac cttcgacgac tacgctatgc actgggtccg acagaccctt   | 180  |
| ggcaaaggac tggaatgggt gtccggcatc tcctggaagt ccaacatcat cggctacgcc   | 240  |
| gactccgtga agggcagatt caccatctcc agagacaacg ccaagaactc cctgtacctg   | 300  |
| cagatgaaca gcctgagagc cgaggacacc gctctgtact actgcgccag agacatcacc   | 360  |
| ggctccggct cttacggatg gttcgatcct tggggccagg gcacactggt cacagtgtcc   | 420  |
| tctgcttcca ccaagggacc cagcgttttc cctctggctc catcctcaa gtctacctct    | 480  |
| ggcggaaacag ctgctctggg ctgcctggtc aaggactact ttcctgagcc tgtgaccgtg  | 540  |
| tcctggaact ctggcgctct gacatctggc gtgcacacct ttccagctgt gctgcagtcc   | 600  |
| tccggcctgt actctctgtc ctctgtcgtg accgtgcctt ccagctctct gggaaccag    | 660  |
| acctacatct gcaatgtgaa ccacaagcct tccaacacca aggtggacaa gagagtggaa   | 720  |
| cccaagtcct gcgacaagac ccacacctgt cctccatgtc ctgctccaga agctgctggc   | 780  |
| ggcccttccg tgtttctgtt ccctccaaag cctaaggaca ccctgatgat ctctcggacc   | 840  |
| cctgaagtga cctgcgtggg ggtggatgtg tctcacgagg acccagaagt gaagttcaat   | 900  |
| tgggtacgtgg acggcgtgga agtgcacaat gccaaagacca agcctagaga ggaacagtac | 960  |
| aactccacct atagagtggg gtccgtgctg accgtgctgc accaggattg gctgaacggc   | 1020 |
| aaagagtaca agtgcgccgt gtccaacaag gccctgcctg ctcttatcga aaagaccatc   | 1080 |
| agcaaggcca agggccagcc tagggaacct caggtttaca ccctgcctcc aagccgggaa   | 1140 |
| gagatgacca agaaccaggt gtccctgacc tgcctcgtga agggattcta cccctccgat   | 1200 |
| atgccgtgg aatgggagtc taatggccag ccagagaaca actacaagac aaccctcct     | 1260 |
| gtgctggact ccgacggctc attcttcctg tactccaagc tgacagtgga caagtccaga   | 1320 |
| tggcagcagg gcaacgtgtt ctctgtctcc gtgatgcacg aggccctgca caatcagtac   | 1380 |
| acacagaagt ccctgtctct gtcccctggc tga                                | 1413 |

<210> 81

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody heavy chain with L239A, L240A, H315A, K327A and H440 variants and signal peptide LHC

<400> 81

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atggactgga cttggagaat cctgttcctg gtggccgctg ctaccggcgc tcattctgaa  | 60   |
| gtgcagctgg tggaatctgg cggcggattg gttcagcctg gcagatccct gagactgtct  | 120  |
| tgtgccgcct ctggcttcac cttcgacgac tacgctatgc actgggtccg acagaccctt  | 180  |
| ggcaaaggac tggaatgggt gtccggcatc tcctggaagt ccaacatcat cggctacgcc  | 240  |
| gactccgtga agggcagatt caccatctcc agagacaacg ccaagaactc cctgtacctg  | 300  |
| cagatgaaca gcctgagagc cgaggacacc gctctgtact actgcgccag agacatcacc  | 360  |
| ggctccggct cttacggatg gttcgatcct tggggccagg gcacactggt cacagtgtcc  | 420  |
| tctgcttcca ccaagggacc cagcgttttc cctctggctc catcctcaa gtctacctct   | 480  |
| ggcggaacag ctgctctggg ctgcctggtc aaggactact ttcctgagcc tgtgaccgtg  | 540  |
| tcctggaact ctggcgctct gacatctggc gtgcacacct ttccagctgt gctgcagtcc  | 600  |
| tccggcctgt actctctgtc ctctgtcgtg accgtgcctt ccagctctct gggaaccag   | 660  |
| acctacatct gcaatgtgaa ccacaagcct tccaacacca aggtggacaa gagagtggaa  | 720  |
| cccaagtcct gcgacaagac ccacacctgt cctccatgtc ctgctccaga agctgctggc  | 780  |
| ggcccttccg tgtttctgtt ccctccaaag cctaaggaca ccctgatgat ctctcggacc  | 840  |
| cctgaagtga cctgcgtggg ggtggatgtg tctcacgagg acccagaagt gaagttcaat  | 900  |
| tggtagctgg acggcgtgga agtgcacaat gccaaagacca agcctagaga ggaacagtac | 960  |
| aactccacct atagagtggg gtccgtgctg accgtgctgg cccaggattg gctgaacggc  | 1020 |
| aaagagtaca agtgcgccgt gtccaacaag gccctgcctg ctctatcga aaagaccatc   | 1080 |
| agcaaggcca agggccagcc tagggaaccc caggtttaca ccctgcctcc aagccgggaa  | 1140 |
| gagatgacca agaaccaggt gtccctgacc tgcctcgtga agggattcta cccctccgat  | 1200 |
| atcgccgtgg aatgggagtc taatggccag ccagagaaca actacaagac aaccctcct   | 1260 |
| gtgctggact ccgacggctc attcttcctg tactccaagc tgacagtgga caagtccaga  | 1320 |
| tggcagcagg gcaacgtgtt ctctgtctcc gtgatgcacg aggccctgca caatcagtac  | 1380 |

acacagaagt ccctgtctct gtcccctggc tga 1413

<210> 82  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody light chain

<400> 82  
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120  
 gggaaagccc ctaagcctct gatctatgtc gcatccagtt tgcaaagtgg ggtcccatca 180  
 tctttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta accctatcac gttcggccaa 300  
 gggaccaggc tggaaatcaa acgaactgtg gctgcacat ctgtcttcat cttcccgcca 360  
 tctgatgagc agcttaagtc cggaactgct agcgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg aaactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 83  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody light chain

<400> 83  
 gacatccaga tgaccagtc tccatcctct ctgtccgcct ctgtgggcga cagagtgacc 60  
 atcacctgtc gggcctctca gtccatctcc tcctacctga actggtatca gcagaagccc 120  
 ggcaaggccc ctaagcctct gatctatgtg gcctccagtc tgcaagtctgg cgtgccctct 180  
 tctttctccg gctctggctc tggcaccgac tttaccctga caatctccag cctgcagcct 240

gaggacttcg ccacctacta ctgccagcag tcctacagca accctatcac cttcggccag 300  
ggcaccagac tggaaatcaa gagaaccgtg gccgctcctt ccgtgttcat cttcccacct 360  
tccgacgagc agctgaagtc cggcacagct tctgtcgtgt gcctgctgaa caacttctac 420  
cctcgggaag ccaaggtgca gtggaaggtg gacaatgctc tgcagtccgg caactcccaa 480  
gagtccgtga ccgagcagga ctccaaggac tctacctaca gcctgtcctc cacactgacc 540  
ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccatcagggc 600  
ctgtctagcc ctgtgaccaa gtctttcaac cggggcgagt gctga 645

<210> 84  
<211> 233  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-PD-L1 antibody light chain with signal peptide C

<400> 84

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala  
1 5 10 15

Thr Gln Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile  
35 40 45

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
50 55 60

Pro Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Ser  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser  
100 105 110

Asn Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr  
 115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu  
 130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro  
 145 150 155 160

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

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr  
 180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His  
 195 200 205

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230

<210> 85  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-PD-L1 antibody light chain with signal peptide LLC

<400> 85

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

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Pro Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val  
65 70 75 80

Pro Ser Ser Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110

Ser Tyr Ser Asn Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 86

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody light chain with signal peptide C

<400> 86

```
atgatgtcct ttgtctctct gtccttggtt ggcatcctat tccatgccac ccaggccgac      60
atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc      120
acttgccggg caagtcagag cattagcagc tatttaaatt ggtatcagca gaaaccaggg      180
aaagccccta agcctctgat ctatgtcgca tccagtttgc aaagtggggt cccatcatct      240
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa      300
gattttgcaa cttactactg tcaacagagt tacagtaacc ctatcacgtt cggccaaggg      360
accaggctgg aatcaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct      420
gatgagcagc ttaagtccgg aactgctagc gttgtgtgcc tgctgaataa cttctatccc      480
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggaaa ctcccaggag      540
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg      600
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg      660
agctcgcccc tcacaaagag cttcaacagg ggagagtgtt ag                          702
```

<210> 87

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized nucleic acid sequence encoding anti-PD-L1 antibody light chain with signal peptide LLC

<400> 87

```
atggacatga gagtgcctgc tcagctgctg ggactgctgc tgttgtgggt gagaggcgcc      60
agatgcgaca tccagatgac ccagtctcca tcctctctgt ccgcctctgt gggcgacaga      120
gtgaccatca cctgtcgggc ctctcagtcc atctcctcct acctgaactg gtatcagcag      180
aagcccggca aggcccctaa gcctctgata tatgtggcct ccagtctgca gtctggcgtg      240
ccctcttctt tctccggctc tggctctggc accgacttta ccctgacaat ctccagcctg      300
cagcctgagg acttcgccac ctactactgc cagcagtcct acagcaacct tatcaccttc      360
ggccagggca ccagactgga aatcaagaga accgtggccg ctcttccgt gttcatcttc      420
ccaccttccg acgagcagct gaagtccggc acagcttctg tcgtgtgcct gctgaacaac      480
```

ttctaccctc gggaagccaa ggtgcagtgg aaggtggaca atgctctgca gtccggcaac 540  
 tcccaagagt ccgtgaccga gcaggactcc aaggactcta cctacagcct gtcctccaca 600  
 ctgaccctgt ccaaggccga ctacgagaag cacaaggtgt acgcctgcga agtgacccat 660  
 cagggcctgt ctagccctgt gaccaagtct ttcaaccggg gcgagtgtg a 711

<210> 88  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Signal peptide C

<400> 88

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala  
 1 5 10 15

Thr Gln Ala

<210> 89  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Signal peptide LLC

<400> 89

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

Leu Arg Gly Ala Arg Cys  
 20

<210> 90  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Signal peptide LHC

<400> 90

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Ala His Ser

<210> 91

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence encoding signal peptide C

<400> 91

atgatgtcct ttgtctctct gctcctggtt ggcatacctat tccatgccac ccaggcc 57

<210> 92

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence encoding signal peptide LLC

<400> 92

atggacatga gagtgcctgc tcagctgctg ggactgctgc tgttgtggtt gagaggcgcc 60

agatgc 66

<210> 93

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence encoding signal peptide LHC

<400> 93

atggactgga cttggagaat cctgttcctg gtggccgctg ctaccggcgc tcattct 57

<210> 94

<211> 118

<212> PRT

<213> Homo sapiens

<400> 94

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  
 115

<210> 95  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 95

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  
100 105

<210> 96  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 96

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> 97  
<211> 214  
<212> PRT  
<213> Homo sapiens

<400> 97

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> 98  
<211> 447  
<212> PRT  
<213> Homo sapiens

<400> 98

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 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 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  
                                  435                      440                      445  
  
 <210> 99  
 <211> 329  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 99  
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1                      5                      10                      15  
  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
                                  20                      25                      30  
  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
                                  35                      40                      45  
  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
                                  50                      55                      60  
  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65                      70                      75                      80  
  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
                                  85                      90                      95  
  
 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
                                  100                      105                      110  
  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
                                  115                      120                      125

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 325

<210> 100

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 atezolizumab antibody heavy chain with L235A, L236A, and K323A variants

<400> 100

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 | Arg | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Ala | Ala | 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 | Ala | 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  
435 440 445

<210> 101

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 atezolizumab antibody heavy chain with L235A, L236A, L311A, and K323A variants

<400> 101

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

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

Lys Cys Ala 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  
435 440 445

<210> 102

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 atezolizumab antibody heavy chain with L235A, L236A, K323A, and H436Q variants

<400> 102

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

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

<210> 103

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 atezolizumab antibody heavy chain with L235A, L236A, L311A, K323A, and H436Q variants

<400> 103

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

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

Lys Cys Ala 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 Gln Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
435 440 445

<210> 104  
<211> 329  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-PD-L1 atezolizumab antibody heavy chain constant region with  
L235A, L236A, and K323A variants

<400> 104

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
325

<210> 105  
<211> 329  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> anti-PD-L1 atezolizumab antibody heavy chain constant region with  
L235A, L236A, L311A, and K323A variants

<400> 105

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 325

<210> 106  
 <211> 329  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> anti-PD-L1 atezolizumab antibody heavy chain constant region with  
 L235A, L236A, K323A, and H436Q variants

<400> 106

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

260

265

270

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 325

<210> 107

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD-L1 atezolizumab antibody heavy chain constant region with  
 L235A, L236A, L311A, K323A, and H436Q variants

<400> 107

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
325

<210> 108  
<211> 329  
<212> PRT  
<213> Homo sapiens

<400> 108

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

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

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

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

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

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

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

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

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

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

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

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