

SEQUENCE LISTING

<110> Numab Therapeutics AG
 <120> ANTIBODIES TARGETING CD137 AND METHODS OF USE THEREOF
 <130> 115159P877PC
 <150> EP18199334.6
 <151> 2018-10-09
 <150> EP19166283.2
 <151> 2019-03-29
 <160> 52
 <170> PatentIn version 3.5
 <210> 1
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Gly Phe Ser Phe Ser Ala Asn Tyr Tyr Pro Cys
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Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp Ala Asn Trp Thr
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Lys

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<400> 3

Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp Leu
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Ala Ser Gly Phe Ser Phe Ser Ala Asn Tyr Tyr
 1 5 10

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<400> 5

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

Gly

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<400> 6

Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp
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<400> 7

Ala Asn Tyr Tyr Pro Cys
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<400> 8

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

Lys

<210> 9
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<400> 9

Ser	Ala	Trp	Tyr	Ser	Gly	Trp	Gly	Gly	Asp	Leu
1				5					10	

<210> 10

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<400> 10

Gly	Phe	Ser	Phe	Ser	Ala	Asn	Tyr
1				5			

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<400> 11

Gly	Gly	Ser	Ser
1			

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<400> 12

Ala	Trp	Tyr	Ser	Gly	Trp	Gly	Gly	Asp
1				5				

<210> 13
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<400> 13

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 Ser Phe Ser Ala Asn
 20 25 30

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

Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp Ala Asn
 50 55 60

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

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

Tyr Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp Leu Trp
 100 105 110

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

<210> 14
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<400> 14

Glu Ser 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 Ser Phe Ser Ala Asn
 20 25 30

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

Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp Ala Asn
 50 55 60

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

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

Phe Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp Leu Trp
 100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 15

<211> 122

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<400> 15

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 Ser Phe Ser Ala Asn
 20 25 30

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

Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp Ala Asn
 50 55 60

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

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

Tyr Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp Leu Trp
 100 105 110

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

<210> 16

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<400> 16

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

<210> 17

<211> 7

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<213> Artificial Sequence

<220>

<223> artificial antibody-based sequence

<400> 17

Ser Ala Ser Thr Leu Ala Ser

1 5

<210> 18

<211> 11

<212> PRT

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<400> 18

Gln Ser Thr Tyr Tyr Gly Asn Asp Gly Asn Ala

1 5 10

<210> 19

<211> 8

<212> PRT

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<400> 19

Ala Ser Gln Ser Ile Ser Asn Arg

1 5

<210> 20

<211> 12

<212> PRT

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<400> 20

Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg

1 5 10

<210> 21
<211> 8
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<400> 21

Thr Tyr Tyr Gly Asn Asp Gly Asn
1 5

<210> 22
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<212> PRT
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<400> 22

Ser Gln Ser Ile Ser Asn Arg
1 5

<210> 23
<211> 3
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<400> 23

Ser Ala Ser
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<210> 24
<211> 8
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<223> artificial antibody-based sequence

<400> 24

Thr Tyr Tyr Gly Asn Asp Gly Asn
 1 5

<210> 25

<211> 110

<212> PRT

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<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 Gln Ala Ser Gln Ser Ile Ser Asn Arg
 20 25 30

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

Tyr Ser Ala Ser Thr Leu Ala 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 Ser Thr Tyr Tyr Gly Asn Asp
 85 90 95

Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
 100 105 110

<210> 26

<211> 110

<212> PRT

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<220>

<223> artificial antibody-based sequence

<400> 26

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

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

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

Tyr Ser Ala Ser Thr Leu Ala 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 Ser Thr Tyr Tyr Gly Asn Asp
 85 90 95

Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
 100 105 110

<210> 27

<211> 110

<212> PRT

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<223> artificial antibody-based sequence

<400> 27

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 Gln Ala Ser Gln Ser Ile Ser Asn Arg
 20 25 30

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

Tyr Ser Ala Ser Thr Leu Ala 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 Ser Thr Tyr Tyr Gly Asn Asp
 85 90 95

Gly Asn Ala Phe Gly Cys Gly Thr Lys Val Thr Val Leu Gly
 100 105 110

<210> 28

<211> 20

<212> PRT

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<220>

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<400> 28

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

Gly Gly Gly Ser
 20

<210> 29

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial antibody-based sequence

<400> 29

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 Gln Ala Ser Gln Ser Ile Ser Asn Arg
20 25 30

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

Tyr Ser Ala Ser Thr Leu Ala 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 Ser Thr Tyr Tyr Gly Asn Asp
85 90 95

Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
145 150 155 160

Ala Asn Tyr Tyr Pro Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp

180

185

190

Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 195 200 205

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 210 215 220

Val Tyr Tyr Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp
 225 230 235 240

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 30

<211> 252

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<400> 30

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

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

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

Tyr Ser Ala Ser Thr Leu Ala 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 Ser Thr Tyr Tyr Gly Asn Asp
85 90 95

Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Ser Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
145 150 155 160

Ala Asn Tyr Tyr Pro Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp
180 185 190

Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Phe Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp
225 230 235 240

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 31
<211> 252
<212> PRT
<213> Artificial Sequence

<220>

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<400> 31

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	Gln	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Arg
			20				25						30		

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

Tyr	Ser	Ala	Ser	Thr	Leu	Ala	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	Ser	Thr	Tyr	Tyr	Gly	Asn	Asp
				85					90					95	

Gly	Asn	Ala	Phe	Gly	Cys	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Gly	Gly
		100						105					110		

Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		115					120					125			

Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro
	130					135						140			

Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser
145					150					155					160

Ala	Asn	Tyr	Tyr	Pro	Cys	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Cys	Leu
				165					170					175	

17
Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser Asp Ile Thr Tyr Asp
180 185 190

Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Ser Ala Trp Tyr Ser Gly Trp Gly Gly Asp
225 230 235 240

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 32
<211> 255
<212> PRT
<213> Homo sapiens

<400> 32

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
35 40 45

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

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
 100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
 115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
 130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
 145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
 165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
 180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
 195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
 210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
 225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 245 250 255

<210> 33

<211> 11

<212> PRT

<213> Homo sapiens

<400> 33

19
Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
1 5 10

<210> 34
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<213> Homo sapiens

<400> 34

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
1 5 10

<210> 35
<211> 11
<212> PRT
<213> Homo sapiens

<400> 35

Phe Gly Gly Gly Thr Gln Leu Ile Ile Leu Gly
1 5 10

<210> 36
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<213> Homo sapiens

<400> 36

Phe Gly Glu Gly Thr Glu Leu Thr Val Leu Gly
1 5 10

<210> 37
<211> 11
<212> PRT
<213> Homo sapiens

<400> 37

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

<210> 38

20

<211> 11
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<213> Homo sapiens

<400> 38

Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
1 5 10

<210> 39
<211> 11
<212> PRT
<213> Homo sapiens

<400> 39

Phe Gly Gly Gly Thr Gln Leu Thr Ala Leu Gly
1 5 10

<210> 40
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<400> 40

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

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

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

Tyr Arg Ala Phe Ile Leu Ala 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 Ser Asn Phe Tyr Ser Asp Ser
 85 90 95

Thr Thr Ile Gly Pro Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
 100 105 110

Leu Gly Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 115 120 125

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 130 135 140

Gly Phe Ser Phe Ser Ala Asn Tyr Tyr Pro Cys Trp Val Arg Gln Ala
 145 150 155 160

Pro Gly Lys Gly Leu Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser
 165 170 175

Asp Ile Thr Tyr Asp Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser
 180 185 190

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
 195 200 205

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ala Trp Tyr Ser
 210 215 220

Gly Trp Gly Gly Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 260 265 270

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser
 275 280 285

Ile Ser Asn Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 290 295 300

Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser
 305 310 315 320

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 325 330 335

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr
 340 345 350

Tyr Gly Asn Asp Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
 355 360 365

Leu Gly Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 385 390 395 400

Gly Phe Ser Phe Asn Ser Asp Tyr Trp Ile Tyr Trp Val Arg Gln Ala
 405 410 415

Pro Gly Lys Gly Leu Glu Trp Ile Ala Ser Ile Tyr Gly Gly Ser Ser
 420 425 430

Gly Asn Thr Gln Tyr Ala Ser Trp Ala Gln Gly Arg Phe Thr Ile Ser
 435 440 445

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
 450 455 460

Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Tyr Val Asp Tyr
465 470 475 480

Gly Gly Ala Thr Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met Thr Gln
500 505 510

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
515 520 525

Cys Gln Ser Ser Glu Ser Val Tyr Ser Asn Asn Gln Leu Ser Trp Tyr
530 535 540

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
545 550 555 560

Asp Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
565 570 575

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
580 585 590

Thr Tyr Tyr Cys Ala Gly Gly Phe Ser Ser Ser Ser Asp Thr Ala Phe
595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Gly Ser Gly
610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
625 630 635 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
645 650 655

Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Asn Ala Met

660

665

670

Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Ile
 675 680 685

Ile Ser Val Gly Gly Phe Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg
 690 695 700

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met
 705 710 715 720

Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Asp
 725 730 735

Arg His Gly Gly Asp Ser Ser Gly Ala Phe Tyr Leu Trp Gly Gln Gly
 740 745 750

Thr Leu Val Thr Val Ser Ser
 755

<210> 41

<211> 759

<212> PRT

<213> Artificial Sequence

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<400> 41

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

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

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

Tyr Arg Ala Phe Ile Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60 25

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 Ser Asn Phe Tyr Ser Asp Ser
85 90 95

Thr Thr Ile Gly Pro Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
100 105 110

Leu Gly Gly Gly Gly Gly Ser Glu Ser Gln Leu Val Glu Ser Gly Gly
115 120 125

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
130 135 140

Gly Phe Ser Phe Ser Ala Asn Tyr Tyr Pro Cys Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Lys Gly Leu Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser
165 170 175

Asp Ile Thr Tyr Asp Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser
180 185 190

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
195 200 205

Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Trp Tyr Ser
210 215 220

Gly Trp Gly Gly Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

245 250 26 255
 Gly Gly Gly Gly Ser Phe Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
 260 265 270
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser
 275 280 285
 Ile Ser Asn Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
 290 295 300
 Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser
 305 310 315 320
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 325 330 335
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr
 340 345 350
 Tyr Gly Asn Asp Gly Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
 355 360 365
 Leu Gly Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 370 375 380
 Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 385 390 395 400
 Gly Phe Ser Phe Asn Ser Asp Tyr Trp Ile Tyr Trp Val Arg Gln Ala
 405 410 415
 Pro Gly Lys Gly Leu Glu Trp Ile Ala Ser Ile Tyr Gly Gly Ser Ser
 420 425 430
 Gly Asn Thr Gln Tyr Ala Ser Trp Ala Gln Gly Arg Phe Thr Ile Ser
 435 440 445

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
 450 455 460

Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Tyr Val Asp Tyr
 465 470 475 480

Gly Gly Ala Thr Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met Thr Gln
 500 505 510

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 515 520 525

Cys Gln Ser Ser Glu Ser Val Tyr Ser Asn Asn Gln Leu Ser Trp Tyr
 530 535 540

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 545 550 555 560

Asp Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 565 570 575

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 580 585 590

Thr Tyr Tyr Cys Ala Gly Gly Phe Ser Ser Ser Ser Asp Thr Ala Phe
 595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Gly Ser Gly
 610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
 625 630 635 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 645 650 655

Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Asn Ala Met
 660 665 670

Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Ile
 675 680 685

Ile Ser Val Gly Gly Phe Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg
 690 695 700

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met
 705 710 715 720

Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Asp
 725 730 735

Arg His Gly Gly Asp Ser Ser Gly Ala Phe Tyr Leu Trp Gly Gln Gly
 740 745 750

Thr Leu Val Thr Val Ser Ser
 755

<210> 42
 <211> 759
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial antibody-based sequence

<400> 42

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

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

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

Tyr Arg Ala Phe Ile Leu Ala 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 Ser Asn Phe Tyr Ser Asp Ser
 85 90 95

Thr Thr Ile Gly Pro Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
 100 105 110

Leu Gly Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 115 120 125

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 130 135 140

Gly Phe Ser Phe Ser Ala Asn Tyr Tyr Pro Cys Trp Val Arg Gln Ala
 145 150 155 160

Pro Gly Lys Cys Leu Glu Trp Ile Gly Cys Ile Tyr Gly Gly Ser Ser
 165 170 175

Asp Ile Thr Tyr Asp Ala Asn Trp Thr Lys Gly Arg Phe Thr Ile Ser
 180 185 190

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
 195 200 205

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ala Trp Tyr Ser
 210 215 220

Gly Trp Gly Gly Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 260 265 270

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser
 275 280 285

Ile Ser Asn Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 290 295 300

Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser
 305 310 315 320

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 325 330 335

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr
 340 345 350

Tyr Gly Asn Asp Gly Asn Ala Phe Gly Cys Gly Thr Lys Val Thr Val
 355 360 365

Leu Gly Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 385 390 395 400

Gly Phe Ser Phe Asn Ser Asp Tyr Trp Ile Tyr Trp Val Arg Gln Ala
 405 410 415

Pro Gly Lys Gly Leu Glu Trp Ile Ala Ser Ile Tyr Gly Gly Ser Ser
 420 425 430

Gly Asn Thr Gln Tyr Ala Ser Trp Ala Gln Gly Arg Phe Thr Ile Ser
 435 440 445

Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
 450 455 460

Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Tyr Val Asp Tyr
 465 470 475 480

Gly Gly Ala Thr Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met Thr Gln
 500 505 510

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 515 520 525

Cys Gln Ser Ser Glu Ser Val Tyr Ser Asn Asn Gln Leu Ser Trp Tyr
 530 535 540

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 545 550 555 560

Asp Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 565 570 575

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 580 585 590

Thr Tyr Tyr Cys Ala Gly Gly Phe Ser Ser Ser Ser Asp Thr Ala Phe
 595 600 605

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

610

615

620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
 625 630 635 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 645 650 655

Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Asn Ala Met
 660 665 670

Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Ile
 675 680 685

Ile Ser Val Gly Gly Phe Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg
 690 695 700

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met
 705 710 715 720

Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Asp
 725 730 735

Arg His Gly Gly Asp Ser Ser Gly Ala Phe Tyr Leu Trp Gly Gln Gly
 740 745 750

Thr Leu Val Thr Val Ser Ser
 755

<210> 43

<211> 758

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial antibody-based sequence

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser 33 Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Arg Ala Phe Ile Leu Ala 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 Ser Asn Phe Tyr Ser Asp Ser
85 90 95

Thr Thr Ile Gly Pro Asn Ala Phe Gly Thr Gly Thr Lys Val Thr Val
100 105 110

Leu Gly Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro
115 120 125

Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Lys Val Ser
130 135 140

Gly Phe Ser Phe Ser Asn Ser Tyr Trp Ile Cys Trp Ile Arg Gln Pro
145 150 155 160

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

Asp Ser Thr Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Val Thr Ile Ser
180 185 190

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

195

200

205

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg His Pro Ser Asp Ala
 210 215 220

Val Tyr Gly Tyr Ala Asn Asn Leu Trp Gly Gln Gly Thr Leu Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 245 250 255

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
 260 265 270

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
 275 280 285

Ser Gln Ser Ile Asn Asn Val Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 290 295 300

Lys Ala Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly
 305 310 315 320

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 325 330 335

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 340 345 350

Ser Ser Tyr Gly Asn Tyr Gly Asp Phe Gly Thr Gly Thr Lys Val Thr
 355 360 365

Val Leu Gly Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
 370 375 380

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Lys Val
 385 390 395 400

Ser Gly Phe Ser Phe Asn Ser Asp Tyr Trp Ile Tyr Trp Ile Arg Gln
 405 410 415

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile Tyr Gly Gly Ser
 420 425 430

Ser Gly Asn Thr Gln Tyr Ala Ser Trp Ala Gln Gly Arg Val Thr Ile
 435 440 445

Ser Val Asp Ser Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
 450 455 460

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Val Asp
 465 470 475 480

Tyr Gly Gly Ala Thr Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val
 485 490 495

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Val Met Thr
 500 505 510

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 515 520 525

Thr Cys Gln Ala Ser Gln Ile Ile Ser Ser Arg Ser Ala Trp Tyr Gln
 530 535 540

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gln Ala Ser Lys
 545 550 555 560

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 565 570 575

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 580 585 590

Tyr Tyr Cys Gln Cys Thr Tyr Ile Asp Ser Asn Phe Gly Ala Phe Gly
 595 600 605

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 625 630 635 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 645 650 655

Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Ser Tyr Trp Ile
 660 665 670

Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Cys
 675 680 685

Val Phe Thr Gly Asp Gly Thr Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
 690 695 700

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
 705 710 715 720

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
 725 730 735

Pro Val Ser Val Tyr Tyr Tyr Gly Met Asp Leu Trp Gly Gln Gly Thr
 740 745 750

Leu Val Thr Val Ser Ser
 755

<210> 44

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial antibody-based sequence

<400> 44

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 Gln Ala Ser Gln Ser Ile Asn Asp Tyr
 20 25 30

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

Tyr Lys Ala Ser Thr Leu Ala 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 Gly Tyr Ile Ile Thr Asp
 85 90 95

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

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
 115 120 125

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Lys Val Ser Gly Phe Ser
 130 135 140

Phe Ser Asn Ser Tyr Trp Ile Cys Trp Ile Arg Gln Pro Pro Gly Lys
 145 150 155 160

Gly Leu Glu Trp Ile Gly Cys Thr Phe Val Gly Ser Ser Asp Ser Thr
 165 170 175

Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Val Thr Ile Ser Val Asp Ser
 180 185 190

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
 195 200 205

Thr Ala Val Tyr Tyr Cys Ala Arg His Pro Ser Asp Ala Val Tyr Gly
 210 215 220

Tyr Ala Asn Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 245 250 255

Gly Gly Gly Ser Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 260 265 270

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile
 275 280 285

Asn Asn Val Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 290 295 300

Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg
 305 310 315 320

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
 325 330 335

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Ser Tyr Gly
 340 345 350

Asn Tyr Gly Asp Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gly
 355 360 365

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
370 375 380 39

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Lys Val Ser Gly Phe Ser
385 390 395 400

Phe Ser Ser Gly Tyr Asp Met Cys Trp Ile Arg Gln Pro Pro Gly Lys
405 410 415

Gly Leu Glu Trp Ile Gly Cys Val Val Ala Gly Ser Val Asp Ile Thr
420 425 430

Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Val Thr Ile Ser Val Asp Ser
435 440 445

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Asp Ala Tyr Ser Asp Ala Phe
465 470 475 480

Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
485 490

<210> 45

<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial construct comprising CD137 extracellular domain(s)

<400> 45

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

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

Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser
 35 40 45

Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys
 50 55 60

Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala
 65 70 75 80

Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser
 85 90 95

Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly
 100 105 110

Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile
 115 120 125

Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val
 130 135 140

Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp
 145 150 155 160

Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu
 165 170 175

Pro Gly His Ser Pro Gln Leu Glu Val Leu Phe Gln Gly Pro Leu Glu
 180 185 190

Val Leu Phe Gln Gly Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 195 200 205

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 210 215 220

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 225 230 235 240

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 245 250 255

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 260 265 270

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 275 280 285

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 290 295 300

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 305 310 315 320

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 325 330 335

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 340 345 350

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 355 360 365

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 385 390 395 400

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 405 410 415

Lys Ser Leu Ser Leu Ser Pro Gly Lys

420

425

<210> 46
 <211> 277
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial construct comprising CD137 extracellular domain(s)

<400> 46

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

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

Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Leu Glu Val Leu Phe Gln
 35 40 45

Gly Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 50 55 60

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 85 90 95

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 100 105 110

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 115 120 125

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 130 135 140

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala
 145 150 155 160

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 165 170 175

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 195 200 205

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 210 215 220

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 225 230 235 240

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 245 250 255

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 260 265 270

Leu Ser Pro Gly Lys
 275

<210> 47
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial construct comprising CD137 extracellular domain(s)

<400> 47

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

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

Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser
 35 40 45

Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys
 50 55 60

Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala
 65 70 75 80

Glu Cys Leu Glu Val Leu Phe Gln Gly Pro Asp Lys Thr His Thr Cys
 85 90 95

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 100 105 110

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 115 120 125

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 130 135 140

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 145 150 155 160

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 165 170 175

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 180 185 190

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
 195 200 205

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
210 215 220 45

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
225 230 235 240

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
245 250 255

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
260 265 270

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
275 280 285

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
290 295 300

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
305 310 315

<210> 48

<211> 349

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial construct comprising CD137 extracellular domain(s)

<400> 48

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

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

Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser
35 40 45

Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys
 50 55 60

Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala
 65 70 75 80

Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser
 85 90 95

Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly
 100 105 110

Cys Lys Leu Glu Val Leu Phe Gln Gly Pro Asp Lys Thr His Thr Cys
 115 120 125

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 130 135 140

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 145 150 155 160

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 165 170 175

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 180 185 190

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 195 200 205

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 210 215 220

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
 225 230 235 240

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
245 250 255 47

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
260 265 270

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
275 280 285

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
290 295 300

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
305 310 315 320

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
325 330 335

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345

<210> 49

<211> 368

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial construct comprising CD137 extracellular domain(s)

<400> 49

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

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

Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg
35 40 45

Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly
 50 55 60

Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys
 65 70 75 80

Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly
 85 90 95

Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys
 100 105 110

Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp
 115 120 125

Val Val Cys Gly Pro Leu Glu Val Leu Phe Gln Gly Pro Asp Lys Thr
 130 135 140

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 145 150 155 160

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 180 185 190

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 195 200 205

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 225 230 235 240

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
245 250 255

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
260 265 270

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
275 280 285

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
290 295 300

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
305 310 315 320

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
325 330 335

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
340 345 350

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
355 360 365

<210> 50

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial construct comprising CD137 extracellular domain(s)

<400> 50

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

Val His Ser Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys
20 25 30

50

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

Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly
50 55 60

Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu
65 70 75 80

Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro Leu Glu Val
85 90 95

Leu Phe Gln Gly Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
 325

<210> 51
 <211> 296
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial construct comprising CD137 extracellular domain(s)

<400> 51

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

Val His Ser Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly
 20 25 30

Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu
 35 40 45

Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro Leu Glu Val
 50 55 60

Leu Phe Gln Gly Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 65 70 75 80

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 85 90 95

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 100 105 110

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 115 120 125

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 130 135 140

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 145 150 155 160

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 165 170 175

Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 180 185 190

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 195 200 205

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 210 215 220

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 225 230 235 240

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
260 265 270

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
275 280 285

Ser Leu Ser Leu Ser Pro Gly Lys
290 295

<210> 52

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial construct comprising CD137 extracellular domain(s)

<400> 52

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

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

Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg
35 40 45

Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly
50 55 60

Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys
65 70 75 80

Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Leu Glu Val Leu Phe
85 90 95

Gln Gly Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 100 105 110

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

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

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

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

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 180 185 190

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

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 210 215 220

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 260 265 270

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300 55

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

Ser Leu Ser Pro Gly Lys
325