

357707_1.txt
SEQUENCE LISTING

<110> Crescendo Biologics Limited

<120> Single domain antibodies that bind to CD137

<130> P34656W01

<150> GB1718734.5
<151> 2017-11-13

<150> GB1718735.2
<151> 2017-11-13

<150> GB1808589.4
<151> 2018-05-24

<160> 902

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Ser His Trp Met Thr
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His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu
1 5 10 15

Gly

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<223> VH that binds CD137

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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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
 50 55 60

Glu Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Gly

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Gly	Gly	Asp	Gly	Tyr	Ser	Asp	Ser	His	Tyr	Gly	Val	Asp	Val
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Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

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

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Tyr Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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Ser Tyr Trp Met Thr
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<400> 10

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

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<400> 11

Gly Gly Leu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
1 5 10

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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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Leu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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Asn Tyr Trp Met Thr
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Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Glu
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Gly

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Gly	Gly	Leu	Gly	Tyr	Gly	Asp	Ser	His	Tyr	Gly	Met	Asp	Val
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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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Leu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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Asn Tyr Trp Met Ile
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<210> 18

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Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 19

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<400> 20

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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Gly Ser His His Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<210> 22
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<400> 22

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 23
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<400> 23

Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
1 5 10

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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 Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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<400> 25

Ser Tyr Trp Met Leu

1 5

<210> 26

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<400> 26

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 27

<211> 14

<212> PRT

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<223> CDR3 OF SEQ ID NO: 28

<400> 27

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Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Thr Asp Val
1 5 10

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<400> 28

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 Gly Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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 <222> (1)..(5)
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Ser Tyr Trp Met Phe
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Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

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<400> 31

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

<210> 32

<211> 123

<212> PRT

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<223> VH that binds CD137

<400> 32

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 Gly Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

Glu 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 Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<400> 33

Asn Tyr Trp Met Thr
1 5

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<223> CDR2 OF SEQ ID NO: 36

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Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 35
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Gly Gly Leu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 36
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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 Asn Tyr
 20 25 30

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

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

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

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

357707_1.txt

Ala Arg Gly Gly Leu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 37
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<400> 37

Asp Tyr Trp Met Asn
1 5

<210> 38
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<400> 38

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

Gly

<210> 39

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<211> 14
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<400> 39

Gly Gly Ala Gly Tyr Ser Met Ser His Tyr Gly Met Asp Val
1 5 10

<210> 40
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<223> VH that binds CD137

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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 Tyr
20 25 30

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

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

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

357707_1.txt

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

Ala Arg Gly Gly Ala Gly Tyr Ser Met Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 41
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Asp Tyr Trp Met Asn
1 5

<210> 42
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<400> 42

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

Gly

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 <223> CDR3 OF SEQ ID NO: 44

<400> 43

Gly Gly Ala Gly Tyr Ser Met Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 44
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 <223> VH that binds to CD137

<400> 44

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 Glu Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

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

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

357707_1.txt

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Thr 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 Gly Gly Ala Gly Tyr Ser Met Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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Ser Tyr Trp Met Leu
1 5

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<400> 46

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 47
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<400> 47

Gly Gly Asp Gly Tyr Ser Asn Ser His Phe Gly Thr Asp Val
 1 5 10

<210> 48
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<400> 48

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 Gly Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

357707_1.txt

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Phe Gly Thr Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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<400> 49

Ser Tyr Trp Met Phe
 1 5

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<400> 50

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Glu
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Gly

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

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

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

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

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

Glu 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 Ile Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Asn Tyr Trp Met Asn
 1 5

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357707_1.txt

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<400> 54

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

Gly

<210> 55
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 56

<400> 55

Gly	Gly	Glu	Gly	Tyr	Ser	Thr	Ser	His	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 56
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 56

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

357707_1.txt

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

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 57
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 60

<400> 57

Thr Tyr Trp Met Leu
1 5

<210> 58
<211> 17

357707_1.txt

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 60

<400> 58

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 59
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 60

<400> 59

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Thr Asp Val
1 5 10

<210> 60
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH that binds to CD137

<400> 60

357707_1.txt

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 Gly Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 61
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 64

<400> 61

Asn Tyr Trp Met Met
1 5

<210> 62
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 64

<400> 62

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Phe	Val	Asp	Ser	Val	Glu
1				5					10					15	

Gly

<210> 63
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 64

<400> 63

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

<210> 64
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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357707_1.txt

<222> (1)..(123)

<223> VH that binds to CD137

<400> 64

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 Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Ser Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 65

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 68

<400> 65

Ser Tyr Trp Met Asn
 1 5

<210> 66

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 68

<400> 66

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

Gly

<210> 67

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 68

<400> 67

Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
 1 5 10

<210> 68

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds to CD137

<400> 68

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 69

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 72

<400> 69

Thr His Trp Met Asn
 1 5

<210> 70
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR 2 OF SEQ ID NO: 72

<400> 70

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 71
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 72

<400> 71

Gly Gly Val Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
 1 5 10

357707_1.txt

<210> 72
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 72

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 Thr His
 20 25 30

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

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

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

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

Ala Arg Gly Gly Val Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
 100 105 110

Trp Gly Leu Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 73
 <211> 5
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 76

<400> 73

Ser Tyr Trp Met Ile

1 5

<210> 74

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 76

<400> 74

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 75

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 76

<400> 75

357707_1.txt

Gly Gly Asp Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
1 5 10

<210> 76
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH that binds to CD137

<400> 76

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

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

357707_1.txt

<210> 77
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 80

<400> 77

Ser	Tyr	Trp	Met	Asn
1				5

<210> 78
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 80

<400> 78

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Gln
1				5					10					15	

Gly

<210> 79
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 80

<400> 79

Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
1 5 10

<210> 80

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds CD137

<400> 80

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

357707_1.txt

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 81
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 84

<400> 81

Ser Tyr Trp Met Phe
1 5

<210> 82
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 84

<400> 82

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

Gly

<210> 83
<211> 14
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 84

<400> 83

Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
 1 5 10

<210> 84
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds CD137

<400> 84

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 Gly Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

Glu 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 Ile Tyr Tyr Cys
 85 90 95

357707_1.txt

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 85
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 88

<400> 85

Asn Tyr Trp Met Asn
1 5

<210> 86
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 88

<400> 86

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

Gly

<210> 87

357707_1.txt

<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 88

<400> 87

Gly Gly Glu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
1 5 10

<210> 88
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH that binds to CD137

<400> 88

Gln 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 Asn Tyr
20 25 30

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

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

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

357707_1.txt

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

Ala Arg Gly Gly Glu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

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

<210> 89
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 92

<400> 89

Ser Tyr Trp Met Asn
1 5

<210> 90
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 92

<400> 90

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 91
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 92

<400> 91

Gly Gly Glu Gly Tyr Gly Asp Asp His Tyr Gly Met Asp Val
 1 5 10

<210> 92
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 92

Gln 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 Ser Tyr
 20 25 30

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

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

357707_1.txt

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 Thr Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Asp Asp His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 93
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 96

<400> 93

Ser Tyr Trp Met Ser
1 5

<210> 94
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 96

<400> 94

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 95
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 96

<400> 95

Gly Gly Glu Gly Tyr Gly Asp Tyr His Tyr Gly Leu Asp Val
 1 5 10

<210> 96
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 96

Gln 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 Ser Tyr
 20 25 30

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

357707_1.txt

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Asp Tyr His Tyr Gly Leu Asp Val
100 105 110

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

<210> 97
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 100

<400> 97

Ser Tyr Trp Met Asn
1 5

<210> 98
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 100

357707_1.txt

<400> 98

Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 99

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 100

<400> 99

Gly	Gly	Asp	Ser	Tyr	Gly	Tyr	Arg	Asp	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 100

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds to CD137

<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	Ser	Tyr
			20					25					30		

357707_1.txt

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

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

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

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

Ala Arg Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 101
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 104

<400> 101

Thr His Trp Met Asn
 1 5

<210> 102
 <211> 17
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 104

<400> 102

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Glu
1				5					10					15	

Gly

<210> 103
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 104

<400> 103

Gly	Gly	Val	Gly	Tyr	Gly	Asp	Ser	His	Phe	Gly	Met	Asp	Val
1				5					10				

<210> 104
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 104

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

357707_1.txt

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

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

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

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

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

Ala Arg Gly Gly Val Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
100 105 110

Trp Gly Leu Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 105
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 108

<400> 105

Ser Tyr Trp Met Leu
1 5

<210> 106
<211> 17

357707_1.txt

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 108

<400> 106

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 107
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 108

<400> 107

Gly Gly Glu Gly Tyr Ser Asp Ser His His Gly Thr Asp Val
1 5 10

<210> 108
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH that binds to CD137

<400> 108

357707_1.txt

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 Gly Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His His Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 109
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 112

<400> 109

Asn Tyr Trp Met Asn
1 5

357707_1.txt

<210> 110
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 112

<400> 110

Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 111
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 112

<400> 111

Gly	Gly	Asp	Asn	Tyr	Ala	Tyr	Arg	Asp	Phe	Gly	Met	Asp	Val
1				5					10				

<210> 112
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

357707_1.txt

<222> (1)..(123)

<223> VH that binds to CD137

<400> 112

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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Asn Tyr Ala Tyr Arg Asp Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 113

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 116

<400> 113

Asn Tyr Trp Met Phe
 1 5

<210> 114

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 116

<400> 114

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

Gly

<210> 115

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 116

<400> 115

Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
 1 5 10

<210> 116

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds to CD137

<400> 116

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 Gly Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

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

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

Glu 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 Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 117

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 120

<400> 117

Ser Tyr Trp Met Asn
 1 5

<210> 118
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 120

<400> 118

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 119
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 120

<400> 119

Gly Gly Glu Glu Tyr Gly Ser Ser His Tyr Gly Met Asp Val
 1 5 10

357707_1.txt

<210> 120
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 120

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 Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Glu Tyr Gly Ser Ser His Tyr Gly Met Asp Val
 100 105 110

Trp Gly Leu Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 121
 <211> 5
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 124

<400> 121

Ser Tyr Trp Met Asn

1 5

<210> 122

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 124

<400> 122

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 123

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 124

<400> 123

357707_1.txt

Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
1 5 10

<210> 124
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH that binds to CD137

<400> 124

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

357707_1.txt

<210> 125
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 128

<400> 125

Ser Tyr Trp Met Asn
 1 5

<210> 126
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 128

<400> 126

Asn Ile Asn Gln Asn Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 127
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 128

<400> 127

Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
1 5 10

<210> 128

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds to CD137

<400> 128

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 129
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 132

<400> 129

Asn Tyr Trp Met Thr
1 5

<210> 130
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 132

<400> 130

Asn Ile Asn Gln Asp Glu Ser Glu Glu Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 131
<211> 14
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(131)

<223> CDR3 OF SEQ ID NO: 132

<400> 131

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

<210> 132

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH that binds to CD137

<400> 132

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

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

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

Ala Asn Ile Asn Gln Asp Glu Ser Glu Glu Tyr Tyr Val Asp Ser Val
50 55 60

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

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

357707_1.txt

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 133
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 136

<400> 133

Asn Tyr Trp Met Asn
1 5

<210> 134
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 136

<400> 134

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

Gly

<210> 135

357707_1.txt

<211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 136

<400> 135

Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 136
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 136

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

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

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

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

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

357707_1.txt

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

Ala Arg Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 137
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 140

<400> 137

Asn Tyr Trp Met Asn
1 5

<210> 138
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 140

<400> 138

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 139
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 140

<400> 139

Gly Gly Glu Gly Tyr Gly Glu Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 140
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 140

Gln 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 Asn Tyr
 20 25 30

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

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

357707_1.txt

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Glu Ser His Tyr Gly Met Asp Val
100 105 110

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

<210> 141
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 144

<400> 141

Thr Tyr Trp Met Asn
1 5

<210> 142
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 144

<400> 142

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 143
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 144

<400> 143

Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
 1 5 10

<210> 144
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH that binds to CD137

<400> 144

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 Thr Tyr
 20 25 30

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

357707_1.txt

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

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

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

Ala Arg Gly Gly Asp Ser Tyr Gly Tyr Arg Asp Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 145
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 148

<400> 145

Tyr Tyr Trp Met Ile
 1 5

<210> 146
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 148

357707_1.txt

<400> 146

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 147

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 148

<400> 147

Gly Gly Asp Gly Tyr Ser Asn Ser His Phe Gly Met Asp Val
1 5 10

<210> 148

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 148

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 Tyr Tyr
20 25 30

357707_1.txt

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Phe Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 149
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(4)
 <223> CDR1 OF SEQ ID NO: 152

<400> 149

Asn Tyr Trp Met Ile
 1 5

<210> 150
 <211> 17
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 152

<400> 150

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1			5					10						15	

Gly

<210> 151
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 152

<400> 151

Gly	Gly	Glu	Gly	Tyr	Ser	Asp	Ser	His	Tyr	Gly	Thr	Asp	Val
1			5					10					

<210> 152
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 152

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

357707_1.txt

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

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 153
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 156

<400> 153

Asn Tyr Trp Met Asn
1 5

<210> 154
<211> 17

357707_1.txt

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 156

<400> 154

Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 155
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 156

<400> 155

Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
1 5 10

<210> 156
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 156

357707_1.txt

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 Asn Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 157
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 160

<400> 157

Asn Tyr Trp Met Phe
1 5

357707_1.txt

<210> 158
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 160

<400> 158

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

Gly

<210> 159
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 160

<400> 159

Gly	Gly	Glu	Gly	Tyr	Ser	Asp	Ser	His	Tyr	Gly	Thr	Asp	Val
1				5					10				

<210> 160
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

357707_1.txt

<222> (1)..(123)

<223> VH binding to CD137

<400> 160

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 Gly Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 161

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 164

<400> 161

Asn Tyr Trp Met Phe
 1 5

<210> 162

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 164

<400> 162

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

Gly

<210> 163

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 164

<400> 163

Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
 1 5 10

<210> 164

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 164

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 Gly Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

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

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

Glu 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 Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Tyr Gly Thr Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 165

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 168

<400> 165

Asn Tyr Trp Met Asn
 1 5

<210> 166
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 168

<400> 166

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 167
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 168

<400> 167

Gly Gly Glu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 1 5 10

357707_1.txt

<210> 168
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 168

Gln 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 Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 100 105 110

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

<210> 169
 <211> 5
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 172

<400> 169

Asn Tyr Trp Met Ile

1 5

<210> 170

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 172

<400> 170

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 171

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 172

<400> 171

357707_1.txt

Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
1 5 10

<210> 172
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 172

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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

357707_1.txt

<210> 173
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 176

<400> 173

Asp Tyr Trp Met Ile
1 5

<210> 174
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 176

<400> 174

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 175
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 176

<400> 175

Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
1 5 10

<210> 176

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 176

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 Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 177
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 180

<400> 177

Lys Tyr Trp Met Ile
 1 5

<210> 178
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 180

<400> 178

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 179
 <211> 14
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 180

<400> 179

Gly Gly Asp Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 180
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 180

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 Lys Tyr
 20 25 30

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

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

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

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

357707_1.txt

Ala Arg Gly Gly Asp Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

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

<210> 181
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 184

<400> 181

Asn Tyr Trp Met Ser
1 5

<210> 182
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 184

<400> 182

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 183

357707_1.txt

<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 184

<400> 183

Gly Gly Glu Glu Tyr Ser Ser Ser His Tyr Gly Met Asp Val
1 5 10

<210> 184
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 184

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 Asn Tyr
20 25 30

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

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

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

357707_1.txt

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

Ala Arg Gly Gly Glu Glu Tyr Ser Ser Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 185
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 188

<400> 185

Asn Tyr Trp Met Asn
1 5

<210> 186
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 188

<400> 186

Asn Ile Lys Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 187
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 188

<400> 187

Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 188
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 188

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 Ile Ala Ser Gly Phe Ser Phe Ser Asn Tyr
 20 25 30

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

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

357707_1.txt

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Thr Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser
115 120

<210> 189
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 192

<400> 189

Ser Tyr Trp Met Ser
1 5

<210> 190
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 192

<400> 190

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 191
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 192

<400> 191

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 192
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 192

Gln 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 Ser Tyr
 20 25 30

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

357707_1.txt

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 193
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 196

<400> 193

Ser Tyr Trp Met Leu
1 5

<210> 194
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 196

357707_1.txt

<400> 194

Asn	Val	Asn	Gln	Asp	Gly	Ser	Glu	Asn	Tyr	Tyr	Val	Asp	Ser	Val	Glu
1				5				10						15	

Gly

<210> 195

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 196

<400> 195

Gly	Gly	Glu	Asp	Tyr	Gly	Asn	Ser	His	Phe	Gly	Met	Asp	Val
1				5					10				

<210> 196

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 196

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	Gly	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		

357707_1.txt

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

Ala Asn Val Asn Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Asp Tyr Gly Asn Ser His Phe Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 197
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 200

<400> 197

Asn Tyr Trp Met Ile
 1 5

<210> 198
 <211> 17
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 200

<400> 198

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1			5					10						15	

Gly

<210> 199
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 200

<400> 199

Gly	Gly	Asp	Gly	Tyr	Ser	Asn	Ser	His	Tyr	Gly	Met	Asp	Val
1			5					10					

<210> 200
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 200

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

357707_1.txt

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

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 201
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 204

<400> 201

Asn Tyr Trp Met Ile
 1 5

<210> 202
 <211> 17

<212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 204

<400> 202

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 203
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 204

<400> 203

Gly	Gly	Asp	Gly	Tyr	Ser	Asn	Ser	His	Tyr	Gly	Met	Asp	Val
1			5					10					

<210> 204
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 204

357707_1.txt

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

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

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

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

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 205
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 208

<400> 205

Lys Tyr Trp Met Ile
1 5

357707_1.txt

<210> 206
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 208

<400> 206

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Glu
1				5					10					15	

Gly

<210> 207
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 208

<400> 207

Gly	Gly	Asp	Asp	Tyr	Ser	Ile	Ser	His	Phe	Gly	Met	Asp	Val
1				5					10				

<210> 208
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

357707_1.txt

<222> (1)..(123)

<223> VH binding to CD137

<400> 208

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

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

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

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

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

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

Ala Arg Gly Gly Asp Asp Tyr Ser Ile Ser His Phe Gly Met Asp Val
100 105 110

Ser Gly Gln Gly Thr Arg Val Thr Val Ser Ser
115 120

<210> 209

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 212

<400> 209

Lys Tyr Trp Met Ile
1 5

<210> 210

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 212

<400> 210

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 211

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 212

<400> 211

Gly Gly Asp Asp Tyr Ser His Ser His Tyr Gly Met Asp Val
1 5 10

<210> 212

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 212

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

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

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

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

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

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

Ala Arg Gly Gly Asp Asp Tyr Ser His Ser His Tyr Gly Met Asp Val
 100 105 110

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

<210> 213

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 216

<400> 213

Asn Tyr Trp Met Asn
 1 5

<210> 214
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 216

<400> 214

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 215
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 216

<400> 215

Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 1 5 10

357707_1.txt

<210> 216
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 216

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 Asn Phe Ser Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 217
 <211> 5
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<213> Homo sapiens

<220>

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<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 220

<400> 217

Ser Tyr Trp Leu Asn

1 5

<210> 218

<211> 17

<212> PRT

<213> Homo sapiens

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<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 220

<400> 218

Asn Ile Asn Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val Glu

1 5 10 15

Gly

<210> 219

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 220

<400> 219

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Gly Gly Glu Asp Tyr Gly Asn Ser His Phe Gly Met Asp Val
1 5 10

<210> 220
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(123)
<223> VH binding to CD137

<400> 220

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 Gly Ser Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Asp Tyr Gly Asn Ser His Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

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<210> 221
 <211> 5
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<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 224

<400> 221

Ser Tyr Trp Met Ser
 1 5

<210> 222
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 224

<400> 222

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 223
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 224

<400> 223

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 224

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 224

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

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

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 225
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 228

<400> 225

Asp Tyr Trp Met Asn
1 5

<210> 226
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO:228

<400> 226

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

Gly

<210> 227
<211> 14
<212> PRT
<213> Homo sapiens

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<220>
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 <223> CDR3 OF SEQ ID NO: 228

<400> 227

Gly	Gly	Glu	Gly	Tyr	Gly	Asp	Asn	His	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 228
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> VH binding to CD137

<400> 228

Gln	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	Thr	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr
			20					25					30		

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

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

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

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

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Ala Arg Gly Gly Glu Gly Tyr Gly Asp Asn His Tyr Gly Met Asp Val
100 105 110

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

<210> 229
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 232

<400> 229

Ser Tyr Trp Met Asn
1 5

<210> 230
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 232

<400> 230

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 231

<211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 232

<400> 231

Gly Gly Pro Asp Tyr Gly Asp Leu His Tyr Gly Met Asp Val
 1 5 10

<210> 232
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 232

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 Arg Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Pro Asp Tyr Gly Asp Leu His Tyr Gly Met Asp Val

100

105

110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 233
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 236

<400> 233

Arg Tyr Trp Met Ser
 1 5

<210> 234
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 236

<400> 234

Asn Ile Asn Gln Asp Gly Arg Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 235
 <211> 14
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 236

<400> 235

Gly Gly Glu Gly Tyr Gly Asp Tyr His Tyr Gly Met Asp Val
1 5 10

<210> 236

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 236

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

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

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

Ala Asn Ile Asn Gln Asp Gly Arg Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Asp Tyr His Tyr Gly Met Asp Val
 100 105 110

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

<210> 237
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 240

<400> 237

Asn Tyr Trp Met Ile
 1 5

<210> 238
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 240

<400> 238

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

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<210> 239
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 240

<400> 239

Gly Gly Asp Gly Tyr Ser Asn Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 240
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 240

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Thr Asn Ser Leu Phe

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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	Gly	Gly	Asp	Gly	Tyr	Ser	Asn	Ser	His	Tyr	Gly	Met	Asp	Val
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
		115					120								

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<210> 241
<211> 5
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 244
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<400> 241

Asn Tyr Trp Met Asn
1 5

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<210> 242
<211> 17
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 244
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<400> 242

Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 243
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 244

<400> 243

Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
 1 5 10

<210> 244
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 244

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 Val Ala Ser Gly Phe Asn Phe Ser Asn Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val

50

55

60

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 245
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 248

<400> 245

Asn Tyr Trp Met Asn
 1 5

<210> 246
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 248

<400> 246

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Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 247
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 248

<400> 247

Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
1 5 10

<210> 248
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(123)
<223> VH binding to CD137

<400> 248

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 Asn Phe Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val

35

40

45

Ala Asn Ile Asn Gln Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Phe Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 249
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 252

<400> 249

Ser Phe Trp Met Asn
 1 5

<210> 250
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 252

<400> 250

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 251

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 252

<400> 251

Gly	Gly	Pro	Asp	Tyr	Gly	Asp	Leu	His	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 252

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 252

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

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

20

25

30

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

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

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

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

Ala Arg Gly Gly Pro Asp Tyr Gly Asp Leu His Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 253
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 256

<400> 253

Ser Tyr Trp Met Asn
 1 5

<210> 254
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 256

<400> 254

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 255
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 256

<400> 255

Gly	Gly	Pro	Asp	Tyr	Gly	Asp	Leu	His	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 256
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 256

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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1              5              10              15

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

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

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

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

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

Ala Arg Gly Gly Pro Asp Tyr Gly Asp Leu His Tyr Gly Met Asp Val
    100              105              110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    115              120

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<210> 257
<211> 5
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 260

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<400> 257

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Asn Tyr Trp Met Ile
1              5

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<210> 258
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 260

<400> 258

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 259
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 260

<400> 259

Gly	Gly	Glu	Asp	Tyr	Gly	Asn	Ser	His	Tyr	Gly	Met	Asp	Val
1				5					10				

<210> 260
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

357707_1.txt

<400> 260

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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Asp Tyr Gly Asn Ser His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 261

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 264

<400> 261

357707_1.txt

Asn Tyr Trp Met Asn
1 5

<210> 262
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 264

<400> 262

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 263
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 264

<400> 263

Gly Gly Glu Gly Tyr Gly Ile Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 264
<211> 123
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 264

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 Asn Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Ile Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 265

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 268

<400> 265

Ser Tyr Trp Met Ser
1 5

<210> 266

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 268

<400> 266

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 267

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 268

<400> 267

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 268

<211> 123

<212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 268

Gln 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 Ser Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 269
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 272

<400> 269

Asn Tyr Trp Met Ile
 1 5

<210> 270
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 272

<400> 270

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 271
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 272

<400> 271

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 272
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 272

Gln 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 Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 273

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

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 276

<400> 273

Asn Tyr Trp Met Asn
 1 5

<210> 274
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 276

<400> 274

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 275
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 276

<400> 275

Gly Gly Thr Gly Tyr Gly Ser Asp His Tyr Gly Met Asp Val
 1 5 10

<210> 276

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 276

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Gly Gly Thr Gly Tyr Gly Ser Asp His Tyr Gly Met Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 277
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 280

<400> 277

Asn Tyr Trp Met Asn
 1 5

<210> 278
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 280

<400> 278

Asn Ile Asn Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 279
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 280

<400> 279

Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val
 1 5 10

<210> 280
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 280

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 Asn Phe Ser Asn Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Asn Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Phe Gly Tyr Gly Asp Ser His Tyr Gly Met Asp Val

100

105

110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 281
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 284

<400> 281

Asn Tyr Trp Met Ile
 1 5

<210> 282
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 284

<400> 282

Asn Ile Asn Gln Asn Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Gln
 1 5 10 15

Gly

<210> 283
 <211> 14
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 284

<400> 283

Gly Gly Ala Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
1 5 10

<210> 284

<211> 123

<212> PRT

<213> Homo sapiens

<400> 284

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 Gly Asn Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asn Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Ala Asp Tyr Ser Asn Ser His Tyr Gly Met Asp Val
100 105 110

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

<210> 285
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 288

<400> 285

Ser Tyr Trp Met Ser
1 5

<210> 286
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 288

<400> 286

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 287
<211> 14
<212> PRT
<213> Homo sapiens

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<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 288

<400> 287

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 288
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 288

Gln 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 Ser Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

357707_1.txt

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 289
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 292

<400> 289

Ser Tyr Trp Met Asn
1 5

<210> 290
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 292

<400> 290

Asn Ile Asn Pro Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Gln
1 5 10 15

Gly

<210> 291

<211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 292

<400> 291

Gly Gly Pro Gly Tyr Gly Asp Leu His Tyr Gly Met Asp Val
 1 5 10

<210> 292
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 292

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 Arg Ser Tyr
 20 25 30

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

Ala Asn Ile Asn Pro Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

357707_1.txt

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

Ala Arg Gly Gly Pro Gly Tyr Gly Asp Leu His Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 293
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 296

<400> 293

Asn Tyr Trp Met Asn
1 5

<210> 294
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 296

<400> 294

Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 295
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 296

<400> 295

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 296
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 296

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

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

357707_1.txt

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 297
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 300

<400> 297

Asp Tyr Tyr Met Ser
1 5

<210> 298
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 300

<400> 298

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys

1 5 10 15

Gly

<210> 299
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 300

<400> 299

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 300
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 300

Gln 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 Tyr
 20 25 30

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

357707_1.txt

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 301
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 304

<400> 301

Asn Tyr Trp Met Asn
1 5

<210> 302
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 304

357707_1.txt

<400> 302

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Arg	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 303

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 304

<400> 303

Gly	Gly	Glu	Gly	Tyr	Gly	Val	Asp	His	Tyr	Gly	Leu	Asp	Val
1				5					10				

<210> 304

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 304

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	Thr	Gly	Phe	Thr	Leu	Ser	Asn	Tyr
			20					25					30		

357707_1.txt

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 305
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 308

<400> 305

Asn Tyr Trp Met Asn
 1 5

<210> 306
 <211> 17
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 308

<400> 306

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Arg	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 307
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 308

<400> 307

Gly	Gly	Glu	Gly	Tyr	Gly	Val	Asp	His	Tyr	Gly	Leu	Asp	Val
1				5					10				

<210> 308
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 308

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

357707_1.txt

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

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 309
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 312

<400> 309

Asn Tyr Trp Met Asn
1 5

<210> 310
<211> 17

<212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 312

<400> 310

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 311
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 312

<400> 311

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 312
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 312

357707_1.txt

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 313
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 316

<400> 313

Asn Tyr Trp Met Asn
1 5

357707_1.txt

<210> 314
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 316

<400> 314

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Arg	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 315
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 316

<400> 315

Gly	Gly	Glu	Gly	Tyr	Gly	Val	Asn	His	Tyr	Gly	Leu	Asp	Val
1				5					10				

<210> 316
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 316

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

 Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

 Ala Arg Gly Gly Glu Gly Tyr Gly Val Asn His Tyr Gly Leu Asp Val
 100 105 110

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

 <210> 317
 <211> 5
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 320

 <400> 317

 Asp Tyr Tyr Met Ser
 1 5

357707_1.txt

<210> 318
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 320

<400> 318

Asn Ile Lys Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 319
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 320

<400> 319

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 320
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

357707_1.txt

<400> 320

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

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

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 321

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 324

<400> 321

Asn Tyr Trp Met Asn
1 5

<210> 322
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 324

<400> 322

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Glu
1 5 10 15

Gly

<210> 323
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 324

<400> 323

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 324
<211> 123
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<223> VH binding to CD137

<400> 324

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

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

<210> 325

<211> 5

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 328

<400> 325

Asn Tyr Trp Met Asn
1 5

<210> 326

<211> 17

<212> PRT

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<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 328

<400> 326

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 327

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 328

<400> 327

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 328

<211> 123

<212> PRT
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 <223> VH binding to CD137

<400> 328

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 329
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 <223> CDR1 OF SEQ ID NO: 332

<400> 329

Asn Tyr Trp Met Asn
 1 5

<210> 330
 <211> 17
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<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 332

<400> 330

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 331
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 332

<400> 331

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 332
 <211> 123
 <212> PRT
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<220>
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 <223> VH binding to CD137

<400> 332

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

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

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 333

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<211> 5
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 336

<400> 333

Asn Tyr Trp Met Asn
1 5

<210> 334
<211> 17
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<213> Homo sapiens

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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 336

<400> 334

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 335
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 336

<400> 335

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 336

<211> 123

<212> PRT

<213> Homo sapiens

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<222> (1)..(123)

<223> VH binding to CD137

<400> 336

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

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

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 337
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 340

<400> 337

Asn Tyr Trp Met Asn
 1 5

<210> 338
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 340

<400> 338

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 339
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 340

<400> 339

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 340
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 340

Gln 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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val

100

105

110

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

<210> 341
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 344

<400> 341

Asn Tyr Trp Met Asn
 1 5

<210> 342
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 344

<400> 342

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Glu
 1 5 10 15

Gly

<210> 343
 <211> 14
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 344

<400> 343

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 344

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 344

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

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

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

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

Leu Gln Met Ser Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 345
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 348

<400> 345

Asn Tyr Trp Met Asn
 1 5

<210> 346
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 348

<400> 346

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

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<210> 347
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 348

<400> 347

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 348
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 348

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

Ser Leu Lys Leu Ser Cys Ala Ala Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr

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65 70 75 80

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

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<210> 349
<211> 5
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 352
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<400> 349

Asn Tyr Trp Met Asn
1 5

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<210> 350
<211> 17
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 352
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<400> 350

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 351
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO:352

<400> 351

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 352
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 352

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

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

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val

50

55

60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 353
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 356

<400> 353

Asp Tyr Gly Met Ser
 1 5

<210> 354
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 356

<400> 354

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Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 355
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 356

<400> 355

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 356
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(123)
<223> VH binding to CD137

<400> 356

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

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

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

35

40

45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

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

<210> 357
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 360

<400> 357

Ser His Trp Met Thr
 1 5

<210> 358
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 360

<400> 358

His	Ile	Lys	Glu	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Glu	Asp	Ser	Val	Glu
1				5					10					15	

Gly

<210> 359

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 360

<400> 359

Gly	Gly	Asp	Gly	Tyr	Ser	Asp	Ser	His	Phe	Gly	Val	Asp	Val
1				5					10				

<210> 360

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 360

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	Ser	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
 50 55 60

Glu Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 361
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 364

<400> 361

Ser His Trp Met Thr
 1 5

<210> 362
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 364

<400> 362

His	Ile	Lys	Glu	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 363
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 364

<400> 363

Gly	Gly	Asp	Gly	Tyr	Ser	Asp	Ser	His	Phe	Gly	Val	Asp	Val
1				5					10				

<210> 364
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 364

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 Ser His
 20 25 30
 Trp Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 365
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 368

<400> 365

Ser His Trp Met Thr
 1 5

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<210> 366
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 368

<400> 366

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Lys
1 5 10 15

Gly

<210> 367
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 368

<400> 367

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 368
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

357707_1.txt

<400> 368

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 369

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 372

<400> 369

Ser His Trp Met Thr
1 5

<210> 370
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 372

<400> 370

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu
1 5 10 15

Gly

<210> 371
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 372

<400> 371

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 372
<211> 123
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 372

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 373

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 376

<400> 373

Ser His Trp Met Thr
1 5

<210> 374

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 376

<400> 374

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu
1 5 10 15

Gly

<210> 375

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 376

<400> 375

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 376

<211> 123

<212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 376

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 377
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 380

<400> 377

Ser His Trp Met Thr
 1 5

<210> 378
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 380

<400> 378

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 379
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 380

<400> 379

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 1 5 10

<210> 380
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 380

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 381

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

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 384

<400> 381

Ser His Trp Met Thr
 1 5

<210> 382
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 384

<400> 382

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 383
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> CDR3 OF SEQ ID NO: 384

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<400> 383

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 384

<211> 123

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(123)

<223> VH binding to CD137

<400> 384

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

200

115

120

<210> 385
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 388

<400> 385

Ser His Trp Met Thr
 1 5

<210> 386
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 388

<400> 386

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 387
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>

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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 388

<400> 387

Gly Gly Val Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
 1 5 10

<210> 388
 <211> 123
 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 388

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Val Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val

100

105

110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 389
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 392

<400> 389

Ser His Trp Met Thr
 1 5

<210> 390
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 392

<400> 390

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 391
 <211> 14
 <212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 392

<400> 391

Gly Gly Glu Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
1 5 10

<210> 392

<211> 123

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(123)

<223> VH binding to CD137

<400> 392

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 393
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 396

<400> 393

Ser His Trp Met Thr
 1 5

<210> 394
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 396

<400> 394

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

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<210> 395
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 396

<400> 395

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 1 5 10

<210> 396
 <211> 123
 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 396

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 397
 <211> 5
 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 400

<400> 397

Ser His Trp Met Thr
 1 5

<210> 398
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 400

<400> 398

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 399
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> CDR3 OF SEQ ID NO: 400

<400> 399

Gly Gly Asp Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
 1 5 10

<210> 400
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> VH binding to CD137

<400> 400

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val

50

55

60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 401
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 404

<400> 401

Ser His Trp Met Thr
 1 5

<210> 402
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 404

<400> 402

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His Ile Lys Glu Gly Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 403
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 404

<400> 403

Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 404
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 404

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 Ser His
20 25 30

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

35

40

45

Ala His Ile Lys Glu Gly Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 405
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 408

<400> 405

Ser His Trp Met Thr
 1 5

<210> 406
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 408

<400> 406

His	Ile	Lys	Glu	Glu	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 407

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 408

<400> 407

Gly	Gly	Asp	Gly	Tyr	Ser	Asp	Ser	His	Phe	Gly	Val	Asp	Val
1				5					10				

<210> 408

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 408

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	Ser	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

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

Ala His Ile Lys Glu Glu Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 409
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 412

<400> 409

Ser His Trp Met Thr
 1 5

<210> 410
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 412

<400> 410

His	Ile	Lys	Glu	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 411
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 412

<400> 411

Gly	Gly	Glu	Gly	Tyr	Ser	Asp	Ser	His	Phe	Gly	Val	Asp	Val
1				5					10				

<210> 412
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 412

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

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1              5              10              15

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

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
    50              55              60

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
    100              105              110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    115              120

<210> 413
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 416

<400> 413

Ser His Trp Met Thr
1              5

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<210> 414
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 416

<400> 414

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 415
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 416

<400> 415

Gly Gly Val Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
1 5 10

<210> 416
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(123)
<223> VH binding to CD137

357707_1.txt

<400> 416

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Val Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 417

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 420

<400> 417

Ser His Trp Met Thr
1 5

<210> 418
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 420

<400> 418

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 419
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 420

<400> 419

Gly Gly Val Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
1 5 10

<210> 420
<211> 123
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 420

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

Ala Arg Gly Gly Val Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 421

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 424

<400> 421

Ser His Trp Met Thr
1 5

<210> 422

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 424

<400> 422

His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 423

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 424

<400> 423

Gly Gly Glu Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
1 5 10

<210> 424

<211> 123

<212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(123)
 <223> VH binding to CD137

<400> 424

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 Ser His
 20 25 30

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

Ala His Ile Lys Glu Asp Glu Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Gly Glu Gly Tyr Ser Ile Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 425
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 428

<400> 425

Asp Tyr Tyr Met Ser
 1 5

<210> 426
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 428

<400> 426

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

Gly

<210> 427
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 428

<400> 427

Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 428
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 428

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 429

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

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 432

<400> 429

Asp Tyr Tyr Met Ser
1 5

<210> 430
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 432

<400> 430

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

Gly

<210> 431
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 432

<400> 431

Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 432

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 432

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr His Cys
 85 90 95

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 433
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> CDR1 OF SEQ ID NO: 436

<400> 433

Asp Tyr Tyr Met Ser
 1 5

<210> 434
 <211> 17
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 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 436

<400> 434

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

Gly

<210> 435
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 436

<400> 435

Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 436
 <211> 122
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 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 436

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

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

Tyr Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr His Cys
 85 90 95

Ala Lys Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Asn Trp

100

105

110

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

<210> 437
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 440

<400> 437

Asp Tyr Tyr Met Ser
 1 5

<210> 438
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 440

<400> 438

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

Gly

<210> 439
 <211> 13
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 440

<400> 439

Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 440

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 440

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Val Ile Asp 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 Val Tyr His Cys

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

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

<210> 441
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 444

<400> 441

Asp Tyr Tyr Met Ser
 1 5

<210> 442
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 444

<400> 442

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

Gly

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<210> 443
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 444

<400> 443

Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 444
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 444

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

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65 70 75 80

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

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

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

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<210> 445
<211> 5
<212> PRT
<213> Homo sapiens
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<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 448
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<400> 445

Asp Tyr Tyr Met Ser
1 5

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<210> 446
<211> 17
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 448
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<400> 446

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

Gly

<210> 447
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 448

<400> 447

Glu Asp Ser Arg Ile Pro Gly Thr Thr Asp Phe Asp Ser
 1 5 10

<210> 448
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 448

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr His Cys
 85 90 95

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

Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 449
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 452

<400> 449

Asp Tyr Tyr Met Ser
 1 5

<210> 450
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 452

<400> 450

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

Gly

<210> 451
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 452

<400> 451

Glu Asp Ile Arg Met Thr Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 452
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH binding to CD137

<400> 452

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

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

Tyr Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

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

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

Ala Arg Glu Asp Ile Arg Met Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 453
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 456

<400> 453

Asp Tyr Tyr Met Ser
 1 5

<210> 454
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 456

<400> 454

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

Gly

<210> 455

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 456

<400> 455

Glu	Asp	Ser	Arg	Met	Pro	Gly	Thr	Thr	Asp	Phe	Asp	Asn
1				5					10			

<210> 456

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 456

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

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

20

25

30

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp 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 Val Tyr His Cys
 85 90 95

Ala Arg Glu Asp Ser Arg Met Pro Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 457
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 460

<400> 457

Asp Tyr Tyr Met Thr
 1 5

<210> 458
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 460

<400> 458

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

Gly

<210> 459
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 460

<400> 459

Glu	Asp	Ser	Arg	Ile	Ala	Gly	Thr	Thr	Asp	Phe	Asp	Asn
1				5					10			

<210> 460
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 460

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

<210> 461
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 464

<400> 461

Asp Tyr Tyr Met Thr
 1 5

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<210> 462
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 464

<400> 462

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

Gly

<210> 463
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 464

<400> 463

Glu Asp Ser Arg Leu Ser Gly Thr Thr Asp Phe Asp Tyr
1 5 10

<210> 464
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH binding to CD137

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<400> 464

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

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

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

Ser Tyr Ile Ser Ser Ser Gly Ser Asn Ile Asp 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 Val Tyr Tyr Cys
85 90 95

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

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

<210> 465

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 468

<400> 465

Asp Tyr Tyr Met Thr
1 5

<210> 466
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 468

<400> 466

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

Gly

<210> 467
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 468

<400> 467

Glu Asp Ser Arg Ile Ala Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 468
<211> 122
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 468

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 Tyr
20 25 30

Tyr Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Ser Tyr Ile Ser Gly Ser Gly Asp Thr Ile Asp Tyr Ala Glu Ser Val
50 55 60

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

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

Ala Arg Glu Asp Ser Arg Ile Ala Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

<210> 469

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 472

<400> 469

Asp Tyr Tyr Met Ser
1 5

<210> 470

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 472

<400> 470

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

Gly

<210> 471

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 472

<400> 471

Glu Asp Ile Arg Met Thr Gly Thr Thr Asp Phe Asp His
1 5 10

<210> 472

<211> 122

<212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 472

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Thr Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

<210> 473
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 476

<400> 473

Asp Tyr Tyr Met Ser
 1 5

<210> 474
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 476

<400> 474

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

Gly

<210> 475
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 476

<400> 475

Glu Asp Pro Arg Leu Pro Gly Thr Thr Asp Phe Asp Tyr
 1 5 10

<210> 476
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 476

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

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

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

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

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

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

<210> 477

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

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 480

<400> 477

Asp Tyr Tyr Met Thr
1 5

<210> 478
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 480

<400> 478

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

Gly

<210> 479
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 480

<400> 479

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
 1 5 10

<210> 480

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 480

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

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

Tyr Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Tyr Ile Ser Gly Ser Gly Asp Thr Ile Asp Tyr Ala Glu Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 481
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 484

<400> 481

Asp Tyr Tyr Met Ser
 1 5

<210> 482
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 484

<400> 482

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

Gly

<210> 483
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 484

<400> 483

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
 1 5 10

<210> 484
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 484

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp

100

105

110

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

<210> 485
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 488

<400> 485

Asp Tyr Tyr Met Ser
 1 5

<210> 486
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 488

<400> 486

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

Gly

<210> 487
 <211> 13
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 488

<400> 487

Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Tyr
1 5 10

<210> 488

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 488

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

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

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

Ser His Ile Ser Ser Ser Gly Ser Thr Ile Asp 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 Val Tyr Tyr Cys

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

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

<210> 489
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 <223> CDR1 OF SEQ ID NO: 492

<400> 489

Asp Tyr Tyr Met Ser
 1 5

<210> 490
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 <223> CDR2 OF SEQ ID NO: 492

<400> 490

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

Gly

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<210> 491
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 492

<400> 491

Glu Asp Pro Arg Ile Ser Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 492
 <211> 122
 <212> PRT
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<220>
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<400> 492

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

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65 70 75 80

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

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

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

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<400> 493

Asp Tyr Tyr Met Ser
1 5

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<223> CDR2 OF SEQ ID NO: 496
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<400> 494

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

Gly

<210> 495
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<220>
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 <223> CDR3 OF SEQ ID NO: 496

<400> 495

Glu Asp Pro Arg Leu Pro Gly Thr Thr Asp Phe Asp Tyr
 1 5 10

<210> 496
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 <212> PRT
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 <223> VH binding to CD137

<400> 496

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

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

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

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

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

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

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 <223> CDR1 OF SEQ ID NO: 500

<400> 497

Asp Tyr Tyr Met Ser
 1 5

<210> 498
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 <223> CDR2 OF SEQ ID NO: 500

<400> 498

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

Gly

<210> 499
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<223> CDR3 OF SEQ ID NO: 500

<400> 499

Glu Asp Pro Arg Leu Pro Gly Thr Ser Glu Phe Asp Asn
1 5 10

<210> 500
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(122)
<223> VH binding to CD137

<400> 500

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

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

Tyr Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Gly Thr Gly Ile Thr Thr Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Pro Arg Leu Pro Gly Thr Ser Glu Phe Asp Asn Trp
 100 105 110

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

<210> 501
 <211> 5
 <212> PRT
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<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 504

<400> 501

Asp Tyr Tyr Met Ser
 1 5

<210> 502
 <211> 17
 <212> PRT
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<220>
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<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 504

<400> 502

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

Gly

<210> 503

<211> 13

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 504

<400> 503

Glu	Asp	Pro	Arg	Met	Pro	Gly	Thr	Phe	Asp	Phe	Asp	Asn
1				5					10			

<210> 504

<211> 122

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(122)

<223> VH binding to CD137

<400> 504

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

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

20

25

30

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

Ser His Ile Ser Ser Ser Gly Ser Thr Ile Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Pro Arg Met Pro Gly Thr Phe Asp Phe Asp Asn Trp
 100 105 110

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

<210> 505
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 508

<400> 505

Asp Tyr Tyr Met Ser
 1 5

<210> 506
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 508

<400> 506

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

Gly

<210> 507
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> CDR3 OF SEQ ID NO: 508

<400> 507

Glu	Asp	Ile	Arg	Met	Pro	Gly	Thr	Thr	Asp	Phe	Asp	His
1				5					10			

<210> 508
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 508

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
    50              55              60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
    100              105              110

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

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<210> 509
<211> 5
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC_FEATURE
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<223> CDR1 OF SEQ ID NO: 512

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<400> 509

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Asp Tyr Tyr Met Ser
1              5

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<210> 510
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<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 512

<400> 510

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

Gly

<210> 511
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 512

<400> 511

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
1 5 10

<210> 512
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<223> VH binding to CD137

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<400> 512

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
100 105 110

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

<210> 513

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 516

<400> 513

Asp Tyr Tyr Met Ser
1 5

<210> 514
<211> 17
<212> PRT
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<220>
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 516

<400> 514

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

Gly

<210> 515
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<212> PRT
<213> Homo sapiens

<220>
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<223> CDR3 OF SEQ ID NO: 516

<400> 515

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
1 5 10

<210> 516
<211> 122
<212> PRT
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<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 516

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
100 105 110

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

<210> 517

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<213> Homo sapiens

<220>

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<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 520

<400> 517

Asp Tyr Tyr Met Ser
1 5

<210> 518

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 520

<400> 518

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

Gly

<210> 519

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 520

<400> 519

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
1 5 10

<210> 520

<211> 122

<212> PRT
 <213> Homo sapiens

<220>
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<400> 520

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

<210> 521
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 <213> Homo sapiens

<220>
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 <223> CDR1 OF SEQ ID NO: 524

<400> 521

Asp Tyr Tyr Met Ser
 1 5

<210> 522
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<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 524

<400> 522

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

Asp

<210> 523
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 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 524

<400> 523

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
 1 5 10

<210> 524
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 <212> PRT
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<220>
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<400> 524

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

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

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

<210> 525

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<211> 5
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 528

<400> 525

Asp Tyr Tyr Met Ser
1 5

<210> 526
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<223> CDR2 OF SEQ ID NO: 528

<400> 526

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

Gly

<210> 527
<211> 13
<212> PRT
<213> Homo sapiens

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Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 528

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<212> PRT

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<220>

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<222> (1)..(122)

<223> VH binding to CD137

<400> 528

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

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

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

Ser His Ile Ser Ser Ser Gly Thr Thr Ile Asp 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 Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

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Asp Tyr Tyr Met Thr
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<210> 530
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 <223> CDR2 OF SEQ ID NO: 532

<400> 530

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

Gly

<210> 531
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 <212> PRT
 <213> Homo sapiens

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 <223> CDR3 OF SEQ ID NO: 532

<400> 531

Glu Asp Ile Arg Met Ser Gly Thr Thr Asp Phe Asp Tyr
 1 5 10

<210> 532
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<400> 532

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

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

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

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

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

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

Ala Arg Glu Asp Ile Arg Met Ser Gly Thr Thr Asp Phe Asp Tyr Trp

100

105

110

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

<210> 533
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 <212> PRT
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<220>
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 <223> CDR1 OF SEQ ID NO: 536

<400> 533

Asp Tyr Tyr Met Ser
 1 5

<210> 534
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 <212> PRT
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<220>
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 <223> CDR2 OF SEQ ID NO: 536

<400> 534

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

Gly

<210> 535
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 <212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(13)

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<400> 535

Glu Asp Pro Arg Leu Ser Gly Thr Ile Asp Phe Asp Ser
1 5 10

<210> 536

<211> 122

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<213> Homo sapiens

<220>

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<222> (1)..(122)

<223> VH binding to CD137

<400> 536

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

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

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

Ser His Ile Ser Ser Ser Gly Ser Ser Ile Asp 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 Val Tyr Tyr Cys

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

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

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<220>
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 <223> CDR1 OF SEQ ID NO: 540

<400> 537

Asp Tyr Tyr Met Ser
 1 5

<210> 538
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<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 540

<400> 538

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

Gly

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<210> 539
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<220>
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 <222> (1)..(13)
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<400> 539

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His
 1 5 10

<210> 540
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 <213> Homo sapiens

<220>
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 <223> VH binding to CD137

<400> 540

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

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

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

Ser His Ile Gly Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Tyr

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65 70 75 80

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

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<400> 541

Asp Tyr Tyr Met Ser
1 5

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<210> 542
<211> 17
<212> PRT
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<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 544
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<400> 542

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

Gly

<210> 543
 <211> 13
 <212> PRT
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<220>
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 <223> CDR3 OF SEQ ID NO: 544

<400> 543

Glu Asp Pro Arg Val Pro Gly Thr Thr Asn Phe Asp Tyr
 1 5 10

<210> 544
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 544

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

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

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

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Pro Arg Val Pro Gly Thr Thr Asn Phe Asp Tyr Trp
 100 105 110

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

<210> 545
 <211> 5
 <212> PRT
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<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 548

<400> 545

Asp Tyr Tyr Met Thr
 1 5

<210> 546
 <211> 17
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<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 548

<400> 546

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

Gly

<210> 547
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<223> CDR3 OF SEQ ID NO: 548

<400> 547

Glu Asp Gly Arg Ile Pro Gly Thr Thr Asp Phe Asp His
1 5 10

<210> 548
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(122)
<223> VH binding to CD137

<400> 548

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

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

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

35

40

45

Ser Tyr Ile Ser Gly Ser Gly Ser Thr Ile Asp 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 Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Asp Gly Arg Ile Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

<210> 549
 <211> 5
 <212> PRT
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<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 552

<400> 549

Asp Tyr Tyr Met Ser
 1 5

<210> 550
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 552

<400> 550

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

Asp

<210> 551

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 552

<400> 551

Glu	Asp	Ile	Arg	Met	Pro	Gly	Thr	Thr	Asp	Phe	Asp	His
1				5					10			

<210> 552

<211> 122

<212> PRT

<213> Homo sapiens

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<222> (1)..(122)

<223> VH binding to CD137

<400> 552

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	Ala	Phe	Ser	Asp	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

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

Ser His Ile Ser Gly Ser Gly Thr Thr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp His Trp
 100 105 110

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

<210> 553
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 556

<400> 553

Asp Tyr Phe Met Ser
 1 5

<210> 554
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 556

<400> 554

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

Gly

<210> 555
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 <213> Homo sapiens

<220>
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 <223> CDR3 OF SEQ ID NO: 556

<400> 555

Glu	Asp	Pro	Arg	Leu	Pro	Gly	Thr	Thr	Asp	Phe	Asp	Tyr
1				5					10			

<210> 556
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 556

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

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

<210> 557
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 560

<400> 557

Asp Ser Tyr Met Ser
 1 5

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<210> 558
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 560

<400> 558

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

Gly

<210> 559
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 560

<400> 559

Glu Asp Pro Arg Leu Pro Gly Thr Ser Asp Phe Asp Tyr
1 5 10

<210> 560
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(122)
<223> VH binding to CD137

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<400> 560

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys 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

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

Ser His Ile Ser Asn Ser Gly Ser Thr Ile Ser 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 Val Tyr Tyr Cys
85 90 95

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

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

<210> 561

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 564

<400> 561

Asp Tyr Tyr Met Ser
1 5

<210> 562
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 564

<400> 562

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

Gly

<210> 563
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 564

<400> 563

Glu Asp Pro Arg Leu Ser Gly Thr Thr Asp Phe Asp Gln
1 5 10

<210> 564
<211> 122
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 564

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

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

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

Ser His Ile Ser Ser Ser Gly Ser Ser Ile Asp 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 Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

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

<210> 565

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 568

<400> 565

Ser Tyr Trp Met Ser
1 5

<210> 566

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 568

<400> 566

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

Gly

<210> 567

<211> 13

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 568

<400> 567

Glu Asp Pro Arg Met Thr Gly Thr Thr Asp Phe Asp Tyr
1 5 10

<210> 568

<211> 122

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<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(122)
<223> VH binding to CD137

<400> 568

Gln 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 Ser Tyr
20 25 30

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

Ser His Ile Ser Ser Ser Gly Ser Thr Ile Asp Tyr Ala Glu Ser Val
50 55 60

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

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

Ala Arg Glu Asp Pro Arg Met Thr Gly Thr Thr Asp Phe Asp Tyr Trp
100 105 110

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

<210> 569
<211> 5
<212> PRT
<213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 572

<400> 569

Asn Tyr Phe Met Ser
 1 5

<210> 570
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 572

<400> 570

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

Gly

<210> 571
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 572

<400> 571

Glu Asp Pro Arg Leu Pro Gly Thr Thr Asp Phe Asp Tyr
 1 5 10

<210> 572
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 572

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

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

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

Ser His Ile Ser Ser Ser Gly Asn Thr Ile Asp 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 Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Glu Asp Pro Arg Leu Pro Gly Thr Thr Asp Phe Asp Tyr Trp
 100 105 110

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

<210> 573

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

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 576

<400> 573

Asp Tyr Tyr Met Thr
 1 5

<210> 574
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 576

<400> 574

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

Gly

<210> 575
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 576

<400> 575

Glu Asn Pro Arg Leu Pro Gly Thr Met Asp Phe Asp Tyr
 1 5 10

<210> 576

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 576

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

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

Tyr Met Thr Trp Ile Arg Gln Gly Pro Gly Lys Gly Gln Glu Trp Ile
 35 40 45

Ser Tyr Ile Ser Ser Gly Gly Ser Thr Ile His 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asn Pro Arg Leu Pro Gly Thr Met Asp Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 577
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 580

<400> 577

Asp His Phe Met Ser
 1 5

<210> 578
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 580

<400> 578

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 579
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 580

<400> 579

Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 580
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 580

Gln 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 His
 20 25 30

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

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

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

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

Ala Arg Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp

100

105

110

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

<210> 581
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 584

<400> 581

Asn Tyr Trp Met Thr
 1 5

<210> 582
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 584

<400> 582

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

Gly

<210> 583
 <211> 13
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 584

<400> 583

Glu Asp Pro Arg Leu Pro Gly Thr Met Asp Phe Asp Tyr
1 5 10

<210> 584

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 584

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

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

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

Ser His Ile Ser Ser Thr Gly Ser Thr Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

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

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

<210> 585
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 588

<400> 585

Asp Tyr Tyr Met Ser
 1 5

<210> 586
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 588

<400> 586

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

Gly

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<210> 587
 <211> 13
 <212> PRT
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<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 588

<400> 587

Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 588
 <211> 122
 <212> PRT
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<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 588

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

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65 70 75 80

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

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

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<210> 589
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<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 592
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<400> 589

Asp Tyr Tyr Met Ser
1 5

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<210> 590
<211> 17
<212> PRT
<213> Homo sapiens
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<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 592
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<400> 590

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

Gly

<210> 591
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 592

<400> 591

Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 592
 <211> 122
 <212> PRT
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<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 592

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 593
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> OF SEQ ID NO: 596

<400> 593

Asp Tyr Tyr Met Ser
 1 5

<210> 594
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 596

<400> 594

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

Gly

<210> 595
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 596

<400> 595

Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 596
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH binding to CD137

<400> 596

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

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

Tyr Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 597
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 600

<400> 597

Asp Tyr Tyr Met Ser
 1 5

<210> 598
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 600

<400> 598

Tyr	Ile	Ser	Gly	Ser	Gly	Asp	Ile	Ile	Asp	Tyr	Ala	Asp	Ser	Val	Lys
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Gly

<210> 599

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 600

<400> 599

Glu	Asp	Ser	Arg	Leu	Thr	Gly	Thr	Thr	Asp	Phe	Asp	Asn
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<210> 600

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 600

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

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

20

25

30

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr His Cys
 85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 601
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 604

<400> 601

Asp Tyr Tyr Met Ser
 1 5

<210> 602
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 604

<400> 602

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

Gly

<210> 603
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 604

<400> 603

Glu	Asp	Ser	Arg	Leu	Thr	Gly	Thr	Thr	Asp	Phe	Asp	Asn
1				5					10			

<210> 604
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 604

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1 5 10 15

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

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

 Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

 <210> 605
 <211> 5
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 608

 <400> 605

 Asp Tyr Tyr Met Ser
 1 5

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<210> 606
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 608

<400> 606

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

Gly

<210> 607
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 608

<400> 607

Glu	Asp	Ser	Arg	Leu	Thr	Gly	Thr	Thr	Asp	Phe	Asp	Asn
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<210> 608
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

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<400> 608

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

<210> 609

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 612

<400> 609

Asp Tyr Tyr Met Ser
1 5

<210> 610
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 612

<400> 610

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

Gly

<210> 611
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CDR3 OF SEQ ID NO: 612

<400> 611

Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 612
<211> 122
<212> PRT
<213> Homo sapiens

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<220>

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<222> (1)..(122)

<223> VH binding to CD137

<400> 612

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

<210> 613

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 616

<400> 613

Asp Tyr Tyr Met Ser
1 5

<210> 614

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 616

<400> 614

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

Gly

<210> 615

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> CDR3 OF SEQ ID NO: 616

<400> 615

Glu Asp Ala Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 616

<211> 122

<212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 616

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Ala Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 617
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> CDR1 OF SEQ ID NO: 620

<400> 617

Asp Tyr Tyr Met Ser
 1 5

<210> 618
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 620

<400> 618

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

Gly

<210> 619
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 620

<400> 619

Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 620
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(122)
 <223> VH binding to CD137

<400> 620

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

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

<210> 621

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

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 624

<400> 621

Asp Tyr Tyr Met Ser
 1 5

<210> 622
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 624

<400> 622

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

Gly

<210> 623
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 624

<400> 623

Glu Asp Ala Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 624

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(122)

<223> VH binding to CD137

<400> 624

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Ala Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 625
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 628

<400> 625

Asp Tyr Tyr Met Ser
 1 5

<210> 626
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 628

<400> 626

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

Gly

<210> 627
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(13)
 <223> CDR3 OF SEQ ID NO: 628

<400> 627

Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn
 1 5 10

<210> 628
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(122)
 <223> VH binding to CD137

<400> 628

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

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Pro Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp

100

105

110

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

<210> 629
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 629
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 tcctgtgcag cctctggatt cacctttagt agccattgga tgacttgggt ccgtcaggct 120
 ccagggaagg ggctggagtg ggtggcccac ataaaggaag acggaagtga gaaatactat 180
 gaggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctcggtatat 240
 ctgcaaatga acagtctgag agccgaagac acggctgtgt attactgtgc gagaggaggt 300
 gatggctaca gtgactccca cttcggtgtg gacgtctggg gccaaaggac cacggtcact 360
 gtctcttca 369

<210> 630
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 630
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 ccagggaagg ggctggagtg ggtggcccac ataaaggaag acggaagtga gaaatactat 180
 gtggactctg tggagggccg attcaccatc tccagagaca acgccaataa ctcgctgtat 240
 ctacaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggaggt 300
 gatggctaca gtgactccca ctacgggtgtg gacgtctggg gccaaaggac cacggtcacc 360
 gtctcctca 369

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<210> 631
<211> 369
<212> DNA
<213> Homo sapiens

<400> 631
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tcctgtgcag cctctggatt cacctttagt agttattgga tgacctgggtt ccgccaggct 120
ccagggagggg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180
gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggggga 300
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gtctcctca 369

<210> 632
<211> 369
<212> DNA
<213> Homo sapiens

<400> 632
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc cgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt aactattgga tgacctgggtt ccgccaggct 120
ccagggggggg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180
gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctactgtat 240
ctacaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggggga 300
ttaggctacg gtgactccca ctacggtatg gacgtctggg gccaaaggac cacggtcact 360
gtctcctca 369

<210> 633
<211> 369
<212> DNA
<213> Homo sapiens

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<400> 633
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tcctgtgcag cctctggatt cacctttagt aactattgga tgatctgggtt ccgccaggct 120
ccaggaaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180
gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaagac acggcttgtt attactgtgc gagaggaggt 300
gatggctaca gtggctccca ccacggtacg gacgtctggg gccaaaggac cacggtcacc 360
gtctcctca 369

<210> 634
<211> 369
<212> DNA
<213> Homo sapiens

<400> 634
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ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180
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gtctcctca 369

<210> 635
<211> 369
<212> DNA
<213> Homo sapiens

<400> 635
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tcctgtggag cctctggatt cacctttagt agctattgga tgctctgggtt ccgccaggct 120
ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

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gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat	240
ctgcaaatga acaccctgag agccgaggac acggctatattt attattgtgc gagaggggggt	300
gatggctaca gtgactccca cttcggtacg gacgtctggg gccaaaggac cacggtcact	360
gtctcctca	369

<210> 636
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 636	
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ccaggagagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat	180
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gatggctaca gtgattccca ctacgggtacg gacgtctggg gccaaaggac cacggtcacc	360
gtctcctca	369

<210> 637
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 637	
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ccagggggggg ggctggagtg ggtggccaac ataaaccaag atgggagtga gaagtactat	180
gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctactggat	240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggga	300
ttaggctacg gtgactccca ctacgggtatg gacgtctggg gccaaaggac cacggtcacc	360

gtctcctca 369

<210> 638
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 638
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 ctgcaaatga acagcctgag agtcgaggac acggctgtgt attactgtgc gagaggaggg 300
 gccgggtata gcatgtctca ctacggtatg gacgtctggg gccaaggac cacggtcact 360
 gtctcttca 369

<210> 639
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 639
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 ccagggaagg ggctggagtg ggtggccaac ataaaggagg atggaagtga gaaatactat 180
 gtggactctg tggagggccg attcaccata tccagagaca acgccaagaa ctcaacgtat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggaggg 300
 gccgggtata gtatgtctca ctacggtatg gacgtctggg gccaaggac cacggtcact 360
 gtctcctca 369

<210> 640
 <211> 369

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<212> DNA

<213> Homo sapiens

<400> 640

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ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat	180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctctctgtat	240
ctgcaaatga acaccctgcg agccgaggac acggctatit attattgtgc gagaggggggt	300
gatggctaca gtaactccca cttcggtacg gacgtctggg gccaaaggac cacggtcacc	360
gtctcttca	369

<210> 641

<211> 369

<212> DNA

<213> Homo sapiens

<400> 641

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tcctgtggag cctctggatt cacctttagt agctattgga tgttctgggtt ccgccaggct	120
ccaggagagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat	180
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ctgcaaatga acagcctgag agccgaggac acggctatit attactgtgc gagaggaggt	300
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357707_1.txt

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<213> Homo sapiens

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 ctgcagatga acaacctgag agccgaggac acggccgtgt atcactgtgc gagagaagat 300
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357707_1.txt

<212> DNA

<213> Homo sapiens

<400> 736

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ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	atcactgtgc	gaaagaagat	300
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<211> 366

<212> DNA

<213> Homo sapiens

<400> 737

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<212> DNA

<213> Homo sapiens

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357707_1.txt

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357707_1.txt

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357707_1.txt

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ctgcagatga acagcctgag agccgaggac acggccgtgt atcactgtgc gagagaagat	300
tcgcgtatag ccggaactac ggactttgac aactggggcc cggaaccct ggtcactgtc	360
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<211> 366

<212> DNA

<213> Homo sapiens

<400> 746

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<212> DNA

<213> Homo sapiens

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ccagggaagg ggctggagtg ggtttcacac attagtagta gtggtaatac catagactac	180

357707_1.txt

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 ccagggaagg gactggagtg gatttcatac attagtggta gtggtgatac catagactac 180
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<212> DNA

<213> Homo sapiens

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<211> 366

<212> DNA

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atcaggatgc ctggaactac ggactttgac cactggggcc aaggaaccct ggtcactgtc	360
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ccagggaagg ggctggagtg ggtttcacac attagtggta gtggaactac catagactac	180
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357707_1.txt

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<212> DNA

<213> Homo sapiens

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<212> DNA

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357707_1.txt

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 <212> DNA
 <213> Homo sapiens

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 gcagactctg tgaagggccg cttcaccatc tccagggaca acgccaagaa ctactgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgttt attactgtgc gaaagaagat 300
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<210> 768
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357707_1.txt

<212> DNA

<213> Homo sapiens

<400> 768

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<213> Homo sapiens

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ctgcaaatga acagcctgag agacgaggac acggccgtgt attactgtgc gagagaagat	300
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<211> 366

<212> DNA

<213> Homo sapiens

<400> 770

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ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat	300
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gcagactctg tgaagggccg cttcaccatc tccagggaca acgccaagaa ctactttat	240
ctgcaaatgg atagtctgag agccgaggac acggccgttt attactgttc gagagaagat	300
cctcgtttac ctggaactac agattttgac tactggggcc agggaaccct ggtcactgtc	360
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ccagggaagg gacaggaatg gatttcatac attagtagtg gtggtagcac catacactac	180
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357707_1.txt

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gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240
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<210> 776
<211> 366
<212> DNA
<213> Homo sapiens

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gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240
ctgcagatga acaacctgag agccgaggac acggccgtgt atcactgtgc gagagaagat 300
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tcctca 366

<210> 777
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357707_1.txt

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ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac	180
gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtgt atcactgtgc gagagaagat	300
tcccgtctaa ctggaactac ggactttgac aattggggcc aggggaaccct ggtcaccgtc	360
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<210> 778

<211> 366

<212> DNA

<213> Homo sapiens

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ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac	180
gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat	240
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tcccgtctaa ctggaactac ggactttgac aattggggcc aggggaaccct ggtcaccgtc	360
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<212> DNA

<213> Homo sapiens

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ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac	180

357707_1.txt

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 <212> DNA
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 tcctca 366

<210> 784
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357707_1.txt

<212> DNA

<213> Homo sapiens

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<211> 366

<212> DNA

<213> Homo sapiens

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tcctca	366

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<211> 255

<212> PRT

<213> Homo sapiens

<400> 786

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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
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
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
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Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu
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<210> 787

<211> 768

<212> DNA

<213> Homo sapiens

<400> 787

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 tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgtga 768

<210> 788
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
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<223> Terminating residues of C- Terminal Domain of a VH domain

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1 5

<210> 789
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 789

His His His His His His
1 5

<210> 790
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<220>
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<400> 790

Gly Gly Gly Gly Ser
1 5

<210> 791
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Linker

<400> 791

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<210> 792

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Linker

<400> 792

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<210> 793

<211> 14

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<213> Artificial Sequence

<220>

<223> Peptide Linker

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<210> 794

<211> 8

<212> PRT

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<220>

<223> Peptide Linker

<400> 794

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1 5

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1 5

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Gly Gly Ser Gly Ser Gly
1 5

<210> 797
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<220>
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Gly Gly Ser Gly
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<210> 798

<211> 276
 <212> PRT
 <213> Artificial Sequence

<220>
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
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Trp Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
 50 55 60

Glu Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 145 150 155 160

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Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Phe Ser Ser His Trp Met Thr Trp Phe Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala His Ile Lys Glu Asp Gly
195 200 205

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

Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln Met Asn Ser Leu Arg
225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asp Gly Tyr
245 250 255

Ser Asp Ser His Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val
260 265 270

Thr Val Ser Ser
275

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<211> 828
<212> DNA
<213> Artificial Sequence

<220>
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ccaggggaagg ggctggagtg ggtggccccc ataaaggaag acggaagtga gaaatactat 180

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 ttcaccgtct ccagagacaa cgccaagaac tcggtatatc tgcaaatgaa cagtctgaga 720
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 ttcggtgtgg acgtctgggg ccaagggacc acggtcactg tctcttca 828

<210> 800
 <211> 274
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Bivalent Molecule

<400> 800

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

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

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val
 50 55 60

357707_1.txt

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

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

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
145 150 155 160

Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Ala
165 170 175

Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser Trp Phe Arg Gln Ala
180 185 190

Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Gly Ser Gly Asp
195 200 205

Ile Ile Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
210 215 220

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Asn Leu Arg Ala
225 230 235 240

Glu Asp Thr Ala Val Tyr His Cys Ala Arg Glu Asp Ser Arg Leu Thr
245 250 255

357707_1.txt

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

Ser Ser

<210> 801
 <211> 822
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Bivalent Molecule of Seq ID NO; 800

<400> 801
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 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtttcatat attagtggta gtggtgatat catagactac 180
 gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240
 ctgcagatga acaacctgag agccgaggac acggccgtgt atcactgtgc gagagaagat 300
 tcccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360
 tcctcagggtg gtggcggttc aggcggagggt ggctctggag gtggagggtc aggagggtgt 420
 ggttctggcg gcgggtggatc ggggtggagggt ggtagtgagg tgcagctgggt ggagtctggg 480
 ggaggcttgg tcaagcctgg aggggtccctg agagtctcct gtgcagcctc tggattcacc 540
 ttcagtgact actacatgag ctggttccgc caggctccag ggaaggggct ggagtggggt 600
 tcatacatta gtggtagtgg tgatatcata gactacgcag actctgtaaa gggccgattc 660
 accatctcca gggacaacgc caagaactct ctgtatctgc agatgaacaa cctgagagcc 720
 gaggacacgg ccgtgtatca ctgtgcgaga gaagattccc gtctaactgg aactacggac 780
 ttgacaatt ggggccaggg aaccctgggtc accgtctcct ca 822

<210> 802

<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> Trivalent molecule

<400> 802

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 Ser His
20 25 30

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

Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val 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 Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
145 150 155 160

357707_1.txt

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Phe Ser Ser His Trp Met Thr Trp Phe Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala His Ile Lys Glu Asp Gly
195 200 205

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

Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln Met Asn Ser Leu Arg
225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asp Gly Tyr
245 250 255

Ser Asp Ser His Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val
260 265 270

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
305 310 315 320

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
325 330 335

Ser His Trp Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu
340 345 350

357707_1.txt

Trp Val Ala His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp
355 360 365

Ser Val Glu Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser
370 375 380

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
385 390 395 400

Tyr Cys Ala Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val
405 410 415

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
420 425

<210> 803
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding the trivalent molecule of Seq ID NO: 802

<400> 803
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc cggggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt agccattgga tgacttgggtt ccgtcaggct 120
ccagggaagg ggctggagtg ggtggccac ataaaggaag acggaagtga gaaatactat 180
gaggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctcggtatat 240
ctgcaaatga acagtctgag agccgaagac acggctgtgt attactgtgc gagaggaggt 300
gatggctaca gtgactccca cttcgggtgtg gacgtctggg gccaaaggac cacggtcact 360
gtctcttcag gtgggtggcgg ttcaggcgga ggtggctctg gaggtggagg ttcaggaggt 420
ggtggttctg gcggcggtgg atcgggtgga ggtggtagtg aggtgcagct ggtggagtct 480
gggggaggct tgggtccagcc ggggggggtcc ctgagactct cctgtgcagc ctctggattc 540

357707_1.txt

acctttagta gccattggat gacttgggtc cgtcaggctc cagggaaggg gctggagtgg 600
 gtggcccaca taaaggaaga cggaagtgag aaatactatg aggactctgt ggagggccga 660
 ttcaccgtct ccagagacaa cgccaagaac tcggtatatc tgcaaatgaa cagtctgaga 720
 gccgaagaca cggctgtgta ttactgtgcg agaggaggtg atggctacag tgactccac 780
 ttcggtgtgg acgtctgggg ccaagggacc acggtcactg tctcttcagg tggtagcggt 840
 tcaggcggag gtggctctgg aggtggaggt tcaggaggtg gtggttctgg cggcgggtgga 900
 tcgggtggag gtggtagtga ggtgcagctg gtggagtctg ggggaggctt ggtccagccg 960
 ggggggtccc tgagactctc ctgtgcagcc tctggattca cctttagtag ccattggatg 1020
 acttgggtcc gtcaggctcc aggggaagggg ctggagtggg tggcccacat aaaggaagac 1080
 ggaagtgaga aatactatga ggactctgtg gagggccgat tcaccgtctc cagagacaac 1140
 gccagaact cggtatatct gcaaatgaac agtctgagag ccgaagacac ggctgtgtat 1200
 tactgtgcga gaggaggtga tggctacagt gactcccact tcggtgtgga cgtctggggc 1260
 caagggacca cggtcactgt ctcttca 1287

<210> 804
 <211> 426
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent molecule

<400> 804

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

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

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

357707_1.txt

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
100 105 110

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
145 150 155 160

Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Ala
165 170 175

Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser Trp Phe Arg Gln Ala
180 185 190

Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Gly Ser Gly Asp
195 200 205

Ile Ile Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
210 215 220

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Asn Leu Arg Ala
225 230 235 240

357707_1.txt

Glu Asp Thr Ala Val Tyr His Cys Ala Arg Glu Asp Ser Arg Leu Thr
245 250 255

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
275 280 285

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
290 295 300

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
305 310 315 320

Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
325 330 335

Tyr Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
340 345 350

Ser Tyr Ile Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val
355 360 365

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
370 375 380

Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
385 390 395 400

Ala Arg Glu Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp
405 410 415

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
420 425

<210> 805
 <211> 1278
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding trivalent molecule of seq ID No: 804

<400> 805
 gaggtgcagc tgggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagagtc 60
 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120
 ccagggaagg ggctggagtg ggtttcatat attagtggta gtggtgatat catagactac 180
 gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240
 ctgcagatga acaacctgag agccgaggac acggccgtgt atcactgtgc gagagaagat 300
 tcccgctctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360
 tcctcaggtg gtggcggttc aggcggagggt ggctctggag gtggagggtc aggagggtgt 420
 ggttctggcg gcggtggatc ggggtggagggt ggtagtgagg tgcagctggg ggagtctggg 480
 ggaggcttgg tcaagcctgg aggggtccctg agagtctcct gtgcagcctc tggattcacc 540
 ttcagtgact actacatgag ctggttccgc caggctccag ggaaggggct ggagtggggt 600
 tcatacatta gtggtagtgg tgatatcata gactacgcag actctgtaaa gggccgattc 660
 accatctcca gggacaacgc caagaactct ctgtatctgc agatgaacaa cctgagagcc 720
 gaggacacgg ccgtgtatca ctgtgcgaga gaagattccc gtctaactgg aactacggac 780
 tttgacaatt ggggccaggg aaccctggtc accgtctcct cagggtgggtg cggttcaggc 840
 ggagggtggct ctggagggtg aggttcaggga ggtggtgggt ctggcggcgg tggatcgggt 900
 ggagggtggta gtgagggtgca gctgggtggag tctggggggag gcttgggtcaa gcctggaggg 960
 tccctgagag tctcctgtgc agcctctgga ttcaccttca gtgactacta catgagctgg 1020
 ttccgccagg ctccaggga ggggctggag tgggtttcat acattagtgg tagtggtgat 1080
 atcatagact acgcagactc tgtaaagggc cgattcacca tctccaggga caacgccaag 1140

357707_1.txt

aactctctgt atctgcagat gaacaacctg agagccgagg acacggccgt gtatcactgt 1200
gcgagagaag attccccgtct aactggaact acggactttg acaattgggg ccagggaacc 1260
ctggtcaccg tctcctca 1278

<210> 806
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Bivalent molecule

<400> 806

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

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

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

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

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

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

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

357707_1.txt

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Trp Met Thr
180 185 190

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala His Ile
195 200 205

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

Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val Trp Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser
275 280

<210> 807

<211> 840

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding the bivalent molecule of Seq ID No 806

357707_1.txt

<400> 807
gaggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt ctcttcagc ggctatggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg 300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg 360
acaatgggtca ccgtctcctc aggtgggtggc gggtcaggcg gaggtggctc tggaggtgga 420
gggtcaggag gtgggtgggtc tggcggcggg ggatcgggtg gaggtggtag tgaggtgcag 480
ctgggtggagt ctggggggagg cttgggtccag ccggggggggc ccctgagact ctctgtgca 540
gcctctggat tcacctttag tagccattgg atgacttggg tccgtcaggc tccagggaag 600
gggctggagt ggggtggcca cataaaggaa gacggaagt agaaatacta tgaggactct 660
gtggagggcc gattcaccgt ctccagagac aacgccaaga actcgggtata tctgcaaatg 720
aacagtctga gagccgaaga cacggctgtg tattactgtg cgagaggagg tgatggctac 780
agtgactccc acttcggtgt ggacgtctgg ggccaaggga ccacggtcac tgtctcttca 840

<210> 808
<211> 279
<212> PRT
<213> Artificial Sequence

<220>
<223> bivalent molecule

<400> 808

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

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

357707_1.txt

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

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

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

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

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
 100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
 165 170 175

Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
 180 185 190

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile
 195 200 205

Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val Lys Gly Arg
 210 215 220

357707_1.txt

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys Ala Arg Glu
245 250 255

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

Thr Leu Val Thr Val Ser Ser
275

<210> 809
<211> 837
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding bivalent molecule of Seq ID NO 808

<400> 809
gaggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt ctcttcagc ggctatggca tgactgggt ccgccaggct 120
ccaggcaagg gactggagt ggtggcatat atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg 300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatattctg gggccaaggg 360
acaatggtca ccgtctcctc aggtggtggc gggtcaggcg gaggtggctc tggaggtgga 420
gggtcaggag gtggtggttc tggcggcggg ggatcgggtg gaggtggtag tgaggtgcag 480
ctggtggagt ctgggggagg cttggtcaag cctggagggt ccctgagagt ctctgtgca 540
gcctctggat tcaccttcag tgactactac atgagctggt tccgccaggc tccagggaag 600
gggctggagt gggtttcata cattagtggg agtggtgata tcatagacta cgcagactct 660

357707_1.txt

gtaaagggcc gattcaccat ctccaggac aacgccaaga actctctgta tctgcagatg 720
aacaacctga gagccgagga cacggccgtg tatcactgtg cgagagaaga ttcccgtcta 780
actggaacta cggactttga caattggggc cagggaaccc tggtcaccgt ctctca 837

<210> 810
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> bivalent molecule

<400> 810

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

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

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

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

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

357707_1.txt

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Trp
165 170 175

Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
180 185 190

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu
195 200 205

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val Trp
245 250 255

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
260 265

<210> 811

<211> 798

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding the bivalent molecule of Seq ID NO: 810

<400> 811

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc

60

357707_1.txt

tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctcag gtggtggcgg ttcaggcgga	360
ggtggctctg gaggtggagg ttcaggaggt ggtggttctg gcggcggtgg atcgggtgga	420
ggtggtagtg aggtgcagct ggtggagtct gggggaggct tgggtccagcc ggggggggtcc	480
ctgagactct cctgtgcagc ctctggattc acctttagta gccattggat gacttggttc	540
cgtcaggctc cagggaaggg gctggagtgg gtggcccaca taaaggaaga cggaagtgag	600
aaatactatg aggactctgt ggagggccga ttcaccgtct ccagagacaa cgccaagaac	660
tcggtatatc tgcaaatgaa cagtctgaga gccgaagaca cggctgtgta ttactgtgcg	720
agaggaggtg atggctacag tgactcccac ttcggtgtgg acgtctgggg ccaagggacc	780
acggtcactg tctcttca	798

<210> 812
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 of SEQ ID NO: 815

<400> 812

Ser	Tyr	Ala	Met	Ser
1				5

<210> 813
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 815

<400> 813

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

Gly

<210> 814
 <211> 4
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(4)
 <223> CDR3 OF SEQ ID NO: 815

<400> 814

Asp	Gly	Val	His
1			

<210> 815
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(113)
 <223> VH binding to PSMA

<400> 815

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Ser

<210> 816
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 816

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

357707_1.txt

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 817
<211> 113
<212> PRT
<213> Homo sapiens

<400> 817

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

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

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

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

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

357707_1.txt

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 818
<211> 113
<212> PRT
<213> Homo sapiens

<400> 818

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

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

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

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 819
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 819

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

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

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

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

Ser

<210> 820
 <211> 113
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<400> 820

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

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

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

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 821

<211> 113

<212> PRT

<213> Homo sapiens

<400> 821

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

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

357707_1.txt

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

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

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 822
<211> 113
<212> PRT
<213> Homo sapiens

<400> 822

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

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

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

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

357707_1.txt

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

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

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 823
<211> 113
<212> PRT
<213> Homo sapiens

<400> 823

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

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

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100

105

110

Ser

<210> 824
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 824

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Ala Tyr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

Ser

<210> 825
 <211> 113

357707_1.txt

<212> PRT

<213> Homo sapiens

<400> 825

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Ala Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 826

<211> 339

<212> DNA

<213> Homo sapiens

<400> 826

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tcctgtgcag cctctggatt cagttttagc agctatgccca tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180

357707_1.txt

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagag tatgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 827
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 827	
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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga ataacgctac cacagactac	180
gcagacttcg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 828
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 828	
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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 829
 <211> 339

357707_1.txt

<212> DNA

<213> Homo sapiens

<400> 829

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagccgacg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 830

<211> 339

<212> DNA

<213> Homo sapiens

<400> 830

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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagacgtcg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 831

<211> 339

<212> DNA

<213> Homo sapiens

<400> 831

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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180

357707_1.txt

gcagccttcg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
 gtccactggg gccagggaac cctggtcacc gtctcctca 339

<210> 832
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 832
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 tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180
 gcagacaccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
 gtccactggg gccagggaac cctggtcacc gtctcctca 339

<210> 833
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 833
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 tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180
 gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
 gtccactggg gccagggaac cctggtcacc gtctcctca 339

<210> 834
 <211> 339
 <212> DNA

357707_1.txt

<213> Homo sapiens

<400> 834

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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagcctccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 835

<211> 339

<212> DNA

<213> Homo sapiens

<400> 835

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagcctacg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt	300
gtccactggg gccagggaac cctggtcacc gtctcctca	339

<210> 836

<211> 339

<212> DNA

<213> Homo sapiens

<400> 836

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac	180
gcagccaccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat	240

357707_1.txt

ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
gtccactggg gccagggaac cctgggcacc gtctcctca 339

<210> 837
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 840

<400> 837

Gly Tyr Gly Met His
1 5

<210> 838
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 of Seq ID NO: 840

<400> 838

Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 839
<211> 18
<212> PRT
<213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(18)
 <223> CDR3 of SEQ ID NO. 840

<400> 839

Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr Asp Phe
 1 5 10 15

Asp Ile

<210> 840
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(127)
 <223> VH domain binding to PSMA

<400> 840

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

357707_1.txt

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 841
<211> 381
<212> DNA
<213> Homo sapiens

<400> 841
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tcctgtgcag cctctggatt ctcttcagt ggctatggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg 300
gcctgggggat tacgtttggg ggagtcacgc tcctatgatt ttgatattctg gggccaaggg 360
acaatggtca ctgtctcttc a 381

<210> 842
<211> 749
<212> PRT
<213> Homo sapiens

<400> 842

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1 5 10 15

Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30

357707_1.txt

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
65 70 75 80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
85 90 95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
100 105 110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
115 120 125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
130 135 140

Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145 150 155 160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
165 170 175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
180 185 190

Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
195 200 205

Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
210 215 220

357707_1.txt

Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225 230 235 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
245 250 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
260 265 270

Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
275 280 285

Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Asp Ala Gln Lys Leu
290 295 300

Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly
305 310 315 320

Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe
325 330 335

Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
340 345 350

Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro Asp
355 360 365

Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Gly
370 375 380

Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg Ser
385 390 395 400

Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu
405 410 415

357707_1.txt

Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu
420 425 430

Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr
435 440 445

Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp
450 455 460

Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu Leu
465 470 475 480

Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser Trp
485 490 495

Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile Ser
500 505 510

Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly
515 520 525

Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys
530 535 540

Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu
545 550 555 560

Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala
565 570 575

Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu
580 585 590

Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala Asp
595 600 605

357707_1.txt

Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr Tyr
610 615 620

Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu
625 630 635 640

Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn
645 650 655

Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg
660 665 670

Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His
675 680 685

Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
690 695 700

Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp Pro
705 710 715 720

Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala Phe
725 730 735

Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745

<210> 843
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding the trivalent molecule in seq ID NO: 844

<400> 843
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60

357707_1.txt

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tcctgtgcag cctctggatt ctccttcagt ggctatggca tgcactgggt ccgccaggct      120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat      180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg      300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatattctg gggccaaggg      360
acaatgggtca ccgtctcctc aggtgggtggc ggttcaggcg gaggtggctc tggaggtgga      420
ggttcaggag gtggtgggtc tggcggcggg ggatcgggtg gaggtggtag tgaggtgcag      480
ctgggtggagt ctgggggagg cttgggtccag ccgggggggt ccctgagact ctcctgtgca      540
gcctctggat tcacctttag tagccattgg atgacttggg tccgtcaggc tccagggaag      600
gggctggagt ggggtggcca cataaaggaa gacggaagtg agaaatacta tgaggactct      660
gtggagggcc gattcaccgt ctccagagac aacgccaaga actcgggtata tctgcaaatg      720
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ttggtacagc cggggggggtc cctgagactc tcctgtgcag cctctggatt cacctttagt     1020
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attagtgata gtggtagtag tgcagactac gcagattccg tgaagggacg gttcaccatc     1140
tccagagaca actccaagaa cacgctgtat cttcaaatga acagcctgag agctgaagac     1200
acggccgtgt attactgtgc gagaggccgg tataactgga acccccgagc tttgggtatc     1260
tggggccaag ggacaatggt caccgtctcc tca                                     1293

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<210> 844

<211> 431

<212> PRT

<213> Artificial Sequence

357707_1.txt

<220>

<223> trivalent molecule

<400> 844

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

357707_1.txt

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Trp Met Thr
180 185 190

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala His Ile
195 200 205

Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu Gly Arg
210 215 220

Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val Trp Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly
305 310 315 320

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
325 330 335

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
340 345 350

Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Ser Gly Ser Ser Ala
355 360 365

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Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
370 375 380

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
385 390 395 400

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Asn Trp Asn Pro Arg
405 410 415

Ala Leu Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
420 425 430

<210> 845
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding trivalent molecule of Seq ID NO: 846

<400> 845
gaggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt ctcttcagt ggctatggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg 300
gcctggggat tacgtttggg ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360
acaatgggtca ccgtctcctc aggtgggtggc ggttcaggcg gaggtggctc tggaggtgga 420
ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag 480
ctgggtggagt ctgggggagg cttgggtcaag cctggagggt ccctgagagt ctctgtgca 540
gcctctggat tcaccttcag tgactactac atgagctggt tccgccaggc tccagggaag 600
gggctggagt ggggtttcata cattagtgggt agtgggtgata tcatagacta cgcagactct 660

357707_1.txt

```

gtaaagggcc gattcaccat ctccagggaac aacgccaaga actctctgta tctgcagatg      720
aacaacctga gagccgagga cacggccgtg tatcactgtg cgagagaaga ttcccgtcta      780
actggaacta cggactttga caattggggc cagggaaccc tggtcaccgt ctctcaggt      840
ggtggcgggtt caggcggagg tggctctgga ggtggagggtt caggagggtg tggttctggc      900
ggcgggtggat cgggtggagg tggtagtcag gtgcagctgg tggagtctgg gggaggcttg      960
gtacagccgg ggggggtccct gagactctcc tgtgcagcct ctggattcac ctttagtagt     1020
tatgcatga gctgggtccg ccaggctcca gggaaggggc tggagtgggt cgcaactatt     1080
agtgatagtg gtagtagtgc agactacgca gattccgtga agggacgggt caccatctcc     1140
agagacaact ccaagaacac gctgtatctt caaatgaaca gcctgagagc tgaagacacg     1200
gccgtgtatt actgtgcgag aggccggtat aactggaacc cccgagcttt gggatatctgg     1260
ggccaaggga caatgggtcac cgtctcctca                                     1290

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<210> 846
 <211> 430
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent Molecule

<400> 846

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1           5           10           15

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
          20           25           30

```

```

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

```

```

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
          50           55           60

```

357707_1.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
165 170 175

Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
180 185 190

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile
195 200 205

Ser Gly Ser Gly Asp Ile Ile Asp Tyr Ala Asp Ser Val Lys Gly Arg
210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys Ala Arg Glu
245 250 255

357707_1.txt

Asp Ser Arg Leu Thr Gly Thr Thr Asp Phe Asp Asn Trp Gly Gln Gly
260 265 270

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
275 280 285

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
290 295 300

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
305 310 315 320

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
325 330 335

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
340 345 350

Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Ser Gly Ser Ser Ala Asp
355 360 365

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
370 375 380

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
385 390 395 400

Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Asn Trp Asn Pro Arg Ala
405 410 415

Leu Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
420 425 430

<210> 847
<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding trivalent molecule in Seq ID NO: 848

<400> 847

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gaggtgcagc tgttggagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt cagtttttagc agctatgccc tcagttgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac      180
gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat      240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatgggt      300
gtccactggg gccagggaac cctggtcacc gtctcctcag gtgggtggcgg ttcaggcggga      360
gggtggctctg gaggtggagg ttcaggagggt ggtggttctg gcggcggtgg atcgggtgga      420
gggtggtagtg aggtgcagct ggtggagtct gggggaggct tgggtccagcc ggggggggtcc      480
ctgagactct cctgtgcagc ctctggattc accttttagta gccattggat gacttggttc      540
cgtcaggctc cagggaaggg gctggagtgg gtggcccaca taaaggaaga cggaagtgag      600
aaatactatg aggactctgt ggagggccga ttcaccgtct ccagagacaa cgccaagaac      660
tcggtatatc tgcaaatgaa cagtctgaga gccgaagaca cggctgtgta ttactgtgcg      720
agaggagggtg atggctacag tgactcccac ttcgggtgtgg acgtctggggg ccaagggacc      780
acggtcactg tctcttcagg tgggtggcgg ttcaggcggag gtggctcttg aggtggagggt      840
tcaggagggtg gtggttcttg cggcggtgga tcgggtggag gtggtagtca ggtgcagctg      900
gtggagtctg ggggagggctt ggtacagccg ggggggtccc tgagactctc ctgtgcagcc      960
tctggattca cctttagtag ttatgccatg agctgggtcc gccaggctcc aggggaagggg     1020
ctggagtggg tcgcaactat tagtgatagt ggtagtagtg cagactacgc agattccgtg     1080
aagggaagggt tcaccatctc cagagacaac tccaagaaca cgctgtatct tcaaatgaac     1140
agcctgagag ctgaagacac ggccgtgtat tactgtgcga gaggccggta taactggaac     1200
ccccgagctt tgggtatctg gggccaaggg acaatggtca ccgtctcctc a               1251

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<210> 848
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent Molecule

<400> 848

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 130 135 140

357707_1.txt

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Trp
 165 170 175

Met Thr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
 180 185 190

His Ile Lys Glu Asp Gly Ser Glu Lys Tyr Tyr Glu Asp Ser Val Glu
 195 200 205

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu
 210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 225 230 235 240

Arg Gly Gly Asp Gly Tyr Ser Asp Ser His Phe Gly Val Asp Val Trp
 245 250 255

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly
 290 295 300

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 305 310 315 320

Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala
 325 330 335

357707_1.txt

Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Ser Gly Ser
 340 345 350

Ser Ala Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 355 360 365

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
 370 375 380

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Asn Trp Asn
 385 390 395 400

Pro Arg Ala Leu Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
 405 410 415

Ser

<210> 849
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 852

<400> 849

Asn Tyr Trp Met Asn
 1 5

<210> 850
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>

357707_1.txt

<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 852

<400> 850

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 851
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 852

<400> 851

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 852
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<223> VH binding to CD137

<400> 852

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

357707_1.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 853
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO:856

<400> 853

Asn Tyr Trp Met Asn
1 5

<210> 854
<211> 17
<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR2 OF SEQ ID NO: 856

<400> 854

Asn	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Arg	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1					5				10					15	

Gly

<210> 855

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(14)

<223> CDR3 OF SEQ ID NO: 856

<400> 855

Gly	Gly	Glu	Gly	Tyr	Gly	Val	Asp	His	Tyr	Gly	Leu	Asp	Val
1				5					10				

<210> 856

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 856

357707_1.txt

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 Thr Gly Phe Thr Leu Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 857
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 860

<400> 857

Asn Tyr Trp Met Asn
1 5

357707_1.txt

<210> 858
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 860

<400> 858

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 859
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 860

<400> 859

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 860
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)

<223> VH binding to CD137

<400> 860

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 Thr Gly Phe Thr Leu Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 861

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDR1 OF SEQ ID NO: 864

<400> 861

357707_1.txt

Asn Tyr Trp Met Asn
1 5

<210> 862
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 864

<400> 862

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 863
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 864

<400> 863

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 864
<211> 123
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 864

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 Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 865

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 868

<400> 865

Asn Tyr Trp Met Asn
 1 5

<210> 866
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 868

<400> 866

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 867
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 868

<400> 867

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 868

<211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 868

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 Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 869
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 872

<400> 869

Asn Tyr Trp Met Asn
 1 5

<210> 870
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 872

<400> 870

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 871
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 872

<400> 871

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val

1 5

10

<210> 872
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 872

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 Thr Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

357707_1.txt

<210> 873
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 876

<400> 873

Asn Tyr Trp Met Asn
1 5

<210> 874
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 876

<400> 874

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 875
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 876

357707_1.txt

<400> 875

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
1 5 10

<210> 876

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> VH binding to CD137

<400> 876

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 Leu Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 877
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 OF SEQ ID NO: 880

<400> 877

Asn Tyr Trp Met Asn
 1 5

<210> 878
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 OF SEQ ID NO: 880

<400> 878

Asn Ile Asn Gln Asp Glu Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 879
 <211> 14
 <212> PRT
 <213> Homo sapiens

357707_1.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR3 OF SEQ ID NO: 880

<400> 879

Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 1 5 10

<210> 880
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH binding to CD137

<400> 880

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 Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Glu Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

357707_1.txt

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 881
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 881
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 tcctgtgccg catctgggtt tacattaagt aactactgga tgaattgggt tcgtcaagcg 120
 cctggaaagg gcttagagtg ggtggctaataa accagg acgggtcaga gcgctactat 180
 gtggattcag taaaaggctc cttcactatc agccgcgata atgctaaaaa ttcgctgtac 240
 cttcagatgt catcacttcg tgcagaggat acagctgtgt atttctgcgc gcgtggaggc 300
 gaggggtacg gggtagacca ctatgggttg gatgtctcgg gacaaggcac gaccgtcact 360
 gtcagtagc 369

<210> 882
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 882
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 cctgggaagg ggtagagtg ggtcgccaac atcaaccaag acggttcgga gcgttactat 180
 gtcgacagcg tgaagggccg tttcacgata tcccgcgata acgctaagaa ctccctgtat 240
 ttgcaaatga atagccttcg tgcggaggat actgcgggtt atttctgtgc tcgtggcggt 300
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 gtgtcatcc 369

357707_1.txt

<210> 883
<211> 369
<212> DNA
<213> Homo sapiens

<400> 883
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ccagggaag gtctggaatg ggtagcgaat atcaaccaag acggctcaga acgtactac 180
gtggactccg taaaaggctc tttcaccatc tctcgtgaca atgctaaaaa ttctttgtat 240
ttgcaaatga gttcacttcg tgctgaggat actgcggctt attactgtgc tcgcgggggg 300
gaaggctacg gagtagacca ctacgggttg gatgtttctg gacagggaac gacgggttact 360
gtaagcagc 369

<210> 884
<211> 369
<212> DNA
<213> Homo sapiens

<400> 884
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ccaggtaaag gtttagaatg ggtcgctaac attaatacga atggttctga acgctattat 180
gtagactcgg taaagggtcg ttttacaatt tctcgcgaca acgcaaaaaa ctctttgtac 240
cttcaaatga attccttacg cgctgaggac actgctgtct atttctgtgc gcgtggaggg 300
gagggatacg gagttgacca ctatgggctg gacgtttcag gacagggcac tacggtaact 360
gtgtcttcg 369

<210> 885
<211> 369
<212> DNA
<213> Homo sapiens

357707_1.txt

<400> 885
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tcttgtgcag ccagcggttt cacattgtct aactattgga tgaattgggt tcgtcaagcg 120
cctggcaagg gactggagtg ggttgcaaac attaataag atggcagcga gcgttattac 180
gtggactcag taaaagggcg cttcacgatt agccgcgata atgctaagaa ctccttatat 240
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gagggatacg gcgtggatca ctatggtttg gacgtatcgg gccaaaggac taccgtgact 360
gtgtcctct 369

<210> 886
<211> 372
<212> DNA
<213> Homo sapiens

<400> 886
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ttatcctgtg ccgctacagg atttacgtta agcaactatt ggatgaactg ggtacgtcaa 120
gctccgggga aggggctgga atgggttgcc aatatcaatc aggatgggtc tgaacgctac 180
tacgttgatt ctgttaaggg tcgctttact atttcacgtg acaatgccaa gaacagtctt 240
taccttcaaa tgaactcgtt acgcgctgag gatactgctg tgtactactg tgcgcgcggc 300
ggagaggggat acggtgtcga tcattatggg cttgacgtaa gcgggcaggg tacgacgggtg 360
acggtatcat ca 372

<210> 887
<211> 369
<212> DNA
<213> Homo sapiens

<400> 887
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tcgtgcgccg cctcgggatt cacattatca aactactgga tgaattgggt ccgccaggct 120

357707_1.txt

ccgggcaaag gtcttgagtg ggtggcgaac attaatacagg acgggagcga gcgttattac 180
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ttacagatga actcacttcg tgctgaggac accgcagtgt actactgtgc tcgcggtggt 300
gaaggatacg gcgtcgatca ctacggcctt gatgtatcag gacaggggac tacagttacc 360
gtctcttcc 369

<210> 888
<211> 369
<212> DNA
<213> Homo sapiens

<400> 888
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tcttgcgccg cctctggggt tactctgtca aattattgga tgaactgggt gcgccaagct 120
cccggcaagg ggttggagtg ggttgccaac attaatacagg acgaatccga gcgttactat 180
gttgattctg taaaagggcg ctctactatc tctcgtgata atgctaagaa cagtttgtac 240
ctgcaaatga attcactgcg tgccgaggat accgcggtgt actattgtgc ccgtggagga 300
gagggatacg gggtcgatca ctatggctta gacgtatcgg gccaggggaa aaccgtcacc 360
gtatcctca 369

<210> 889
<211> 900
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding bivalent molecule of Seq ID NO: 890

<400> 889
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tcctgtgcag cctctggatt ctcttcagt ggctatggca tgactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

357707_1.txt

```

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg      300
gcctgggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg      360
acaatgggtca ccgtctcctc aggtgggtggc ggttcaggcg gaggtggctc tggaggtgga      420
ggttcaggag gtggtgggttc tggcggcggg ggatcgggtg gaggtggtag tgaggtgcag      480
ttagttgaga gcggaggtgg tttagttcag ccgggggggct cgcttcgcct gtcgtgcgcc      540
gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa      600
ggctctgagt ggggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg      660
gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg      720
aactcacttc gtgctgagga caccgcagtg tactactgtg ctgcgggtgg tgaaggatac      780
ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc      840
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<210> 890
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Bivalent Molecule

<400> 890

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

357707_1.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn
180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
195 200 205

Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Asp Ser Val Lys Gly Arg Phe
210 215 220

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
225 230 235 240

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly
245 250 255

357707_1.txt

Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln Gly
260 265 270

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
275 280 285

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295

<210> 891
<211> 858
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding bivalent molecule of seq ID NO.892

<400> 891
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tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180
gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
gtccactggg gccagggaac cctggtcacc gtctcctcag gtggtggcgg ttcaggcgga 360
ggtggctctg gaggtggagg ttcaggaggt ggtggttctg gcggcggtgg atcgggtgga 420
ggtggtagtg aggtgcagtt agttgagagc ggaggtggtt tagttcagcc ggggggctcg 480
cttcgcctgt cgtgcgccgc ctcgggattc acattatcaa actactggat gaattgggtc 540
cgccaggctc cgggcaaagg tcttgagtgg gtggcgaaca ttaatcagga cgggagcgag 600
cgttattacg ttgattcggg aaaaggacgt ttactatca gtcgtgacaa cgctaaaaat 660
tccttgact tacagatgaa ctacttcgt gctgaggaca ccgcagtgt ctactgtgct 720
cgcggtggtg aaggatacgg cgtcgatcac tacggccttg atgtatcagg acaggggact 780

acagttaccg tctcttccgg cggaggtggc tctggaggag gaggttcagg aggtggtgga 840
tctggcggcg gtggtagt 858

<210> 892
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Bivalent Molecule

<400> 892

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

357707_1.txt

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp
165 170 175

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
180 185 190

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser
245 250 255

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
275 280 285

<210> 893

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding trivalent molecule of seq ID NO. 894

357707_1.txt

<400> 893

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ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg	300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg	360
acaatggtca ccgtctctc aggtgggtggc gggtcaggcg gaggtggctc tggagggtga	420
gggtcaggag gtgggtggtc tggcggcggg ggatcgggtg gaggtggtag tgagggtgcag	480
ttagttgaga gcggagggtg tttagttcag ccggggggct cgcttcgcct gtcgtgcgcc	540
gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa	600
ggctctgagt ggggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg	660
gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg	720
aactcacttc gtgctgagga caccgcagtg tactactgtg ctgcgggtgg tgaaggatac	780
ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc	840
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ggaggagggtg gttctggagg cggtggctct gaagtacaac tggttgaatc ggggtgggtga	960
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cactatgcta tgcactgggt gagacaagcc cctggtaagg gcttggaatg ggtgtccgga	1080
atctcctgga atggtaacaa aataacatat gcagattccg ttaagggtag atttactatt	1140
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acagctcttt actattgtgt gcgtgactca tcgttggtca ttgtcggagc cccaactttc	1260
gaacattggg gtagaggtag cctagttacg gttagctcag gcggagggtg ctctggagga	1320
ggcggatcgg ggggtggagg aagtggcggc ggtggtagt	1359

357707_1.txt

<210> 894
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent molecule

<400> 894

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
 100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 145 150 155 160

480

357707_1.txt

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn
180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
195 200 205

Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys Gly Arg
210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
305 310 315 320

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
325 330 335

Phe Thr Phe His His Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly
340 345 350

357707_1.txt

Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Gly Asn Lys Ile
355 360 365

Thr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
370 375 380

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
385 390 395 400

Thr Ala Leu Tyr Tyr Cys Val Arg Asp Ser Ser Leu Phe Ile Val Gly
405 410 415

Ala Pro Thr Phe Glu His Trp Gly Arg Gly Thr Leu Val Thr Val Ser
420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
435 440 445

Gly Gly Gly Gly Ser
450

<210> 895
<211> 2634
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding trivalent molecule of Seq ID no. 896

<400> 895
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ccagggaagg ggctggagtg ggtttcaagt attggtgaga atgatggtac cacagactac 180
gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
ctacaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300

357707_1.txt

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gggtggctctg gaggtggagg ttcaggaggt ggtgggttctg gcggcggtgg atcgggtgga	420
gggtggtagtg aagtacaact ggttgaatcg ggtgggtggat tggccaacc tggaagatca	480
ttgaggcttt cttgtgcagc ttccggattc acctttcatc actatgctat gcactgggtg	540
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agtttatact tgcagatgaa ttccttgagg gctgaggata cagctcttta ctattgtgtg	720
cgtgactcat cgttgttcat tgtcggagcc ccaactttcg aacattgggg tagaggtagc	780
ctagttacgg ttagctcagg cggaggtggc tctggaggag gaggttcagg aggtgggtgga	840
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aaaggacgtt tcactatcag tcgtgacaac gctaaaaatt cttgtactt acagatgaac	1140
tcacttcgtg ctgaggacac cgagtgtagc tactgtgtc gcgggtggtag aggatacggc	1200
gtcgatcact acggccttga tgtatcagga caggggacta cagttaccgt ctcttcggc	1260
ggaggtggct ctggaggagg cggatcgggg ggtggaggaa gtggcggcgg tggtagttag	1320
gtgcagctgt tggagtctgg gggaggcttg gtacagcctg gggggtcct gagactctcc	1380
tgtgcagcct ctggattcag ttttagcagc tatgccctca gttgggtccg ccaggctcca	1440
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gacgccgtga agggccgatt caccatctcc agagacaatt ccaagaatac gctgtatcta	1560
caaatgaaca gcctgagagt cgaggacacg gccgtctatt actgtgtgaa agatgggtgc	1620
cactggggcc agggaaacct ggtcaccgtc tcctcagggt gtggcgggtt aggcggaggt	1680
ggctctggag gtggagggtt aggaggtggt ggttctggcg gcgggtggatc ggggtggaggt	1740

357707_1.txt

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 caagcccctg gtaagggctt ggaatgggtg tccggaatct cctggaatgg taacaaaata 1920
 acatatgcag attccgtaa gggtagattt actattagcc gtgataatgc aaaaaacagt 1980
 ttatacttgc agatgaattc cttgagggct gaggatacag ctctttacta ttgtgtgcgt 2040
 gactcatcgt tgttcattgt cggagcccca actttcgaac attggggtag aggtacccta 2100
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 ggaggaggcg gatcgggggg tggaggaaagt ggcggcgggt gtagtgaggt gcagttagtt 2220
 gagagcggag gtggtttagt tcagccgggg ggctcgcttc gcctgtcgtg cgccgcctcg 2280
 ggattcacat tatcaaacta ctggatgaat tgggtccgcc aggctccggg caaaggctctt 2340
 gagtgggtgg cgaacattaa tcaggacggg agcgagcgtt attacgttga ttcggtaaaa 2400
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 cttcgtgctg aggacaccgc agtgtactac tgtgctcgcg gtggtgaagg atacggcgtc 2520
 gatcactacg gccttgatgt atcaggacag gggactacag ttaccgtctc ttccggcgga 2580
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<210> 896
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent molecule

<400> 896

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

357707_1.txt

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His His Tyr Ala
165 170 175

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
180 185 190

Gly Ile Ser Trp Asn Gly Asn Lys Ile Thr Tyr Ala Asp Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
210 215 220

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Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Val
225 230 235 240

Arg Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His Trp
245 250 255

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
290 295 300

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
305 310 315 320

Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala
325 330 335

Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Ser
340 345 350

Glu Arg Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
355 360 365

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
370 375 380

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Glu Gly Tyr Gly
385 390 395 400

Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln Gly Thr Thr Val Thr
405 410 415

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Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 420 425 430

Gly Ser Gly Gly Gly Gly Ser
 435

<210> 897
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding trivalent molecule of seq ID no. 898

<400> 897
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 ccagggaagg ggctggagtg ggtttcaagt attggtgaga atgatggtag cacagactac 180
 gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctacaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggg 300
 gtccactggg gccagggaac cctggtcacc gtctcctcag gtgggtggcgg ttcaggcgga 360
 ggtggctctg gaggtggagg ttcaggagggt ggtgggttctg gcggcggtgg atcgggtgga 420
 ggtggtagtg aggtgcagtt agttgagagc ggaggtgggt tagttcagcc ggggggctcg 480
 cttgcctgt cgtgcgccgc ctcgggattc acattatcaa actactggat gaattgggtc 540
 cgccaggctc cgggcaaagg tcttgagtgg gtggcgaaca ttaatcagga cgggagcgag 600
 cgttattacg ttgattcggg aaaaggacgt ttcactatca gtcgtgacaa cgctaaaaat 660
 tccttgtagt tacagatgaa ctacttcgt gctgaggaca ccgcagtgt ctactgtgct 720
 cgcggtgggt aaggatacgg cgtcgatcac tacggccttg atgtatcagg acaggggact 780
 acagttaccg tctcttccgg cggaggtggc tctggaggag gcggatcggg ggggtggagga 840
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gttgaatcgg gtggtggatt ggtccaacct ggaagatcat tgaggctttc ttgtgcagct 960
 tccggattca cctttcatca ctatgctatg cactgggtga gacaagcccc tggtaagggc 1020
 ttggaatggg tgtccggaat ctcttggaat ggtaacaaaa taacatatgc agattccggt 1080
 aagggtagat ttactattag ccgtgataat gcaaaaaaca gtttatactt gcagatgaat 1140
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<210> 898
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent molecule

<400> 898

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

357707_1.txt

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp
165 170 175

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
180 185 190

Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser
245 250 255

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

357707_1.txt

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
290 295 300

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala
305 310 315 320

Ser Gly Phe Thr Phe His His Tyr Ala Met His Trp Val Arg Gln Ala
325 330 335

Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Gly Asn
340 345 350

Lys Ile Thr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
355 360 365

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
370 375 380

Glu Asp Thr Ala Leu Tyr Tyr Cys Val Arg Asp Ser Ser Leu Phe Ile
385 390 395 400

Val Gly Ala Pro Thr Phe Glu His Trp Gly Arg Gly Thr Leu Val Thr
405 410 415

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser
435

<210> 899

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding trivalent molecule of seq ID no. 900

<400> 899

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gaggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggct cctgagactc      60
tcctgtgcag cctctggatt ctccctcagt ggctatggca tgcactgggt ccgccaggct      120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat      180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg      300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg      360
acaatggtca ccgtctcctc aggtgggtggc gggtcaggcg gaggtggctc tggaggtgga      420
gggtcaggag gtgggtggtc tggcggcggg ggatcgggtg gaggtggtag tgaagtacaa      480
ctggttgaat cgggtgggtg attgggtcaa cctggaagat cattgaggct ttcttgtgca      540
gcttccggat tcacctttca tcactatgct atgcactggg tgagacaagc ccctggtaag      600
ggcttggaat ggggtgtccg aatctcctgg aatggtaaca aaataacata tgcagattcc      660
gttaagggtg gatttactat tagccgtgat aatgcaaaaa acagtttata cttgcagatg      720
aattccttga gggctgagga tacagctctt tactattgtg tgcgtgactc atcgttggtc      780
attgtcggag ccccaacttt cgaacattgg ggtagaggta ccctagttac ggtagctca      840
ggcggagggtg gctctggagg aggaggttca ggaggtgggt gatctggagg aggcggatcg      900
gggggtggag gaagtggcgg cgggtggtagt gaggtgcagt tagttgagag cggaggtggt      960
ttagttcagc cgggggggctc gcttcgcctg tcgtgcgccg cctcgggatt cacattatca     1020
aactactgga tgaattgggt ccgccaggct ccgggcaaag gtcttgagtg ggtggcgaac     1080
attaatcagg acgggagcga gcgttattac gttgattcgg taaaaggacg tttcactatc     1140
agtcgtgaca acgctaaaaa ttccttgtag ttacagatga actcacttcg tgctgaggac     1200
accgcagtgt actactgtgc tcgcggtggt gaaggatacg gcgtcgatca ctacggcctt     1260
gatgtatcag gacaggggac tacagttacc gtctcttccg gcggaggtgg ctctggagga     1320
ggcggatcgg ggggtggagg aagtggcggc ggtggtagt                                1359

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<210> 900
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Trivalent molecule

<400> 900

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
 100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

357707_1.txt

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His His Tyr Ala Met His
180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
195 200 205

Ser Trp Asn Gly Asn Lys Ile Thr Tyr Ala Asp Ser Val Lys Gly Arg
210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Val Arg Asp
245 250 255

Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His Trp Gly Arg
260 265 270

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
305 310 315 320

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
325 330 335

357707_1.txt

Phe Thr Leu Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly
340 345 350

Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg
355 360 365

Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
370 375 380

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
385 390 395 400

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp
405 410 415

His Tyr Gly Leu Asp Val Ser Gly Gln Gly Thr Thr Val Thr Val Ser
420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
435 440 445

Gly Gly Gly Gly Ser
450

<210> 901
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH that binds to HSA

<400> 901

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

357707_1.txt

Ser Leu Arg Ser Cys Ala Ala Ser Gly Phe Thr Phe His His Tyr Ala
20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
35 40 45

Gly Ile Ser Trp Asn Gly Asn Lys Ile Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Val
85 90 95

Arg Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 902
<211> 750
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(750)
<223> Nucleotide encoding VH that binds to HSA of Seq ID 901

<400> 902
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gcaatcgcaa tcgcagtcgc tctggcgggt ttcgcaactg tagcgcaagc cgaggtgcaa 180
ctggtcgagt ctggtggtgg tttggtgcaa cctggtagaa gcttgcgttt gagttgtgcc 240

357707_1.txt

gcttccggct tcactttcca tcattatgct atgcactggg ttcgtcaagc tcccggaaaa	300
ggtttggagt gggtttccgg aatttcctgg aatggcaata agattacgta cgctgattca	360
gtgaaaggaa ggtttacaat cagtagagat aatgctaaaa actcattgta tctacaaatg	420
aacagcctaa gagcagaaga taccgctctg tactactgtg ttagagatag ctcgttattc	480
attgtaggtg caccaacttt tgaacattgg ggtcggggta ctcttgtgac tgtctcatcc	540
gcggccgcac accaccatca tcaccactaa ctcgagcgcc taatgaaagc ttccccaagg	600
gcgacacccc ctaattagcc cgggcgaaag gccagtcctt tcgactgagc ctttcgtttt	660
atttgatgcc tggcagttcc ctactctcgc atggggagtc cccacactac catcggcgct	720
acggcgtttc acttctgagt tcggcatgga	750