SEQUENCE LISTING

<110> Crescendo Biologics Limited

<120> Single domain antibodies that bind to CD137

<130> P34656WO1

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

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

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

<160> 902

<170> PatentIn version 3.5

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Ser His Trp Met Thr
1 5

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1 5 10 15

Gly

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<400> 3

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

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<400> 4

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
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1               5


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<400> 6

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

Gly

<210> 7
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Gly Gly Asp Gly Tyr Ser Asp Ser His Tyr Gly Val Asp Val
1   5   10

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<400> 8

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
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Ser Tyr Trp Met Thr
1               5


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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

<210> 11
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<400> 11

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

<210> 12
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<400> 12

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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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<400>  13

Asn Tyr Trp Met Thr
1               5
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<210> 14
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<222> (1)..(17)
<223> CRD2 OF SEQ ID NO. 16

<400> 14

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

Gly

<210> 15
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<223> CDR3 OF SEQ ID NO.16

<400> 15

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

<210> 16
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<400> 16

```
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
        115                 120
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Asn Tyr Trp Met Ile
1 5

<210> 18
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<400> 18

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

<210> 20
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<400> 20

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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 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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<223> CDR 1 OF SEQ ID NO: 24

<400> 21

Ser Tyr Trp Met Ser
1 5

<210> 22
<211> 17
<212> PRT
<213> Homo sapiens

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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO:24

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

<220>
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<223> CDR3 OF SEQ ID NO:24

<400> 23

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

<210> 24
<211> 123
<212> PRT
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<223> VH that binds to CD137

<400> 24

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

<210> 25
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<400> 25

Ser Tyr Trp Met Leu
1 5

<210> 26
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 28

<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
<213> Homo sapiens

<220>
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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 28

<400> 27

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

<210> 28
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<212> PRT
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<220>
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<223> VH that binds to CD137

<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

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

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 32

<400> 29

Ser Tyr Trp Met Phe
1 5

<210> 30
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<212> PRT
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO:32

<400> 30

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

Gly

<210> 31
<211> 14
<212> PRT
<213> Homo sapiens

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

<223> CDR3 OF SEQ ID NO:32

<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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<222> (1)..(123)
<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

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

<210> 33
<211> 5
<212> PRT
<213> Homo sapiens

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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 36

<400> 33

Asn Tyr Trp Met Thr
1 5

<210> 34
<211> 17
<212> PRT
<213> Homo sapiens

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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 36

<400> 34

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

Gly

<210> 35
<211> 14
<212> PRT
<213> Homo sapiens

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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 36

<400> 35

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

<210> 36
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<212> PRT
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<223> VH that binds to CD137

<400> 36

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

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

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 40

<400> 37

Asp Tyr Trp Met Asn
1 5

<210> 38
<211> 17
<212> PRT
<213> Homo sapiens

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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 40

<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

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

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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 40

<400> 39

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

<210> 40
<211> 123
<212> PRT
<213> Homo sapiens

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<223> VH that binds CD137

<400> 40

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

```
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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<223>  CDR1 OF SEQ ID NO: 44

<400>  41

Asp Tyr Trp Met Asn
1               5


<210>  42
<211>  17
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<223>  CDR2 OF SEQ ID NO: 44

<400>  42

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


Gly
```

<210> 43
<211> 14
<212> PRT
<213> Homo sapiens

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

```
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


<210>  45
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<213>  Homo sapiens


<220>
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<400>  45

Ser Tyr Trp Met Leu
1               5


<210>  46
<211>  17
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<220>
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<223>  CDR2 OF SEQ ID NO: 48

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

<220>
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<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 48

<400> 47

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

<210> 48
<211> 123
<212> PRT
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<223> VH that binds to CD137

<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

```
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


<210>  49
<211>  5
<212>  PRT
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<400>  49

Ser Tyr Trp Met Phe
1               5


<210>  50
<211>  17
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<223>  CDR2 OF SEQ ID NO: 52
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<400> 50

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

Gly

<210> 51
<211> 14
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<223> CDR3 OF SEQ ID NO: 52

<400> 51

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

<210> 52
<211> 123
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<223> VH that binds to CD137

<400> 52

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

```
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


<210>  53
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<222>  (1)..(5)
<223>  CDR1 OF SEQ ID NO: 56

<400>  53

Asn Tyr Trp Met Asn
1               5


<210>  54
<211>  17
<212>  PRT
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<220>
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<223> CDR2 OF SEQ ID NO: 56

<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>
<221> MISC_FEATURE
<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

```
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
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<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

```
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>
<221> MISC_FEATURE

<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

<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

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

<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

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

<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

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

<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

```
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

```
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

```
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
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<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

```
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
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<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>
<221> MISC_FEATURE
<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

```
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
```

<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

```
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>
<221>  MISC_FEATURE
<222>  (1)..(5)
<223>  CDR1 OF SEQ ID NO: 112

<400>  109

Asn Tyr Trp Met Asn
1               5
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<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

<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

<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

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

<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

<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

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

<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

```
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

```
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

```
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
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<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

```
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
```

<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

```
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
```

<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

```
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
```

<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

<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<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

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

<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

<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

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

<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

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

```
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

```
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
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<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

```
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
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<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

```
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
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<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

```
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
```

<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

<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

<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
<212> PRT

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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

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

<400> 219

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

<210> 221
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<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>
<221> MISC_FEATURE
<222> (1)..(123)
<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

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>
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<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>
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<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>
<221> MISC_FEATURE
<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>
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<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

85 90 95

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

<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

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> 241
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 244

<400> 241

Asn Tyr Trp Met Asn
1 5

<210> 242
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 244

<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

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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE

<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>
<221> MISC_FEATURE
<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

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

<210> 257
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 260

<400> 257

Asn Tyr Trp Met Ile
1 5

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

<400> 260

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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 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
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<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

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

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

<400> 268

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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
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<210> 269
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

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

```
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

```
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>
<221> MISC_FEATURE
<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

```
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
```

<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

```
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
```

<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>
<221> MISC_FEATURE
<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

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

<400> 312

```
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
```

<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
```

<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

<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
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<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>
<221> MISC_FEATURE
<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
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<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
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<210> 329
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 332

<400> 329

Asn Tyr Trp Met Asn
1   5

<210> 330
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(123)
<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

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

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 336

<400> 333

Asn Tyr Trp Met Asn
1 5

<210> 334
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

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> 345
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<210> 347
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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

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> 349
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 352

<400> 349

Asn Tyr Trp Met Asn
1 5

<210> 350
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 352

<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 356

<400> 354

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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<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

<400> 368

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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


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
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<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

<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

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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


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
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<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDR3 OF SEQ ID NO: 384

<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>
<221> MISC_FEATURE
<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

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>
<221> MISC_FEATURE
<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>

<221> MISC_FEATURE
<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

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

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> 393
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<210> 395
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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

<220>
<221> MISC_FEATURE
<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

<220>
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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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<222> (1)..(14)
<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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<222> (1)..(123)
<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

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>
<221> MISC_FEATURE
<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

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

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

<400> 416

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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


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
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<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

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

<400> 424

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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


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
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<210> 425
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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

<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>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 436

<400> 433

Asp Tyr Tyr Met Ser
1 5

<210> 434
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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
<212> PRT
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

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> 441
<211> 5
<212> PRT
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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>
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<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

<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
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<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

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> 445
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 448

<400> 445

Asp Tyr Tyr Met Ser
1 5

<210> 446
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 448

<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>
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<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>
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<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>
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<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 452

<400> 450

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>
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<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>
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<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>
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<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>
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<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>
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<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
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<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>
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<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>
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<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>
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<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

<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

<400> 464

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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 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
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<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

<220>
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<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>
<221> MISC_FEATURE
<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

<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>
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<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

85 90 95

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

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 492

<400> 489

Asp Tyr Tyr Met Ser
1 5

<210> 490
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
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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

<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
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH binding to CD137

<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

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

<210> 493
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 496

<400> 493

Asp Tyr Tyr Met Ser
1 5

<210> 494
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 496

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

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<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
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<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

<210> 497
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<223> CDR1 OF SEQ ID NO: 500

<400> 497

Asp Tyr Tyr Met Ser
1 5

<210> 498
<211> 17
<212> PRT
<213> Homo sapiens

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<223> CDR2 OF SEQ ID NO: 500

<400> 498

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

Gly

<210> 499
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(13)
<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
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<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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<223> CDR1 OF SEQ ID NO: 504

<400> 501

Asp Tyr Tyr Met Ser
1 5

<210> 502
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<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>
<221> MISC_FEATURE
<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>
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<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
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<223> VH binding to CD137

<400> 508

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 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> 509
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<223> CDR1 OF SEQ ID NO: 512

<400> 509

Asp Tyr Tyr Met Ser
1 5

<210> 510
<211> 17
<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>
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<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
<211> 122
<212> PRT
<213> Homo sapiens

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<223> VH binding to CD137

<400> 512

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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 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
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<210> 513
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<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
<213> Homo sapiens

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

<220>
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<222> (1)..(13)
<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
<213> Homo sapiens

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

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<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>
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<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
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<212> PRT
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<220>
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<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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<222> (1)..(122)
<223> VH binding to CD137

<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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<223> CDR1 OF SEQ ID NO: 524

<400> 521

Asp Tyr Tyr Met Ser
1   5

<210> 522
<211> 17
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<213> Homo sapiens

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

<220>
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<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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<223> VH binding to CD137

<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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<212> PRT
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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
<211> 17
<212> PRT
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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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<223> CDR3 OF SEQ ID NO: 528

<400> 527

Glu Asp Ile Arg Met Pro Gly Thr Thr Asp Phe Asp Asn
1 5 10

<210> 528
<211> 122
<212> PRT
<213> Homo sapiens

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<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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<223> CDR1 OF SEQ ID NO: 532

<400> 529

Asp Tyr Tyr Met Thr
1 5

<210> 530
<211> 17
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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
<211> 13
<212> PRT
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<400> 531

Glu Asp Ile Arg Met Ser Gly Thr Thr Asp Phe Asp Tyr
1 5 10

<210> 532
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<212> PRT
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<223> VH binding to CD137

<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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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 536

<400> 533

Asp Tyr Tyr Met Ser
1 5

<210> 534
<211> 17
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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

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<223> CDR3 OF SEQ ID NO: 536

<400> 535

Glu Asp Pro Arg Leu Ser Gly Thr Ile Asp Phe Asp Ser
1 5 10

<210> 536
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<212> PRT
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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

85 90 95

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

<210> 537
<211> 5
<212> PRT
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<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 540

<400> 537

Asp Tyr Tyr Met Ser
1 5

<210> 538
<211> 17
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<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

<210> 539
<211> 13
<212> PRT
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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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<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

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> 541
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<223> CDR1 OF SEQ ID NO: 544

<400> 541

Asp Tyr Tyr Met Ser
1 5

<210> 542
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<212> PRT
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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
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<212> PRT
<213> Homo sapiens

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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
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<212> PRT
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<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

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<212> PRT
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<223> CDR1 OF SEQ ID NO: 548

<400> 545

Asp Tyr Tyr Met Thr
1 5

<210> 546
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<223> CDR2 OF SEQ ID NO: 548

<400> 546

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

Gly

<210> 547
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<212> PRT
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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
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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
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<212> PRT
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<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
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<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
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<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
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<212> PRT
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<223> CDR1 OF SEQ ID NO: 556

<400> 553

Asp Tyr Phe Met Ser
1 5

<210> 554
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<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 560

<400> 557

Asp Ser Tyr Met Ser
1 5

<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

<400> 560

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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
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<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

<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>
<221> MISC_FEATURE
<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

<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(122)
<223> VH binding to CD137

<400> 568

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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
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<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
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<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>
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<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>
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<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

85 90 95

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>
<221> MISC_FEATURE
<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

<210> 587
<211> 13
<212> PRT
<213> Homo sapiens

<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
<213> Homo sapiens

<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

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> 589
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 OF SEQ ID NO: 592

<400> 589

Asp Tyr Tyr Met Ser
1 5

<210> 590
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 592

<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
<213> Homo sapiens

<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>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR2 OF SEQ ID NO: 596

<400> 594

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
1   5   10   15

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
1   5   10

<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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

<210> 606
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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
1 5 10

<210> 608
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> VH binding to CD137

<400> 608

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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 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
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<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>
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<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

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<222> (1)..(5)
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc cgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agccattgga tgacttggtt 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 gccaagggac cacggtcact 360

gtctcttca 369

<210> 630
<211> 369
<212> DNA
<213> Homo sapiens

<400> 630
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc cgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgacttggtt ccgtcaggct 120

ccagggaagg ggctggagtg ggtggcccac ataaaggaag acggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaataa ctcgctgtat 240

ctacaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggaggt 300

gatggctaca gtgactccca ctacggtgtg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 631
<211> 369
<212> DNA
<213> Homo sapiens

<400> 631
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgacctggtt ccgccaggct 120

ccagggaggg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggggga 300

ttaggctacg gtgactccca ctacggtatg gacgtctggg gccaagggac cacggtcact 360

gtctcctca 369

<210> 632
<211> 369
<212> DNA
<213> Homo sapiens

<400> 632
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc cgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt aactattgga tgacctggtt ccgccaggct 120

ccagggggGG ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctcactgtat 240

ctacaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggggga 300

ttaggctacg gtgactccca ctacggtatg gacgtctggg gccaagggac cacggtcact 360

gtctcctca 369

<210> 633
<211> 369
<212> DNA
<213> Homo sapiens

<400> 633
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttagt aactattgga tgatctggtt ccgccaggct 120

ccaggaaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagaggaggt 300

gatggctaca gtggctccca ccacggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 634
<211> 369
<212> DNA
<213> Homo sapiens

<400> 634
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tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggg 300

gaaggctata gcacctcgca ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 635
<211> 369
<212> DNA
<213> Homo sapiens

<400> 635
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tcctgtggag cctctggatt cacctttagt agctattgga tgctctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acaccctgag agccgaggac acggctattt attattgtgc gagaggggt 300

gatggctaca gtgactccca cttcggtacg gacgtctggg gccaagggac cacggtcact 360

gtctcctca 369

<210> 636
<211> 369
<212> DNA
<213> Homo sapiens

<400> 636
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtggag cctctggatt cacctttagt agctattgga tgttctggtt ccgccaggct 120

ccaggagagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctctctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctattt attactgtgc gagaggaggt 300

gatggctaca gtgattccca ctacggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 637
<211> 369
<212> DNA
<213> Homo sapiens

<400> 637
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc cgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt aactattgga tgacctggtt ccgccaggct 120

ccaggggggg ggctggagtg ggtggccaac ataaaccaag atgggagtga gaagtactat 180

gtggactctg tggagggccg attcaccgtc tccagagaca acgccaagaa ctcactggat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggggga 300

ttaggctacg gtgactccca ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 638
<211> 369
<212> DNA
<213> Homo sapiens

<400> 638
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt gactattgga tgaactgggc ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaggagg atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccata tccagagaca acgccaagaa ctcaacgtat 240

ctgcaaatga acagcctgag agtcgaggac acggctgtgt attactgtgc gagaggaggg 300

gccgggtata gcatgtctca ctacggtatg gacgtctggg gccaagggac cacggtcact 360

gtctcttca 369

<210> 639
<211> 369
<212> DNA
<213> Homo sapiens

<400> 639
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgaag cctctggatt cacctttagt gactattgga tgaactgggc ccgccaggct 120

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 gccaagggac cacggtcact 360

gtctcctca 369

<210> 640
<211> 369

<212> DNA
<213> Homo sapiens

<400> 640
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tcctgtggag cctctggatt cacctttagt agctattgga tgctctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acaccctgcg agccgaggac acggctattt attattgtgc gagagggggt 300

gatggctaca gtaactccca cttcggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcttca 369

<210> 641
<211> 369
<212> DNA
<213> Homo sapiens

<400> 641
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctgggggtc cctgagactc 60

tcctgtggag cctctggatt cacctttagt agctattgga tgttctggtt ccgccaggct 120

ccaggagagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctctctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctattt attactgtgc gagaggaggt 300

gatggctaca gtgattccca ctacggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 642
<211> 369
<212> DNA
<213> Homo sapiens

<400> 642
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt aattattgga tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaggaag atggaagtga gaattactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagaggggag 300

gaaggctata gcacctcgca ctacggtatg gacgtctggg gccaagggac cacggtcact 360

gtctcctca 369

<210> 643
<211> 369
<212> DNA
<213> Homo sapiens

<400> 643
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtggag cctctggatt cacctttagt acctattgga tgctctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtct 240

ctacaaatga acagcctgag agccgaggac acggcaactt attactgtgc gagaggaggt 300

gatggctaca gtgactccca cttcggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 644
<211> 369
<212> DNA
<213> Homo sapiens

<400> 644
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttagt aactattgga tgatgtggtt ccgccaggct 120

ccaggaaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatacttt 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagaggaggt 300

gatggctaca gtagctctca ctacggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcttca 369

<210> 645
<211> 369
<212> DNA
<213> Homo sapiens

<400> 645
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaggaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggg 300

gacagctatg gttacaggga ctacggtatg gacgtctggg gccaagggac cacggtcact 360

gtctcctca 369

<210> 646
<211> 369
<212> DNA
<213> Homo sapiens

<400> 646
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt acccattgga tgaactgggc ccgccaggct 120

ccagggaagg agctggaatg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaacaa ttcactgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtat attactgtgc gagagggggg 300

gttggctacg gtgactccca cttcggtatg gacgtctggg gcctagggac cacggtcacc 360

gtctcctca 369

<210> 647
<211> 369
<212> DNA
<213> Homo sapiens

<400> 647
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgatctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaggaggt 300

gatgactaca gtaactccca ctacggtatg gacgtctcgg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 648
<211> 369
<212> DNA
<213> Homo sapiens

<400> 648
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgcagggccg attcaccatc tccagagaca atgccaataa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggg 300

tttggctacg gtgactccca ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 649
<211> 369
<212> DNA
<213> Homo sapiens

<400> 649
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtggag cctctggatt cacctttagt agttattgga tgttctggtt ccgccaggct 120

ccaggaaagg agctggagtg ggtggccaat gttaaccaag atggaagtga gaaatactat 180

gtggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctattt attactgtgc gagaggaggt 300

gagggctaca gtgattccca ctacggtacg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> 650
<211> 369
<212> DNA
<213> Homo sapiens

<400> 650
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gtctcctca 369

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<212> DNA
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gtctcctca 369

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<212> DNA
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gtctcctca 369

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<212> DNA
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<212> DNA
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gatggctaca gtgactccca cttcggtgtg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

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gatggctaca gtgactccca cttcggtgtg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

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gttggctaca gtatctccca cttcggtgtg gacgtctggg gccaagggac cacggtcacc 360

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gagggctaca gtatctccca cttcggtgtg gacgtctggg gccaagggac cacggtcacc 360

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ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

tcccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 781
<211> 366
<212> DNA
<213> Homo sapiens

<400> 781
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

tcccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 782
<211> 366
<212> DNA
<213> Homo sapiens

<400> 782
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

gcccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 783
<211> 366
<212> DNA
<213> Homo sapiens

<400> 783
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

ccccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 784
<211> 366

<212> DNA
<213> Homo sapiens

<400> 784
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

gcccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 785
<211> 366
<212> DNA
<213> Homo sapiens

<400> 785
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtggta gtggtgatat catagactac 180

gcagactctg taaagggccg attcaccatc tccagggaca acgccaagaa ctctctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaagat 300

ccccgtctaa ctggaactac ggactttgac aattggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 786
<211> 255
<212> PRT
<213> Homo sapiens

<400> 786

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu

```
1               5                   10                  15

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

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

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

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

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

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

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

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

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

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

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

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
```

195 200 205

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

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

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

<210> 787
<211> 768
<212> DNA
<213> Homo sapiens

<400> 787
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acaagatcat tgcaggatcc ttgtagtaac tgcccagctg gtacattctg tgataataac 120

aggaatcaga tttgcagtcc ctgtcctcca aatagtttct ccagcgcagg tggacaaagg 180

acctgtgaca tatgcaggca gtgtaaaggt gttttcagga ccaggaagga gtgttcctcc 240

accagcaatg cagagtgtga ctgcactcca gggtttcact gcctgggggc aggatgcagc 300

atgtgtgaac aggattgtaa acaaggtcaa gaactgacaa aaaaaggttg taaagactgt 360

tgctttggga catttaacga tcagaaacgt ggcatctgtc gaccctggac aaactgttct 420

ttggatggaa agtctgtgct tgtgaatggg acgaaggaga gggacgtggt ctgtggacca 480

tctccagccg acctctctcc gggagcatcc tctgtgaccc cgcctgcccc tgcgagagag 540

ccaggacact ctccgcagat catctccttc tttcttgcgc tgacgtcgac tgcgttgctc 600

ttcctgctgt tcttcctcac gctccgtttc tctgttgtta aacggggcag aaagaaactc 660

ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 720

tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgtga 768

<210> 788
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> Terminating residues of C- Terminal Domain of a VH domain

<400> 788

Val Thr Val Ser Ser
1 5

<210> 789
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Hexa-His Tag

<400> 789

His His His His His His
1 5

<210> 790
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<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
1 5 10

<210> 792
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 792

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

<210> 793
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 793

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

<210> 794
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 794

Gly Ser Gly Ser Gly Ser Gly Ser
1   5

<210> 795
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 795

Gly Gly Ser Gly Ser Gly Ser Gly
1   5

<210> 796
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 796

Gly Gly Ser Gly Ser Gly
1   5

<210> 797
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 797

Gly Gly Ser Gly
1

<210> 798

<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> Bivalent molecule

<400> 798

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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


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
```

```
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


<210>  799
<211>  828
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  DNA encoding Bivalent Molecule of SEQ ID NO: 798

<400>  799
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ggggggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagt agccattgga tgacttggtt 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 gccaagggac cacggtcact 360

gtctcttcag gtggtggcgg ttcaggcgga ggtggctctg gaggtggagg ttcaggaggt 420

ggtggttctg gcggcggtgg atcgggtgga ggtggtagtg aggtgcagct ggtggagtct 480

gggggaggct tggtccagcc gggggggtcc ctgagactct cctgtgcagc ctctggattc 540

acctttagta gccattggat gacttggttc cgtcaggctc cagggaaggg gctggagtgg 600

gtggcccaca taaaggaaga cggaagtgag aaatactatg aggactctgt ggagggccga 660

ttcaccgtct ccagagacaa cgccaagaac tcggtatatc tgcaaatgaa cagtctgaga 720

gccgaagaca cggctgtgta ttactgtgcg agaggaggtg atggctacag tgactcccac 780

ttcggtgtgg acgtctgggg ccaagggacc acggtcactg tctcttca 828

<210> 800
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Bivalent Molecule

<400> 800

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 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
```

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
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagagtc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac 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

tcctcaggtg gtggcggttc aggcggaggt ggctctggag gtggaggttc aggaggtggt 420

ggttctggcg gcggtggatc gggtggaggt ggtagtgagg tgcagctggt ggagtctggg 480

ggaggcttgg tcaagcctgg agggtccctg agagtctcct gtgcagcctc tggattcacc 540

ttcagtgact actacatgag ctggttccgc caggctccag ggaaggggct ggagtgggtt 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 ca 822

<210> 802

<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> Trivalent molecule

<400> 802

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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


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
```

```
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
```

```
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 tggtggagtc tgggggaggc ttggtccagc ggggggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagt agccattgga tgacttggtt 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 gccaagggac cacggtcact      360

gtctcttcag gtggtggcgg ttcaggcgga ggtggctctg gaggtggagg ttcaggaggt      420

ggtggttctg gcggcggtgg atcgggtgga ggtggtagtg aggtgcagct ggtggagtct      480

gggggaggct tggtccagcc gggggggtcc ctgagactct cctgtgcagc ctctggattc      540
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acctttagta gccattggat gacttggttc cgtcaggctc cagggaaggg gctggagtgg 600

gtggcccaca taaaggaaga cggaagtgag aaatactatg aggactctgt ggagggccga 660

ttcaccgtct ccagagacaa cgccaagaac tcggtatatc tgcaaatgaa cagtctgaga 720

gccgaagaca cggctgtgta ttactgtgcg agaggaggtg atggctacag tgactcccac 780

ttcggtgtgg acgtctgggg ccaagggacc acggtcactg tctcttcagg tggtggcggt 840

tcaggcggag gtggctctgg aggtggaggt tcaggaggtg gtggttctgg cggcggtgga 900

tcgggtggag gtggtagtga ggtgcagctg gtggagtctg ggggaggctt ggtccagccg 960

gggggtccc tgagactctc ctgtgcagcc tctggattca cctttagtag ccattggatg 1020

acttggttcc gtcaggctcc agggaagggg ctggagtggg tggcccacat aaaggaagac 1080

ggaagtgaga aatactatga ggactctgtg gagggccgat tcaccgtctc cagagacaac 1140

gccaagaact 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

```
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
```

```
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
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<210> 805
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding trivalent molecule of seq ID No: 804

<400> 805
gaggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagagtc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac 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

tcctcaggtg gtggcggttc aggcggaggt ggctctggag gtggaggttc aggaggtggt 420

ggttctggcg gcggtggatc gggtggaggt ggtagtgagg tgcagctggt ggagtctggg 480

ggaggcttgg tcaagcctgg agggtccctg agagtctcct gtgcagcctc tggattcacc 540

ttcagtgact actacatgag ctggttccgc caggctccag ggaaggggct ggagtgggtt 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 caggtggtgg cggttcaggc 840

ggaggtggct ctggaggtgg aggttcagga ggtggtggtt ctggcggcgg tggatcgggt 900

ggaggtggta gtgaggtgca gctggtggag tctgggggag gcttggtcaa gcctggaggg 960

tccctgagag tctcctgtgc agcctctgga ttcaccttca gtgactacta catgagctgg 1020

ttccgccagg ctccagggaa ggggctggag tgggtttcat acattagtgg tagtggtgat 1080

atcatagact acgcagactc tgtaaagggc cgattcacca tctccaggga caacgccaag 1140

aactctctgt atctgcagat gaacaacctg agagccgagg acacggccgt gtatcactgt 1200

gcgagagaag attcccgtct 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

```
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

<400> 807
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga 420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag 480

ctggtggagt ctgggggagg cttggtccag ccgggggggt ccctgagact ctcctgtgca 540

gcctctggat tcacctttag tagccattgg atgacttggt tccgtcaggc tccagggaag 600

gggctggagt gggtggccca cataaaggaa gacggaagtg agaaatacta tgaggactct 660

gtggagggcc gattcaccgt ctccagagac aacgccaaga actcggtata 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

```
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
```

```
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 tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg      360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga      420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag      480

ctggtggagt ctgggggagg cttggtcaag cctggagggt ccctgagagt ctcctgtgca      540

gcctctggat tcaccttcag tgactactac atgagctggt tccgccaggc tccagggaag      600

gggctggagt gggtttcata cattagtggt agtggtgata tcatagacta cgcagactct      660
```

gtaaagggcc gattcaccat ctccagggac aacgccaaga actctctgta tctgcagatg 720

aacaacctga gagccgagga cacggccgtg tatcactgtg cgagagaaga ttcccgtcta 780

actggaacta cggactttga caattggggc cagggaaccc tggtcaccgt ctcctca 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

```
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 ctgggggtc cctgagactc 60

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 tggtccagcc gggggggtcc 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

```
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
```

```
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

<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

```
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
```

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

<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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cagttttagc agctatgcca tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

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

<212> DNA
<213> Homo sapiens

<400> 829
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc 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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

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

<213> Homo sapiens

<400> 834
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

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 ctgggggGTC 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 ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180

gcagccaccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240

ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300

gtccactggg gccagggaac cctggtcacc 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

<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

```
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
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

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 ggagtcatcg tcctatgatt ttgatatctg 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
```

```
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
```

```
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
```

```
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
```

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 trvialent molecule in seq ID NO: 844

<400> 843
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga 420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag 480

ctggtggagt ctgggggagg cttggtccag ccgggggggt ccctgagact ctcctgtgca 540

gcctctggat tcacctttag tagccattgg atgacttggt tccgtcaggc tccagggaag 600

gggctggagt gggtggccca cataaaggaa gacggaagtg agaaatacta tgaggactct 660

gtggagggcc gattcaccgt ctccagagac aacgccaaga actcggtata tctgcaaatg 720

aacagtctga gagccgaaga cacggctgtg tattactgtg cgagaggagg tgatggctac 780

agtgactccc acttcggtgt ggacgtctgg ggccaaggga ccacggtcac tgtctcttca 840

ggtggtggcg gttcaggcgg aggtggctct ggaggtggag gttcaggagg tggtggttct 900

ggcggcggtg gatcgggtgg aggtggtagt caggtgcagc tggtggagtc tgggggaggc 960

ttggtacagc cgggggggtc cctgagactc tcctgtgcag cctctggatt cacctttagt 1020

agttatgcca tgagctgggt ccgccaggct ccagggaagg ggctggagtg ggtcgcaact 1080

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

<210> 844
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> trivalent molecule

<400> 844

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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


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 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
```

```
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

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gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg      360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga      420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag      480

ctggtggagt ctgggggagg cttggtcaag cctggagggt ccctgagagt ctcctgtgca      540

gcctctggat tcaccttcag tgactactac atgagctggt tccgccaggc tccagggaag      600

gggctggagt gggtttcata cattagtggt agtggtgata tcatagacta cgcagactct      660
```

gtaaagggcc gattcaccat ctccagggac aacgccaaga actctctgta tctgcagatg 720

aacaacctga gagccgagga cacggccgtg tatcactgtg cgagagaaga ttcccgtcta 780

actggaacta cggactttga caattggggc cagggaaccc tggtcaccgt ctcctcaggt 840

ggtggcggtt caggcggagg tggctctgga ggtggaggtt caggaggtgg tggttctggc 900

ggcggtggat cgggtggagg tggtagtcag gtgcagctgg tggagtctgg gggaggcttg 960

gtacagccgg gggggtccct gagactctcc tgtgcagcct ctggattcac ctttagtagt 1020

tatgccatga gctgggtccg ccaggctcca gggaaggggc tggagtgggt cgcaactatt 1080

agtgatagtg gtagtagtgc agactacgca gattccgtga agggacggtt caccatctcc 1140

agagacaact ccaagaacac gctgtatctt caaatgaaca gcctgagagc tgaagacacg 1200

gccgtgtatt actgtgcgag aggccggtat aactggaacc cccgagcttt gggtatctgg 1260

ggccaaggga caatggtcac cgtctcctca 1290

<210> 846
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Trivalent Molecule

<400> 846

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

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
```

```
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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

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 tggtccagcc gggggggtcc 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 tctcttcagg tggtggcggt tcaggcggag gtggctctgg aggtggaggt 840

tcaggaggtg gtggttctgg cggcggtgga tcgggtggag gtggtagtca ggtgcagctg 900

gtggagtctg ggggaggctt ggtacagccg ggggggtccc tgagactctc ctgtgcagcc 960

tctggattca cctttagtag ttatgccatg agctgggtcc gccaggctcc agggaagggg 1020

ctggagtggg tcgcaactat tagtgatagt ggtagtagtg cagactacgc agattccgtg 1080

aagggacggt tcaccatctc cagagacaac tccaagaaca cgctgtatct tcaaatgaac 1140

agcctgagag ctgaagacac ggccgtgtat tactgtgcga gaggccggta taactggaac 1200

ccccgagctt tgggtatctg gggccaaggg acaatggtca ccgtctcctc a 1251

<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
```

```
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
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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>

<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

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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
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<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

```
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
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<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
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<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

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

<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

<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

<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

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
gaggtgcaat tagtcgaatc ggggggtgga ctggttcagc cgggaggtag cctgcgcctg 60

tcctgtgccg catctggttt tacattaagt aactactgga tgaattgggt tcgtcaagcg 120

cctggaaagg gcttagagtg ggtggctaat attaaccagg acgggtcaga gcgctactat 180

gtggattcag taaaaggtcg 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
gaggtccagt tggttgagtc cggcggcggc ttggtccaac cagggggtc gcttcgctta 60

tcttgcgctg ccacagggtt taccctgagc aactactgga tgaactgggt gcgccaagcg 120

cctgggaagg ggttagagtg ggtcgccaac atcaaccaag acggttcgga gcgttactat 180

gtcgacagcg tgaagggccg tttcacgatc tcccgcgata acgctaagaa ctccctgtat 240

ttgcaaatga atagccttcg tgcggaggat actgcggttt atttctgtgc tcgtggcggt 300

gaaggatatg gggttgacca ttatgggttg gatgtctccg ggcaagggac aacggtgacc 360

gtgtcatcc 369

<210> 883
<211> 369
<212> DNA
<213> Homo sapiens

<400> 883
gaggttcaac ttgttgaatc gggtggcgga ttagtacaac ccggcggctc gctgcgttta 60

tcgtgtgcgg caaccggatt tactttatca aactattgga tgaattgggt gcgccaggct 120

ccagggaaag gtctggaatg ggtagcgaat atcaaccaag acggctcaga acgctactac 180

gtggactccg taaaaggtcg tttcaccatc tctcgtgaca atgctaaaaa ttctttgtat 240

ttgcaaatga gttcacttcg tgctgaggat actgcggtct attactgtgc tcgcgggggg 300

gaaggctacg gagtagacca ctacgggttg gatgtttctg gacagggaac gacggttact 360

gtaagcagc 369

<210> 884
<211> 369
<212> DNA
<213> Homo sapiens

<400> 884
gaggttcagt tagttgagtc cggcgggga ttagttcaac ctggcggaag ccttcgtctg 60

agttgtgccg cgagcgggtt tacccttagc aattactgga tgaactgggt acgtcaagct 120

ccaggtaaag gtttagaatg ggtcgctaac attaatcaag atggttctga acgctattat 180

gtagactcgg taaagggtcg ttttacaatt tctcgcgaca acgccaaaaa 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

<400> 885
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tcttgtgcag ccagcggttt cacattgtct aactattgga tgaattgggt tcgtcaagcg 120

cctggcaagg gactggagtg ggttgcaaac attaatcaag atggcagcga gcgttattac 180

gtggactcag taaaagggcg cttcacgatt agccgcgata atgctaagaa ctccttatat 240

ctgcagatgt catctttgcg tgccgaggac acggcagttt actattgcgc acgtggtggc 300

gagggatacg gcgtggatca ctatggtttg gacgtatcgg gccaagggac 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

ggagagggat acggtgtcga tcattatggg cttgacgtaa gcgggcaggg tacgacggtg 360

acggtatcat ca 372

<210> 887
<211> 369
<212> DNA
<213> Homo sapiens

<400> 887
gaggtgcagt tagttgagag cggaggtggt ttagttcagc cgggggggctc gcttcgcctg 60

tcgtgcgccg cctcgggatt cacattatca aactactgga tgaattgggt ccgccaggct 120

ccgggcaaag gtcttgagtg ggtggcgaac attaatcagg acgggagcga gcgttattac 180

gttgattcgg taaaaggacg tttcactatc agtcgtgaca acgctaaaaa ttccttgtac 240

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
gaggtgcagt tggtagagag tgggggtggc ctggtccaac caggtgggtc ccttcgtttg 60

tcttgcgccg cctctgggtt tactctgtca aattattgga tgaactgggt gcgccaagct 120

cccggcaagg ggttggagtg ggttgccaac attaatcagg acgaatccga gcgttactat 180

gttgattctg taaaagggcg cttcactatc tctcgtgata atgctaagaa cagtttgtac 240

ctgcaaatga attcactgcg tgccgaggat accgcggtgt actattgtgc ccgtggagga 300

gagggatacg gggtcgatca ctatggctta gacgtatcgg gccagggaac 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 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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga 420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag 480

ttagttgaga gcggaggtgg tttagttcag ccgggggggct cgcttcgcct gtcgtgcgcc 540

gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa 600

ggtcttgagt gggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg 660

gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg 720

aactcacttc gtgctgagga caccgcagtg tactactgtg ctcgcggtgg tgaaggatac 780

ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc 840

ggcggaggtg gctctggagg aggaggttca ggaggtggtg gatctggcgg cggtggtagt 900

<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

```
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
```

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

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 ttgattcggt aaaaggacgt ttcactatca gtcgtgacaa cgctaaaaat 660

tccttgtact tacagatgaa ctcacttcgt gctgaggaca ccgcagtgta 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

```
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

<400> 893

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga 420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag 480

ttagttgaga gcggaggtgg tttagttcag ccgggggggct cgcttcgcct gtcgtgcgcc 540

gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa 600

ggtcttgagt gggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg 660

gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg 720

aactcacttc gtgctgagga caccgcagtg tactactgtg ctcgcggtgg tgaaggatac 780

ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc 840

ggcggaggtg gctctggagg aggcggatcg gggggtggag gaagtggcgg cggtggtagt 900

ggaggaggtg gttctggagg cggtggctct gaagtacaac tggttgaatc gggtggtgga 960

ttggtccaac ctggaagatc attgaggctt tcttgtgcag cttccggatt cacctttcat 1020

cactatgcta tgcactgggt gagacaagcc cctggtaagg gcttggaatg ggtgtccgga 1080

atctcctgga atggtaacaa aataacatat gcagattccg ttaagggtag atttactatt 1140

agccgtgata atgcaaaaaa cagtttatac ttgcagatga attccttgag ggctgaggat 1200

acagctcttt actattgtgt gcgtgactca tcgttgttca ttgtcggagc cccaactttc 1260

gaacattggg gtagaggtac cctagttacg gttagctcag gcggaggtgg ctctggagga 1320

ggcggatcgg ggggtggagg aagtggcggc ggtggtagt 1359

<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
```

```
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
```

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcaagt attggtgaga atgatggtac cacagactac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240

ctacaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300

gtccactggg gccagggaac cctggtcacc gtctcctcag gtggtggcgg ttcaggcgga 360

ggtggctctg gaggtggagg ttcaggaggt ggtggttctg gcggcggtgg atcgggtgga 420

ggtggtagtg aagtacaact ggttgaatcg ggtggtggat tggtccaacc tggaagatca 480

ttgaggcttt cttgtgcagc ttccggattc acctttcatc actatgctat gcactgggtg 540

agacaagccc ctggtaaggg cttggaatgg gtgtccggaa tctcctggaa tggtaacaaa 600

ataacatatg cagattccgt taagggtaga tttactatta gccgtgataa tgcaaaaaac 660

agtttatact tgcagatgaa ttccttgagg gctgaggata cagctcttta ctattgtgtg 720

cgtgactcat cgttgttcat tgtcggagcc ccaactttcg aacattgggg tagaggtacc 780

ctagttacgg ttagctcagg cggaggtggc tctggaggag gaggttcagg aggtggtgga 840

tctggaggag gcggatcggg gggtggagga agtggcggcg gtggtagtga ggtgcagtta 900

gttgagagcg gaggtggttt agttcagccg gggggctcgc ttcgcctgtc gtgcgccgcc 960

tcgggattca cattatcaaa ctactggatg aattgggtcc gccaggctcc gggcaaaggt 1020

cttgagtggg tggcgaacat taatcaggac gggagcgagc gttattacgt tgattcggta 1080

aaaggacgtt tcactatcag tcgtgacaac gctaaaaatt ccttgtactt acagatgaac 1140

tcacttcgtg ctgaggacac cgcagtgtac tactgtgctc gcggtggtga aggatacggc 1200

gtcgatcact acggccttga tgtatcagga caggggacta cagttaccgt ctcttccggc 1260

ggaggtggct ctggaggagg cggatcgggg ggtggaggaa gtggcggcgg tggtagtgag 1320

gtgcagctgt tggagtctgg gggaggcttg gtacagcctg gggggtccct gagactctcc 1380

tgtgcagcct ctggattcag ttttagcagc tatgccctca gttgggtccg ccaggctcca 1440

gggaaggggc tggagtgggt ttcaagtatt ggtgagaatg atggtaccac agactacgca 1500

gacgccgtga agggccgatt caccatctcc agagacaatt ccaagaatac gctgtatcta 1560

caaatgaaca gcctgagagt cgaggacacg gccgtctatt actgtgtgaa agatggtgtc 1620

cactggggcc agggaaccct ggtcaccgtc tcctcaggtg gtggcggttc aggcggaggt 1680

ggctctggag gtggaggttc aggaggtggt ggttctggcg gcggtggatc gggtggaggt 1740

ggtagtgaag tacaactggt tgaatcgggt ggtggattgg tccaacctgg aagatcattg 1800

aggctttctt gtgcagcttc cggattcacc tttcatcact atgctatgca ctgggtgaga 1860

caagcccctg gtaagggctt ggaatgggtg tccggaatct cctggaatgg taacaaaata 1920

acatatgcag attccgttaa gggtagattt actattagcc gtgataatgc aaaaaacagt 1980

ttatacttgc agatgaattc cttgagggct gaggatacag ctctttacta ttgtgtgcgt 2040

gactcatcgt tgttcattgt cggagcccca actttcgaac attggggtag aggtacccta 2100

gttacggtta gctcaggcgg aggtggctct ggaggaggag gttcaggagg tggtggatct 2160

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ggattcacat tatcaaacta ctggatgaat tgggtccgcc aggctccggg caaaggtctt 2340

gagtgggtgg cgaacattaa tcaggacggg agcgagcgtt attacgttga ttcggtaaaa 2400

ggacgtttca ctatcagtcg tgacaacgct aaaaattcct tgtacttaca gatgaactca 2460

cttcgtgctg aggacaccgc agtgtactac tgtgctcgcg gtggtgaagg atacggcgtc 2520

gatcactacg gccttgatgt atcaggacag gggactacag ttaccgtctc ttccggcgga 2580

ggtggctctg gaggaggcgg atcgggggt ggaggaagtg gcggcggtgg tagt 2634

<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

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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
```

```
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
```

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cagttttagc agctatgccc tcagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcaagt attggtgaga atgatggtac cacagactac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240

ctacaaatga 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 ttgattcggt aaaaggacgt ttcactatca gtcgtgacaa cgctaaaaat 660

tccttgtact tacagatgaa ctcacttcgt gctgaggaca ccgcagtgta ctactgtgct 720

cgcggtggtg aaggatacgg cgtcgatcac tacggccttg atgtatcagg acaggggact 780

acagttaccg tctcttccgg cggaggtggc tctggaggag gcggatcggg gggtggagga 840

agtggcggcg gtggtagtgg aggaggtggt tctggaggcg gtggctctga agtacaactg 900

gttgaatcgg gtggtggatt ggtccaacct ggaagatcat tgaggctttc ttgtgcagct 960

tccggattca cctttcatca ctatgctatg cactgggtga gacaagcccc tggtaagggc 1020

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aagggtagat ttactattag ccgtgataat gcaaaaaaca gtttatactt gcagatgaat 1140

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gtcggagccc caactttcga acattggggt agaggtaccc tagttacggt tagctcaggc 1260

ggaggtggct ctggaggagg cggatcgggg ggtggaggaa gtggcggcgg tggtagt 1317

<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

```
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
```

```
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
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

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 ggagtcatcg tcctatgatt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcctc aggtggtggc ggttcaggcg gaggtggctc tggaggtgga 420

ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaagtacaa 480

ctggttgaat cgggtggtgg attggtccaa cctggaagat cattgaggct ttcttgtgca 540

gcttccggat tcacctttca tcactatgct atgcactggg tgagacaagc ccctggtaag 600

ggcttggaat gggtgtccgg aatctcctgg aatggtaaca aaataacata tgcagattcc 660

gttaagggta gatttactat tagccgtgat aatgcaaaaa acagtttata cttgcagatg 720

aattccttga gggctgagga tacagctctt tactattgtg tgcgtgactc atcgttgttc 780

attgtcggag ccccaacttt cgaacattgg ggtagaggta ccctagttac ggttagctca 840

ggcggaggtg gctctggagg aggaggttca ggaggtggtg gatctggagg aggcggatcg 900

gggggtggag gaagtggcgg cggtggtagt gaggtgcagt tagttgagag cggaggtggt 960

ttagttcagc cgggggggctc gcttcgcctg tcgtgcgccg cctcgggatt cacattatca 1020

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<220>
<223> Trivalent molecule

<400> 900

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
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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
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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
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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
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Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
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Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Val Arg Asp
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Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His Trp Gly Arg
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Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
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Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
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Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
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Phe Thr Leu Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly
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Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg
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Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
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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
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His Tyr Gly Leu Asp Val Ser Gly Gln Gly Thr Thr Val Thr Val Ser
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Gly Gly Gly Gly Ser
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<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
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<222>  (1)..(122)
<223>  VH that binds to HSA

<400>  901

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1               5                   10                  15
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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
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<220>
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gcaatcgcaa tcgcagtcgc tctggcgggt ttcgcaactg tagcgcaagc cgaggtgcaa      180

ctggtcgagt ctggtggtgg tttggtgcaa cctggtagaa gcttgcgttt gagttgtgcc      240
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aacagcctaa gagcagaaga taccgctctg tactactgtg ttagagatag ctcgttattc 480

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