

SEQUENCE LISTING

<110> NANJING LEGEND BIOTECH CO., LTD.
<120> CD19 BINDING MOLECULES AND USES THEREOF
<130> 14651-025-228
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<150> PCT/CN2020/102457
<151> 2020-07-16
<160> 114
<170> PatentIn version 3.5
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<223> CDR1 of VHH-083 (IMGT) or VHH-131 (IMGT)
<400> 1

Gly Asn Ile Asn Ser Arg Asn Cys
1 5

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<400> 2

Gly Asp Thr Leu Ser Asn Lys Trp
1 5

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<223> CDR1 of 77LICA542 (IMGT)

<400> 3

Gly Tyr Thr Tyr Ser Ser Gly Cys
1 5

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<220>

<223> CDR1 of 77LICA519 (IMGT)

<400> 4

Gly Leu Pro Tyr Thr Gly Tyr Cys
1 5

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<223> CDR1 of 77LICA602 (IMGT)

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Gly Tyr Thr Ser Ser Tyr Ala Tyr
1 5

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<223> CDR1 of LIC1157 (IMGT)

<400> 6

Gly Phe Thr Phe Ser Asp Ala Val
1 5

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<223> CDR1 of LIC1159 (IMGT)

<400> 7

Gly Arg Thr Phe Ser Ser Leu Ala
1 5

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<223> CDR2 of VHH-083 (IMGT) or VHH-131 (IMGT)

<400> 8

Ile Gly Gln Val Thr Gly Arg Ser
1 5

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<220>

<223> CDR2 of VHH-111 (IMGT)

<400> 9

Ile Arg Thr Asp His Ala Gly Thr
1 5

<210> 10

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<220>

<223> CDR2 of 77LICA542 (IMGT)

<400> 10

Ile Asp Ser Asp Gly Met Thr
1 5

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<220>
<223> CDR2 of 77LICA519 (IMGT)

<400> 11

Ile Ser Thr Gly Ser Gly Gly Thr
1 5

<210> 12
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<220>
<223> CDR2 of 77LICA602 (IMGT)

<400> 12

Ile Gly Ser Asn Gly Arg Thr
1 5

<210> 13
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<220>
<223> CDR2 of LIC1157 (IMGT)

<400> 13

Ile Ser Asn Gly Gly Ile Thr Arg
1 5

<210> 14
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<220>
<223> CDR2 of LIC1159 (IMGT)

<400> 14

Ile Ser Trp Ser Gly Gly Ser Ile
1 5

<210> 15
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<220>
<223> CDR3 of VHH-083 (IMGT) or VHH-131 (IMGT)

<400> 15

Ala Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
1 5 10 15

Arg Asn

<210> 16
<211> 12
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<220>
<223> CDR3 of VHH-111 (IMGT)

<400> 16

Ala Ala Ser Tyr Ser Gly Ala Thr Thr Phe Arg Tyr
1 5 10

<210> 17
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<220>
<223> CDR3 of 77LICA542 (IMGT)

<400> 17

Ala Ala Asp Pro Asp Cys Tyr Tyr Ser Asp Tyr Ala Ile Ser Pro Ala
1 5 10 15

Phe Gly Tyr

<210> 18
<211> 19
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<213> Artificial Sequence

<220>

<223> CDR3 of 77LICA519 (IMGT)

<400> 18

Ala Ala Gly Leu Arg Leu Pro Gly Arg Ala Cys Thr Thr Ser His Lys
1 5 10 15

Tyr Asn Tyr

<210> 19

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of 77LICA602 (IMGT)

<400> 19

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

Tyr Asn Asn

<210> 20

<211> 9

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<220>

<223> CDR3 of LIC1157 (IMGT)

<400> 20

Ala Lys Arg Ala Pro Gly Asp Lys Val
1 5

<210> 21

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of LIC1159 (IMGT)

<400> 21

Ala Ala Asp Arg Thr Leu Gln Ala Thr Met Ser Glu Ile Ser Tyr
1 5 10 15

<210> 22
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<220>
<223> CDR1 of VHH-083 (Kabat) or VHH-131 (Kabat)

<400> 22

Gly Asn Ile Asn Ser Arg Asn Cys Met Gly
1 5 10

<210> 23
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<213> Artificial Sequence

<220>
<223> CDR1 of VHH-111 (Kabat)

<400> 23

Gly Asp Thr Leu Ser Asn Lys Trp Met Gly
1 5 10

<210> 24
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<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of 77LICA542 (Kabat)

<400> 24

Gly Tyr Thr Tyr Ser Ser Gly Cys Met Gly
1 5 10

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of 77LICA519 (Kabat)

<400> 25

Gly Leu Pro Tyr Thr Gly Tyr Cys Met Gly
1 5 10

<210> 26

<211> 10

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<213> Artificial Sequence

<220>

<223> CDR1 of 77LICA602 (Kabat)

<400> 26

Gly Tyr Thr Ser Ser Tyr Ala Tyr Met Gly
1 5 10

<210> 27

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of LIC1157 (Kabat)

<400> 27

Gly Phe Thr Phe Ser Asp Ala Val Met Ser
1 5 10

<210> 28

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of LIC1159 (Kabat)

<400> 28

Gly Arg Thr Phe Ser Ser Leu Ala Met Gly
1 5 10

<210> 29

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of VHH-083 (Kabat)

<400> 29

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

Gly

<210> 30

<211> 16

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<220>

<223> CDR2 of VHH-111 (Kabat)

<400> 30

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

<210> 31

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<220>

<223> CDR2 of 77LICA542 (Kabat)

<400> 31

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

<210> 32

<211> 17

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<220>

<223> CDR2 of 77LICA519 (Kabat)

<400> 32

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

Gly

<210> 33
<211> 16
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<220>
<223> CDR2 of 77LICA602 (Kabat)

<400> 33

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

<210> 34
<211> 17
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<220>
<223> CDR2 of LIC1157 (Kabat)

<400> 34

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

Gly

<210> 35
<211> 17
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<220>
<223> CDR2 of LIC1159 (Kabat)

<400> 35

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

Gly

<210> 36
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<220>
<223> CDR3 of VHH-083 (Kabat) or VHH-131 (Kabat)

<400> 36

Ala	Pro	Gly	Cys	Leu	Leu	Ser	Ala	Leu	Arg	Ser	Ala	Asp	Tyr	Arg	Asn
1				5					10					15	

<210> 37
<211> 10
<212> PRT
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<220>
<223> CDR3 of VHH-111 (Kabat)

<400> 37

Ser	Tyr	Ser	Gly	Ala	Thr	Thr	Phe	Arg	Tyr
1				5					10

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of 77LICA542 (Kabat)

<400> 38

Asp	Pro	Asp	Cys	Tyr	Tyr	Ser	Asp	Tyr	Ala	Ile	Ser	Pro	Ala	Phe	Gly
1				5					10					15	

Tyr

<210> 39
<211> 17
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<213> Artificial Sequence

<220>
<223> CDR3 of 77LICA519 (Kabat)

<400> 39

Gly Leu Arg Leu Pro Gly Arg Ala Cys Thr Thr Ser His Lys Tyr Asn
1 5 10 15

Tyr

<210> 40

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of 77LICA602 (Kabat)

<400> 40

Arg Arg Trp Gly Trp Gly Glu Leu Pro Leu Thr Pro Ser Glu Tyr Asn
1 5 10 15

Asn

<210> 41

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<213> Artificial Sequence

<220>

<223> CDR3 of LIC1157 (Kabat)

<400> 41

Arg Ala Pro Gly Asp Lys Val
1 5

<210> 42

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of LIC1159 (Kabat)

<400> 42

Asp Arg Thr Leu Gln Ala Thr Met Ser Glu Ile Ser Tyr
1 5 10

<210> 43
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH-083 (amino acid)

<400> 43

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

Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Asn Ile Asn Ser Arg Asn
20 25 30

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

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

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

Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 44
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<213> Artificial Sequence

<220>
<223> VHH-111 (amino acid)

<400> 44

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

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

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

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

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

Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Ala Ser Tyr Ser Gly Ala Thr Thr Phe Arg Tyr Trp Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser
115

<210> 45
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> 77LICA542 (amino acid)

<400> 45

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

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

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

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

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

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

Ala Asp Pro Asp Cys Tyr Tyr Ser Asp Tyr Ala Ile Ser Pro Ala Phe
100 105 110

Gly Tyr Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 46
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> 77LICA519 (amino acid)

<400> 46

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

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

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

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

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

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

Ala Ala Gly Leu Arg Leu Pro Gly Arg Ala Cys Thr Thr Ser His Lys
100 105 110

Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 47

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> 77LICA602 (amino acid)

<400> 47

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

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

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

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

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

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

Ala Arg Arg Trp Gly Trp Gly Glu Leu Pro Leu Thr Pro Ser Glu Tyr
100 105 110

Asn Asn Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 48

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> LIC1157 (amino acid)

<400> 48

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

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

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

Ser Asp Ile Ser Asn Gly Gly Ile Thr Arg Arg Tyr Ser Asp Ser Val
50 55 60

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

Leu Gln Met Thr Lys Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Arg Ala Pro Gly Asp Lys Val Arg Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser
115

<210> 49

<211> 122

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<213> Artificial Sequence

<220>

<223> LIC1159 (amino acid)

<400> 49

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

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

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

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

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

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

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

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

<210> 50
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<220>
<223> CDR3 of A592H2 (IMGT)

<400> 50

Ala Lys Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
1 5 10 15

Arg Asn

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

<220>
<223> huVHH-773 (amino acid)

<400> 51

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 Asn Ile Asn Ser Arg Asn
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Leu 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 Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
100 105 110

Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 52

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> huVHH-776 (amino acid)

<400> 52

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 Asn Ile Asn Ser Arg Asn
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Leu 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 Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
100 105 110

Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 53
<211> 125
<212> PRT
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<220>
<223> A592H1 (amino acid)

<400> 53

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 Asn Ile Asn Ser Arg Asn
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Leu 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 Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
100 105 110

Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 54

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> A592H2 (amino acid)

<400> 54

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 Asn Ile Asn Ser Arg Asn
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Leu 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 Ala Pro Gly Cys Leu Leu Ser Ala Leu Arg Ser Ala Asp Tyr
100 105 110

Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 55

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> A592H3 (amino acid)

<400> 55

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

Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Asn Ile Asn Ser Arg Asn
20 25 30

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

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

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

Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 56

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> A593H4 (amino acid)

<400> 56

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

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Asn Ile Asn Ser Arg Asn
20 25 30

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

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

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

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

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

Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 57

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH-083-CAR (amino acid)

<400> 57

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Asn
35 40 45

Ile Asn Ser Arg Asn Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

Glu Arg Glu Gly Val Ala Ala Ile Gly Gln Val Thr Gly Arg Ser Tyr
65 70 75 80

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu
115 120 125

Arg Ser Ala Asp Tyr Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 58
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<220>
<223> VHH-111-CAR (amino acid)

<400> 58

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asp
35 40 45

Thr Leu Ser Asn Lys Trp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

Glu Arg Asp Trp Val Ala Thr Ile Arg Thr Asp His Ala Gly Thr Tyr
65 70 75 80

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

Asn Met Ile Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Ala Ser Tyr Ser Gly Ala Thr Thr Phe Arg Tyr
115 120 125

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Thr Ser Thr Thr Thr
130 135 140

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
145 150 155 160

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

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
180 185 190

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
195 200 205

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
210 215 220

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

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
245 250 255

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
260 265 270

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
275 280 285

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
290 295 300

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
305 310 315 320

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
325 330 335

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
340 345 350

Tyr Asp Ala Leu His Met Gln
355

<210> 59

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> 77LICA542-CAR (amino acid)

<400> 59

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr
35 40 45

Thr Tyr Ser Ser Gly Cys Met Gly Trp Phe Arg Gln Ala Pro Ala Lys
50 55 60

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

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

Asn Thr Leu His Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Ala Asp Pro Asp Cys Tyr Tyr Ser Asp Tyr Ala
115 120 125

Ile Ser Pro Ala Phe Gly Tyr Arg Gly Gln Gly Thr Gln Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 60

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> 77LICA519-CAR (amino acid)

<400> 60

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu
35 40 45

Pro Tyr Thr Gly Tyr Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

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

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

Gly Asn Thr Met Phe Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Ala Gly Leu Arg Leu Pro Gly Arg Ala Cys
115 120 125

Thr Thr Ser His Lys Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
130 135 140

Val Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
145 150 155 160

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
165 170 175

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
180 185 190

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
195 200 205

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
210 215 220

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
225 230 235 240

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
245 250 255

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

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
275 280 285

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
290 295 300

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
305 310 315 320

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
325 330 335

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
340 345 350

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
355 360 365

Leu Pro Pro Arg
370

<210> 61
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> 77LICA602-CAR (amino acid)

<400> 61

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ser Gly Gly Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Tyr
35 40 45

Thr Ser Ser Tyr Ala Tyr Met Gly Trp Phe Arg Gln Val Leu Gly Lys
50 55 60

Glu Arg Glu Gly Val Ala Ala Ile Gly Ser Asn Gly Arg Thr Asn Tyr
65 70 75 80

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

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

Met Tyr Tyr Cys Ala Ala Arg Arg Trp Gly Trp Gly Glu Leu Pro Leu
115 120 125

Thr Pro Ser Glu Tyr Asn Asn Trp Gly Gln Gly Thr Gln Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 62
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> huVHH-773 CAR (amino acid)

<400> 62

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn
35 40 45

Ile Asn Ser Arg Asn Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

Gly Arg Glu Gly Val Ala Ala Ile Gly Gln Val Thr Gly Arg Ser Tyr
65 70 75 80

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

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

Ala Val Tyr Tyr Cys Ala Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu
115 120 125

Arg Ser Ala Asp Tyr Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 63
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> huVHH-776 CAR (amino acid)

<400> 63

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn
35 40 45

Ile Asn Ser Arg Asn Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

Gly Arg Glu Gly Val Ala Ala Ile Gly Gln Val Thr Gly Arg Ser Tyr
65 70 75 80

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

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

Ala Val Tyr Tyr Cys Ala Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu
115 120 125

Arg Ser Ala Asp Tyr Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 64
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> VHH-083 (nucleic acid)

<400> 64
caggtgcagc tgggtggagag cggaggtggc tctgtgcagg ctgggtgggtc gctcaggctg 60
tcatgcgggg cgtccggcaa cattaactcc cgcaactgca tgggctgggtt ccgtcaagcc 120
ccaggcaagg agcgcgaggg cgtagccgct atcggtcagg tcaccggccg cagctactac 180
gtggattctg ttaaaggccg cttcaccatc tcgttggaca acgcaagaa cacgctgtac 240
ctgcagatga acacactgaa gcccgaagac accgccatgt attactgtgc tgcagccccg 300
gggtgtctgc tgtccgctct gcgctccgcg gactaccgga attggggcca gggcacccag 360
gtcaccgtgt ccagt 375

<210> 65
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> VHH-111 (nucleic acid)

<400> 65
gaggtgcagc tgggtggagag cggaggggga tccgtgcaag ccggcggctc cttg'gcctg 60
tcatgcgccg cttccggtga tactcttagc aacaaatgga tgggctgggtt ccgccaggcc 120
cccggcaagg agcgcgattg ggtcgcgacg attcgtaccg accacgccgg gacctacgcg 180
gacagtgtga agggccgctt caccatctcg cgggacaact ttaagaatat gatctacctg 240
cagatgaaca acctgaagcc tgaagacacc gccatgtatt actgtgctgc tagctactcc 300
ggtgcaacca cttcagata ctggggccag ggcacccagg tcaccgtttc ttct 354

<210> 66
<211> 375
<212> DNA
<213> Artificial Sequence

<220>

<223> huVHH-773 (nucleic acid)

<400> 66
caggtgcagc tggaggagag cggaggcggg ctggtgcagc cgggcggctc cctccgcctg 60
tcatgcgccg cttccggcaa cattaattcc cgcaactgca tgggctggtt ccgccaggcc 120
cccggcaagg gcagggaggg cgtggcggcc atcggtcagg tcaccggccg cagctattac 180
gtggattctg tgaaggagc cttcaccatc tctctggaca actccaagaa cacgctgtac 240
ctgcagatga acagcctgcg cgccaggagc accgccgtgt actactgtgc cgcggcgcca 300
gggtgcctgc tgtccgccct gcgctcggcg gactacagga actggggcca gggcaccctg 360
gttaccgtgt cctcc 375

<210> 67
<211> 375
<212> DNA
<213> Artificial Sequence

<220>

<223> huVHH-776 (nucleic acid)

<400> 67
caggtgcagc tggaggagag cggaggcggg gtggtgcagc caggcgatc tcttcgcctg 60
tcatgcgccg cttccggcaa cattaattcc cgcaactgca tgggctggtt ccgccaggcc 120
cccggcaaag gcagggaggg cgtggcggcc atcggtcagg tcaccggccg cagctattac 180
gtggattctg tgaagggccg cttcaccatc tctctggaca actccaagaa cacgctgtac 240
ctgcagatga acagcctgcg cgccaggagc accgccgtgt actactgtgc tgcggctccc 300
gggtgcctgc tgtccgccct gcgctcggcg gactaccgga actggggcca gggcaccctg 360
gtgaccgtgt cctcc 375

<210> 68
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>

<223> VHH-083 CAR (nucleic acid)

<400> 68

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atggcccttc ctgtgactgc gcttctgctg cccttggcac tcctactcca cgccgcccga      60
cctcaggtgc agctggtgga gagcggaggt ggctctgtgc aggctggtgg gtcgctcagg      120
ctgtcatgcg gggcgtccgg caacattaac tcccgcaact gcatgggctg gttccgtcaa      180
gccccaggca aggagcgcga gggcgtagcc gctatcggtc aggtcaccgg ccgcagctac      240
tacgtggatt ctgttaaagg ccgcttcacc atctcgttgg acaacgcgaa gaacacgctg      300
tacctgcaga tgaacacact gaagcccgaa gacaccgcca tgtattactg tgctgcagcc      360
ccgggggtgtc tgctgtccgc tctgcgctcc gcggactacc ggaattgggg ccagggcacc      420
caggtcaccg tgtccagtac tagtaccacg acgccagcgc cgcgaccacc aacaccggcg      480
cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg      540
ggcgcagtg c acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg      600
gccgggactt gtgggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc      660
agaaagaaac tcctgtatat attcaaaca ccatthtatga gaccagtaca aactactcaa      720
gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga      780
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat      840
aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg      900
gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa      960
ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg     1020
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac     1080
gacgcccttc acatgcaggc cctgccccct cgctaa                                1116
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<210> 69

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH-111 CAR (nucleic acid)

<400> 69

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atggcgtgc cggtgactgc tctactgctg cccctggcgc tcctcttgca tgcagccagg      60
ccagaggtgc agctggtgga gagcggaggg ggatccgtgc aagccggcgg ctccttgccg     120
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ctgtcatgcg ccgcttccgg tgatactctt agcaacaaat ggatgggctg gttccgccag	180
gccccgggca aggagcgcgga ttgggtcgcg acgattcgta ccgaccacgc cgggacctac	240
gcggacagtg tgaagggccg cttcaccatc tcgcgggaca actttaagaa tatgatctac	300
ctgcagatga acaacctgaa gcctgaagac accgccatgt attactgtgc tgctagctac	360
tccggtgcaa ccaccttcag atactggggc cagggcaccc aggtcaccgt ttctttctact	420
agtaccacga cgccagcgcc gcgaccacca acaccggcgc ccaccatcgc gtcgcagccc	480
ctgtccctgc gcccagaggc gtgccggcca gcggcggggg gcgcagtgca cacgaggggg	540
ctggacttcg cctgtgatat ctacatctgg gcgcccttgg ccgggacttg tggggtcctt	600
ctcctgtcac tggttatcac cttttactgc aaacggggca gaaagaaact cctgtatata	660
ttcaaacaac catttatgag accagtacaa actactcaag aggaagatgg ctgtagctgc	720
cgatttccag aagaagaaga aggaggatgt gaactgagag tgaagttcag caggagcgca	780
gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga	840
agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag	900
ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg	960
gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc	1020
ctttaccagg gtctcagtag agccaccaag gacacctacg acgcccttca catgcaggcc	1080
ctgccccctc gctaa	1095

<210> 70
 <211> 1116
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huVHH-773 CAR (nucleic acid)

<400> 70	
atggcgctgc ccgtcactgc tctgctcttg cccctggccc tgctgcttca cgccgccagg	60
cctcaggtgc agctggtgga gagcggaggc gggctggtgc agccgggicgg ctccctccgc	120
ctgtcatgcg ccgcttccgg caacattaat tcccgaact gcatgggctg gttccgccag	180
gccccgggca agggcaggga gggcgtggcg gccatcggtc aggtcaccgg ccgcagctat	240
tacgtggatt ctgtgaaggg acgcttcacc atctctctgg acaactccaa gaacacgctg	300

tacctgcaga tgaacagcct gcgcgccgag gacaccgccg tgtactactg tgccgcggcg	360
ccagggtgcc tgctgtccgc cctgcgctcg gcggactaca ggaactgggg ccagggcacc	420
ctggttaccg tgtcctccac tagtaccacg acgccagcgc cgcgaccacc aacaccggcg	480
cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg	540
ggcgcagtgc acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg	600
gccgggactt gtgggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc	660
agaaagaaac tcctgtatat attcaaaca ccatthtatga gaccagtaca aactactcaa	720
gaggaagatg gctgtagctg ccgattttcca gaagaagaag aaggaggatg tgaactgaga	780
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	840
aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg	900
gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa	960
ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1020
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1080
gacgcccttc acatgcaggc cctgccccct cgctaa	1116

<210> 71

<211> 1116

<212> DNA

<213> Artificial Sequence

<220>

<223> huVHH-776 CAR (nucleic acid)

<400> 71

atggcgctcc cggtgactgc tcttctgctg cccctggcgc tgctgctcca cgccgccagg	60
cctcaggtgc agctgggtgga gagcggaggc ggtgtggtgc agccagggcg atctcttcgc	120
ctgtcatgcg ccgcttcgg caacattaat tcccgcaact gcatgggctg gttccgccag	180
gccccggca aaggcaggga gggcgtggcg gccatcggtc aggtcaccgg ccgcagctat	240
tacgtggatt ctgtgaaggg ccgcttcacc atctctctgg acaactcaa gaacacgctg	300
tacctgcaga tgaacagcct gcgcgccgag gacaccgccg tgtactactg tgctgcggct	360
cccgggtgcc tgctgtccgc cctgcgctcg gcggactacc ggaactgggg ccagggcacc	420
ctggtgaccg tgtcctccac tagtaccacg acgccagcgc cgcgaccacc aacaccggcg	480

cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg	540
ggcgcagtg acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg	600
gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc	660
agaaagaaac tcctgtatat attcaaaca ccatatatga gaccagtaca aactactcaa	720
gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga	780
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	840
aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg	900
gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa	960
ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1020
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1080
gacgcccttc acatgcaggc cctgccccct cgctaa	1116

<210> 72
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide (CD8Alpha)

<400> 72

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro
			20	

<210> 73
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hinge (CD8Alpha)

<400> 73

Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala
1				5					10					15	

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 74
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Transmembrane domain (CD8Alpha)

<400> 74

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 75
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Co-stimulatory signaling domain (CD137)

<400> 75

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 76
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Primary intracellular signaling domain (CD3Zeta)

<400> 76

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 77

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> huIgG1Fc

<400> 77

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 78
<211> 9
<212> DNA
<213> Artificial Sequence

<220>

<223> Kozak sequence

<400> 78

gccgccacc

9

<210> 79

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 1

<220>

<221> MISC_FEATURE

<222> (1)..(2)

<223> can be repeated n times, where n is an integer including, e.g.,
1, 2, 3, 4, 5, and 6

<400> 79

Gly Ser

1

<210> 80

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 2

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> can be repeated n times, where n is an integer including, e.g.,
1, 2, 3, 4, 5, and 6

<400> 80

Gly Ser Gly Gly Ser

1

5

<210> 81

<211> 4

<212> PRT

<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 3

<220>
<221> MISC_FEATURE
<222> (1)..(4)
<223> can be repeated n times, where n is an integer including, e.g.,
1, 2, 3, 4, 5, and 6

<400> 81

Gly Gly Gly Ser
1

<210> 82
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 4

<400> 82

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

Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
20 25 30

Gly Ser

<210> 83
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 5

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> can be repeated n times, where n is an integer including, e.g.,
1, 2, 3, 4, 5, and 6

<400> 83

Gly Gly Gly Gly Ser
1 5

<210> 84

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 6

<400> 84

Asp Gly Gly Gly Ser
1 5

<210> 85

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 7

<400> 85

Thr Gly Glu Lys Pro
1 5

<210> 86

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 8

<400> 86

Gly Gly Arg Arg
1

<210> 87

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 9

<400> 87

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

Ser Gly Ser Gly Gly Gly Gly Ser
20

<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 10

<400> 88

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
1 5 10

<210> 89

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 11

<400> 89

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15

<210> 90

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary peptide linker 12

<400> 90

Gly Gly Arg Arg Gly Gly Gly Ser
1 5

<210> 91
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 13

<400> 91

Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 14

<400> 92

Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

<210> 93
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 15

<400> 93

Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
1 5 10 15

<210> 94
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 16

<400> 94

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

<210> 95
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 17

<400> 95

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 96
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary peptide linker 18

<400> 96

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15

Leu Asp

<210> 97
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> EcoRI restriction site

<400> 97

gaattc

6

<210> 98
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> SpeI restriction site

<400> 98
actagt

6

<210> 99
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> FMC63 scFv

<400> 99

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

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

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

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser

<210> 100
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 scFv CAR

<400> 100

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

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

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 101
<211> 223
<212> PRT
<213> Artificial Sequence

<220>

<223> FMC63 VH-CH1

<400> 101

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

Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

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

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

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

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

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

<210> 102
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FMC63 VL-CL

<400> 102

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

<210> 103
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of VHH-131 (Kabat)

<400> 103

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

Gly

<210> 104
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH-131 (amino acid)

<400> 104

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

Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Asn Ile Asn Ser Arg Asn
20 25 30

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

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

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

Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 105
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH-131-CAR (amino acid)

<400> 105

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Asn
35 40 45

Ile Asn Ser Arg Asn Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60

Glu Arg Glu Gly Val Ala Gly Ile Gly Gln Val Thr Gly Arg Ser Tyr
65 70 75 80

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

Lys Asn Met Leu Tyr Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Ala Ala Pro Gly Cys Leu Leu Ser Ala Leu
115 120 125

Arg Ser Ala Asp Tyr Arg Asn Trp Gly Gln Gly Thr Gln Val Thr Val
130 135 140

Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
145 150 155 160

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
165 170 175

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
180 185 190

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
195 200 205

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
210 215 220

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
225 230 235 240

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

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
260 265 270

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
275 280 285

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
290 295 300

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
305 310 315 320

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
325 330 335

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
340 345 350

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
355 360 365

Pro Pro Arg
370

<210> 106
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> VHH-131 (nucleic acid)

<400> 106
caggtgcagc tggaggagag cggaggaggc tccgtgcagg ccggcggctc cctgcgctg 60
tcatgcgggg cttccggcaa cattaactcc cgcaactgca tgggctggtt ccgccaggcc 120
cccggcaagg agcgcgaggg cgtggctggc atcggtcagg tcaccggccg cagctactac 180
gcggacagcg tgaagggccg cttcaccatc tctctggaca acgccaagaa catgctgtac 240
ctgcagatga acacgctgaa gcctgaagac accgccatgt attactgtgc cgcggctccc 300
gggtgcctgc tgagcgcgct ccgtagtgcg gactacagga attggggcca gggcaccag 360
gtcaccgtgt cgtcc 375

<210> 107
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>

<223> VHH-131 CAR (nucleic acid)

<400> 107

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cctcaggtgc agctggtgga gagcggagga ggctccgtgc aggccggcgg ctccctgcgc      120
ctgtcatgcg gggcttccgg caacattaac tcccgcaact gcatgggctg gttccgccag      180
gccccgggca aggagcgcga gggcgtggct ggcatcggtc aggtcaccgg ccgcagctac      240
tacgcggaca gcgtgaaggg ccgcttcacc atctctctgg acaacgcaa gaacatgctg      300
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cccgggtgcc tgctgagcgc gctccgtagt gcggactaca ggaattgggg ccagggcacc      420
caggtcaccg tgtcgtccac tagtaccacg acgccagcgc cgcgaccacc aacaccggcg      480
cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg      540
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agaaagaaac tcctgtatat attcaaaca ccatTTatga gaccagtaca aactactcaa      720
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aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg      900
gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa      960
ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg     1020
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac     1080
gacgcccttc acatgcaggc cctgccccct cgctaa                                1116
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<210> 108

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of VHH-083 & VHH-131 (Kabat with 5aa)

<400> 108

Arg Asn Cys Met Gly
1 5

<210> 109
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of VHH-111 (Kabat with 5aa)

<400> 109

Asn Lys Trp Met Gly
1 5

<210> 110
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of 77LICA542 (Kabat with 5aa)

<400> 110

Ser Gly Cys Met Gly
1 5

<210> 111
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of 77LICA519 (Kabat with 5aa)

<400> 111

Gly Tyr Cys Met Gly
1 5

<210> 112
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of 77LICA602 (Kabat with 5aa)

<400> 112

Tyr Ala Tyr Met Gly
1 5

<210> 113
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of LIC1157 (Kabat with 5aa)

<400> 113

Asp Ala Val Met Ser
1 5

<210> 114
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of LIC1159 (Kabat with 5aa)

<400> 114

Ser Leu Ala Met Gly
1 5