

SEQUENCE LISTING

<110> INSERM
UNIVERSITE DE NANTES
CENTRE HOSPITALIER UNIVERSITAIRE DE NANTES
GUILLONNEAU Carole
ANEGON Ignacio

<120> ANTI-HUMAN CD45RC ANTIBODIES AND USES THEREOF

<130> CV - 1093/PCT

<150> EP18306230.6
<151> 2018-09-21

<160> 129

<170> BiSSAP 1.3.6

<210> 1
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<220>
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<400> 1
Asn Tyr Tyr Ile Gly
1 5

<210> 2
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<220>
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<223> Xaa is selected from Asp (D), Ile (I) and Arg (R)

<220>
<223> VH-CDR2

<220>
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<223> Xaa is selected from Pro and Ser (S)

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<223> Xaa is selected from Asp (D), Ser (S) and Gly (G)

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<223> Xaa is selected from Ala (A) and Thr (T)

<220>
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<223> Xaa is selected from Ser (S) and Tyr (Y)

<220>
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<223> Xaa is selected from Asn (N), Ala (A) and Ser (S)

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<223> Xaa is selected from Glu (E), Asp (D), Pro (P) and Gln (Q)

<220>
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<223> Xaa is selected from Lys (K) and Ser (S)

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<223> Xaa is selected from Phe (F) and Val (V)

<220>
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<222> 16
<223> Xaa is selected from Lys (K) and Gln (Q)

<400> 2
Xaa Ile Phe Xaa Gly Gly Xaa Tyr Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Gly

<210> 3
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<220>

<223> VH-CDR3

<400> 3

Arg Asn Phe Asp Tyr
1 5

<210> 4

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 4

Asp Ile Phe Pro Gly Gly Asp Tyr Ala Asn Ser Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 5

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 5

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

<210> 6

<211> 17

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<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 6

Asp Ile Phe Pro Gly Gly Gly Tyr Thr Asn Tyr Ala Glu Lys Phe Gln
1 5 10 15
Gly

<210> 7
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<220>
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<400> 7
Asp Ile Phe Pro Gly Gly Ser Tyr Thr Asn Tyr Ser Glu Ser Phe Gln
1 5 10 15
Gly

<210> 8
<211> 17
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<213> Artificial Sequence

<220>
<223> VH-CDR2

<400> 8
Asp Ile Phe Pro Gly Gly Ser Tyr Thr Asn Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-CDR2

<400> 9
Arg Ile Phe Pro Gly Gly Gly Tyr Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15
Gly

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-CDR2

<400> 10
Ile Ile Phe Pro Gly Gly Ser Tyr Thr Asn Tyr Ser Pro Ser Phe Gln
1 5 10 15
Gly

<210> 11
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<220>
<223> VH-CDR2

<400> 11
Asp Ile Phe Ser Gly Gly Ser Tyr Thr Asn Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 12
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<223> Xaa is selected from Ser (S) and Arg (R)

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<223> VL-CDR1

<220>
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<222> 8
<223> Xaa is absent, or is selected from Asn (N), Ser (S) and Gly (G)

<400> 12

Xaa Ala Ser Ser Ser Val Ser Xaa Tyr Met His
1 5 10

<210> 13
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<222> 1
<223> Xaa is selected from Asn (N) and Ala (A); or Xaa is any amino acid but Ala (A) or Asn (N)

<220>
<223> VL-CDR2

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<223> Xaa is selected from Leu (L), Ser (S) and Arg (R)

<220>
<221> SITE
<222> 6
<223> Xaa is selected from Pro (P), Ala (A) and Gln (Q)

<220>
<221> SITE
<222> 7
<223> Xaa is selected from Ser (S) and Thr (T)

<400> 13
Xaa Thr Ser Asn Xaa Xaa Xaa
1 5

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

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<221> SITE
<222> 1
<223> Xaa is selected from Gln (Q) and His (H)

<220>
<223> VL-CDR3

<400> 14

Xaa Gln Arg Ser Ser Tyr Pro Leu Thr Phe
1 5 10

<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> VL-CDR1

<220>

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<222> 8

<223> Xaa is absent or is selected from Asn (N), Ser (S) and Gly (G)

<400> 15

Ser Ala Ser Ser Ser Val Ser Xaa Tyr Met His
1 5 10

<210> 16

<211> 7

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<213> Artificial Sequence

<220>

<223> VL-CDR2

<400> 16

Asn Thr Ser Asn Leu Pro Ser
1 5

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> VL-CDR3

<400> 17

Gln Gln Arg Ser Ser Tyr Pro Leu Thr Phe
1 5 10

<210> 18

<211> 11
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<220>
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<220>
<221> SITE
<222> 8
<223> Xaa is absent or is selected from Asn (N), Ser (S) and Gly (G)

<400> 18
Arg Ala Ser Ser Ser Val Ser Xaa Tyr Met His
1 5 10

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR2

<400> 19
Asn Thr Ser Asn Ser Pro Ser
1 5

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR2

<400> 20
Ala Thr Ser Asn Leu Gln Ser
1 5

<210> 21
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> VL-CDR3

<400> 21

His Gln Arg Ser Ser Tyr Pro Leu Thr Phe
1 5 10

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> VL-CDR2

<400> 22

Asn Thr Ser Asn Arg Ala Thr
1 5

<210> 23

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<223> C determinant of hCD45RC

<400> 23

Asp Val Pro Gly Glu Arg Ser Thr Ala Ser Thr Phe Pro Thr Asp Pro
1 5 10 15
Val Ser Pro Leu Thr Thr Thr Leu Ser Leu Ala His His Ser Ser Ala
20 25 30
Ala Leu Pro Ala Arg Thr Ser Asn Thr Thr Ile Thr Ala Asn Thr Ser
35 40 45

<210> 24

<211> 144

<212> DNA

<213> Homo sapiens

<220>

<223> Exon 6 of hCD45RC

<400> 24

gatgtcccag gagagaggag tacagccagc acctttccta cagacccagt ttccccattg

60

acaaccaccc tcagccttgc acaccacagc tctgctgcct tacctgcacg cacctccaac 120

accaccatca cagcgaacac ctca 144

<210> 25

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR1

<400> 25

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Thr
1			5					10						15	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ala	Gly	Tyr	Thr	Phe	Thr		
			20				25						30		

<210> 26

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> VH-FR2

<400> 26

Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile	Gly
1			5					10					

<210> 27

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR3

<400> 27

Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln
1			5					10						15	
Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Ile	Tyr	Tyr	Cys	Val	Arg
			20				25						30		

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR4

<400> 28
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 29
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR1

<400> 29
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR2

<400> 30
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10

<210> 31
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR3

<400> 31

Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	Met	Glu
1				5					10					15	
Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys	Val	Arg
			20					25					30		

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR4

<400> 32

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 33

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR1

<400> 33

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		
			20					25					30		

<210> 34

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR2

<400> 34

Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly
1				5					10				

<210> 35

<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR3

<400> 35
Gln Val Thr Leu Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15
Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Val Arg
20 25 30

<210> 36
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR1

<400> 36
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 Tyr Thr Phe Thr
20 25 30

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-FR2

<400> 37
Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 38
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> VH-FR3

<400> 38

Arg	Phe	Thr	Leu	Ser	Ala	Asp	Thr	Ala	Lys	Asn	Ser	Ala	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	Arg
			20					25					30		

<210> 39

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR1

<400> 39

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	Thr		
			20					25					30		

<210> 40

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR1

<400> 40

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		
			20					25					30		

<210> 41

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-FR3

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 45
Trp Phe Gln Gln Lys Thr Gly Thr Ser Pro Arg Leu Trp Ile Tyr
1 5 10 15

<210> 46
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR3

<220>
<221> SITE
<222> 15
<223> Xaa is selected from Tyr (Y) and Phe (F)

<400> 46
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Xaa Ser
1 5 10 15
Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR4

<400> 47
Gly Ala Gly Thr Lys Leu Glu Leu Lys
1 5

<210> 48

<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR1

<400> 48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
20

<210> 49
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 49
Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
1 5 10 15

<210> 50
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR3

<220>
<221> SITE
<222> 15
<223> Xaa is selected from Tyr (Y) and Phe (F)

<400> 50
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Xaa Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 51

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

<220>
<223> VL-FR4

<400> 51
Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5

<210> 52
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR1

<400> 52
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Ile Thr Cys
20

<210> 53
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 53
Trp Phe Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Ile Tyr
1 5 10 15

<210> 54
<211> 32
<212> PRT
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<220>
<223> VL-FR3

<220>

<221> SITE
<222> 15
<223> Xaa is selected from Tyr (Y) and Phe (F)

<400> 54
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Xaa Thr
1 5 10 15
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 55
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR1

<400> 55
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys
20

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 56
Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
1 5 10 15

<210> 57
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR3

<220>

<221> SITE
<222> 15
<223> Xaa is selected from Tyr (Y) and Phe (F)

<400> 57
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Xaa Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 58
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
1 5 10 15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 59
Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Ile Tyr
1 5 10 15

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-FR2

<400> 60
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
1 5 10 15

<210> 61
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine HCVR

<400> 61
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Tyr Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45
Gly Asp Ile Phe Pro Gly Gly Asp Tyr Ala Asn Ser Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95
Val Arg Arg Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 62
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized HCVR

<400> 62
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Tyr Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Asp Ile Phe Pro Gly Gly Asp Tyr Ala Asn Ser Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Val Val Tyr Tyr Cys
85 90 95

Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 63
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

<400> 63															
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20				25						30		
Tyr	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	Asp	Ile	Phe	Pro	Gly	Gly	Asp	Tyr	Ala	Asn	Ser	Asn	Glu	Lys	Phe
	50					55					60				
Lys	Gly	Gln	Val	Thr	Leu	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75				80	
Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90				95		
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 64
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

<400> 64															
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	Tyr	Thr	Phe	Thr	Asn	Tyr
			20				25						30		
Tyr	Ile	Gly	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	Asp	Ile	Phe	Pro	Gly	Gly	Asp	Tyr	Ala	Asn	Ser	Asn	Glu	Lys	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Leu	Ser	Ala	Asp	Thr	Ala	Lys	Asn	Ser	Ala	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 65
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
		20						25					30		
Tyr	Ile	Gly	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	Ala	Glu	Lys	Phe
	50				55					60					
Gln	Gly	Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys
			85					90						95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 66
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1			5						10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
		20						25					30		

Tyr Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Phe Pro Gly Gly Ser Tyr Thr Asn Tyr Ser Glu Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Leu Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Val Arg Arg Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110
 Ser Ser

<210> 67
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

<400> 67
 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 Asn Tyr
 20 25 30
 Tyr Ile Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Phe Pro Gly Gly Ser Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Leu Ser Ala Asp Thr 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
 Val Arg Arg Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110
 Ser Ser

<210> 68
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

<400> 68

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25						30	
Tyr	Ile	Gly	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40						45		
Gly	Arg	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys
				85					90					95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 69

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized HCVR

<400> 69

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Asn	Tyr
			20					25						30	
Tyr	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40						45		
Gly	Ile	Ile	Phe	Pro	Gly	Gly	Ser	Tyr	Thr	Asn	Tyr	Ser	Pro	Ser	Phe
	50					55					60				
Gln	Gly	Gln	Val	Thr	Leu	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
			85						90					95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 70

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized HCVR

<400> 70

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	Asn	Tyr
		20						25					30		
Tyr	Ile	Gly	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			
Gly	Asp	Ile	Phe	Ser	Gly	Gly	Ser	Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Leu	Ser	Ala	Asp	Thr	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	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 71

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 71

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Thr	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
		20						25				30			
Met	His	Trp	Phe	Gln	Gln	Lys	Thr	Gly	Thr	Ser	Pro	Arg	Leu	Trp	Ile
		35				40						45			
Tyr	Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly
	50				55						60				
Ser	Gly	Ser	Gly	Thr	Ser	Phe	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala
65					70					75				80	
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
			85					90						95	
Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys					
			100					105							

<210> 72
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized LCVR

<220>
<221> SITE
<222> 31
<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 72
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Xaa Tyr
 20 25 30
Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile
 35 40 45
Tyr Asn Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu
 85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 73
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized LCVR

<220>
<221> SITE
<222> 31
<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 73
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Xaa Tyr
 20 25 30

Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Asp	Gln	Ser	Pro	Lys	Leu	Trp	Ile
		35					40					45			
Tyr	Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala
65					70					75					80
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 74
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>
 <221> SITE
 <222> 31
 <223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
			20					25					30		
Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Trp	Ile
		35					40					45			
Tyr	Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 75
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 75

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
			20					25					30		
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile
			35				40					45			
Tyr	Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85				90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 76

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 76

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Phe	Gln	Ser	Val	Thr	Pro	Lys
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
			20					25					30		
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gln	Ser	Pro	Lys	Leu	Trp	Ile
			35				40					45			
Tyr	Asn	Thr	Ser	Asn	Ser	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala
65					70					75				80	
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85				90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized LCVR

<220>
<221> SITE
<222> 31
<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 77
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Xaa Tyr
20 25 30
Met His Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile
35 40 45
Tyr Asn Thr Ser Asn Leu Pro Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 78
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized LCVR

<220>
<221> SITE
<222> 31
<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 78
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Xaa Tyr
20 25 30

Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile
	35						40					45			
Tyr	Ala	Thr	Ser	Asn	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
			85						90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> 79
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>
 <221> SITE
 <222> 31
 <223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Phe	Gln	Ser	Val	Thr	Pro	Lys
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
		20						25				30			
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gln	Ser	Pro	Lys	Leu	Trp	Ile
	35						40					45			
Tyr	Asn	Thr	Ser	Asn	Ser	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala
65					70					75					80
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
			85						90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> 80
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 80

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
			20					25					30		
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Trp	Ile
		35					40					45			
Tyr	Asn	Thr	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85				90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 81

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine LCVR

<400> 81

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Thr	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Thr	Gly	Thr	Ser	Pro	Arg	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70					75				80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
				85				90						95	
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys						
			100					105							

<210> 82

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 82

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
          20           25           30
His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
          35           40           45
Asn Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
          50           55           60
Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65           70           75           80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
          85           90           95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

<210> 83

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 83

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1           5           10           15
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
          20           25           30
His Trp Phe Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Ile Tyr
          35           40           45
Asn Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
          50           55           60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
          85           90           95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

<210> 84

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 84

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
		20						25					30		
His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu
65				70						75				80	
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

<210> 85

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 85

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
		20						25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Glu	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
65				70						75				80	
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

<210> 86

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 86

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Phe	Gln	Ser	Val	Thr	Pro	Lys
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gln	Ser	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ser	Asn	Ser	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala	Glu
65				70						75				80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

<210> 87

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 87

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu
65				70						75				80	
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

<210> 88

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 88

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
          20          25          30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
          35          40          45
Ala Thr Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
          50          55          60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65          70          75          80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
          85          90          95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

<210> 89

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 89

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1           5           10           15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
          20          25          30
His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Ile Tyr
          35          40          45
Asn Thr Ser Asn Ser Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
          50          55          60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu
65          70          75          80
Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Leu Thr
          85          90          95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

<210> 90

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 90

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1      5      10      15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
      20      25      30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
      35      40      45
Asn Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
      50      55      60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65      70      75      80
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
      85      90      95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100      105
```

<210> 91

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Human HCCR

<400> 91

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1      5      10      15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20      25      30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35      40      45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      50      55      60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65      70      75      80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85      90      95
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
      100      105      110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
      115      120      125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
      130      135      140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
```

145					150					155					160
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
				165					170						175
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			180					185							190
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195					200					205			
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	210					215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu
225					230					235					240
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			245						250						255
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
		260						265					270		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
	275						280					285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
	290					295					300				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
			325						330						

<210> 92

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Human LCCR

<400> 92

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
1			5					10						15	
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
		20					25						30		
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
	35					40					45				
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
	50					55				60					
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
65				70					75					80	
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
			85					90						95	
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
			100					105							

<210> 93

<211> 323
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine HCCR

<400> 93

Ala	Lys	Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	1	5	10	15
Ala	Gln	Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	20	25	30	
Phe	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	35	40	45	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	50	55	60	
Ser	Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	65	70	75	80
Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	85	90	95	
Ile	Val	Pro	Arg	Asp	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	100	105	110	
Glu	Val	Ser	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	115	120	125	
Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	130	135	140	
Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	145	150	155	160
Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	165	170	175	
Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	180	185	190	
Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	195	200	205	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	210	215	220	
Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	225	230	235	240
Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	245	250	255	
Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	260	265	270	
Pro	Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	275	280	285	
Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	290	295	300	
Leu	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	305	310	315	320
Ser	Pro	Gly																	

<210> 94
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine LCCR

<400> 94
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 1 5 10 15
 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 20 25 30
 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 35 40 45
 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 50 55 60
 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 65 70 75 80
 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 85 90 95
 Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 100 105

<210> 95
 <211> 342
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Murine HCVR

<400> 95
 caggtccagc tgcaacagtc tggcgctgag ctggttaggc ctgggacttc agtgaagatg 60
 tcctgcaagg ccgctggata caccttcact aactactaca taggttgggt aaagcagagg 120
 cctggacatg gccttgagtg gatcggagat attttccttg gaggtgacta tgccaacagc 180
 aatgagaagt tcaagggaag agccacactg actgcagaca catcctccag cacagcctac 240
 atgcagctca gcagcctgac atctgaggac tctgccatct attactgtgt gagaaggaac 300
 ttgactact ggggccaagg caccactctc acagtgtcct ca 342

<210> 96
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine LCVR

<400> 96
caaattgttc tcacccagtc tccaacaatc atgtctgcat ctccagggga gaagggtgacc 60
ataacctgca gtgccagctc aagtgttaagt tacatgcact gggtccagca gaagacaggc 120
acttctccca gactctggat ttataacaca tccaacctgc cttctggagt ccccgctcgc 180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
gatgctgcca cttattactg ccagcaaagg agtagttacc cactcacgtt cgggtgctggg 300
accaagctgg agctgaaa 318

<210> 97
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Human HCCR

<400> 97
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300
aaatcttggt acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 420
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 480
tacgtggacg gcgtggagggt gcataatgcc aagacaaagc cgcggggagga gcagtacaac 540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag	720
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	840
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtgg	900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	960
cagaagagcc tctccctgtc cccgggtaaa	990

<210> 98
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human LCCR

<400> 98	
cgaactgtgg ctgcaccatc tgtcttcac tccccgcat ctgatgagca gttgaaatct	60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	120
tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac	180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag	240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag	300
agcttcaaca ggggagagtg t	321

<210> 99
 <211> 1306
 <212> PRT
 <213> Homo sapiens

<220>
 <223> hCD45

<300>

<308> UniProt Accession P08575-3

<309> 2018 03 28

<400> 99

Met	Thr	Met	Tyr	Leu	Trp	Leu	Lys	Leu	Leu	Ala	Phe	Gly	Phe	Ala	Phe
1				5				10						15	
Leu	Asp	Thr	Glu	Val	Phe	Val	Thr	Gly	Gln	Ser	Pro	Thr	Pro	Ser	Pro
			20					25					30		
Thr	Gly	Leu	Thr	Thr	Ala	Lys	Met	Pro	Ser	Val	Pro	Leu	Ser	Ser	Asp
		35					40					45			
Pro	Leu	Pro	Thr	His	Thr	Thr	Ala	Phe	Ser	Pro	Ala	Ser	Thr	Phe	Glu
	50					55					60				
Arg	Glu	Asn	Asp	Phe	Ser	Glu	Thr	Thr	Thr	Ser	Leu	Ser	Pro	Asp	Asn
65					70					75				80	
Thr	Ser	Thr	Gln	Val	Ser	Pro	Asp	Ser	Leu	Asp	Asn	Ala	Ser	Ala	Phe
			85						90					95	
Asn	Thr	Thr	Gly	Val	Ser	Ser	Val	Gln	Thr	Pro	His	Leu	Pro	Thr	His
			100					105						110	
Ala	Asp	Ser	Gln	Thr	Pro	Ser	Ala	Gly	Thr	Asp	Thr	Gln	Thr	Phe	Ser
		115					120					125			
Gly	Ser	Ala	Ala	Asn	Ala	Lys	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Asn	Ala
	130					135					140				
Ile	Ser	Asp	Val	Pro	Gly	Glu	Arg	Ser	Thr	Ala	Ser	Thr	Phe	Pro	Thr
145					150					155					160
Asp	Pro	Val	Ser	Pro	Leu	Thr	Thr	Thr	Leu	Ser	Leu	Ala	His	His	Ser
				165					170					175	
Ser	Ala	Ala	Leu	Pro	Ala	Arg	Thr	Ser	Asn	Thr	Thr	Ile	Thr	Ala	Asn
			180					185					190		
Thr	Ser	Asp	Ala	Tyr	Leu	Asn	Ala	Ser	Glu	Thr	Thr	Thr	Leu	Ser	Pro
		195				200						205			
Ser	Gly	Ser	Ala	Val	Ile	Ser	Thr	Thr	Thr	Ile	Ala	Thr	Thr	Pro	Ser
	210					215					220				
Lys	Pro	Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	Ile	Thr	Val	Asp	Tyr	Leu
225					230					235					240
Tyr	Asn	Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	Lys	Leu	Asn	Val	Asn	Glu
			245						250					255	
Asn	Val	Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His	Asn
			260					265					270		
Leu	Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys
		275					280					285			
Thr	Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu
	290					295					300				
Lys	Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr
305					310					315					320
Ile	Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln
			325						330					335	
Asn	Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys
			340					345					350		
Glu	Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp

		355					360				365				
Ser	Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile
	370					375					380				
Ile	Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys
385					390					395					400
Arg	Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln
				405					410					415	
Arg	Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys
			420					425					430		
Asp	Cys	Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn
		435					440					445			
Leu	Lys	Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile
	450					455					460				
Ala	Lys	Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr
465					470					475					480
Lys	Ser	Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr
				485					490					495	
Ser	Asp	Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn
			500					505					510		
Gly	Pro	His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu
		515					520					525			
Val	Arg	Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu
	530					535					540				
Gln	Tyr	Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp
545					550					555					560
Tyr	Pro	Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn	Ser
				565					570					575	
Lys	Ala	Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile
			580					585					590		
Ala	Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg
		595					600					605			
Ser	Cys	Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu
	610					615					620				
Lys	Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu
625					630					635					640
Thr	Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu
				645					650					655	
Phe	Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala
			660					665					670		
Arg	Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro
		675					680					685			
Tyr	Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly
					695						700				
Ser	Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg
705					7										

		755					760				765				
Met	Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn
	770					775					780				
Gln	His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val
785					790					795					800
Asn	Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln	Phe
			805						810					815	
Thr	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu
			820					825					830		
Lys	Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro
		835					840				845				
Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile
	850					855					860				
Gly	Ile	Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val	Asp
865					870					875					880
Val	Tyr	Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met	Val
			885					890						895	
Gln	Val	Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu	Tyr
			900					905					910		
Asn	Gln	Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro	Tyr
		915					920					925			
Leu	His	Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro	Leu
	930					935					940				
Glu	Ala	Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr	Gln
945					950					955					960
His	Ile	Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn
			965						970					975	
Val	Ile	Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu
			980					985					990		
Met	Ser	Lys	Glu	Ser	Glu	His	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp
		995					1000					1005			
Ser	Asp	Ser	Glu	Glu	Pro	Ser	Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met
	1010					1015					1020				
Ser	Tyr	Trp	Lys	Pro	Glu	Val	Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys
1025					1030					1035					1040
Glu	Thr	Ile	Gly	Asp	Phe	Trp	Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys
			1045						1050					1055	
Val	Ile	Val	Met	Leu	Thr	Glu	Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys
			1060					1065				1070			
Ala	Gln	Tyr	Trp	Gly	Glu	Gly	Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val
		1075					1080					1085			
Asp	Leu	Lys	Asp	Thr	Asp	Lys	Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe
	1090					1095					1100				
Glu	Leu	Arg	His	Ser	Lys	Arg	Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr
1105					1110					1115					1120
Gln	Tyr	Thr	Asn	Trp	Ser	Val	Glu	Gln	Leu	Pro	Ala	Glu	Pro	Lys	Glu
			1125						1130					1135	
Leu	Ile	Ser	Met	Ile	Gln	Val	Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn
			1140					1145					1150		
Ser	Ser	Glu	Gly	Asn	Lys	His	His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His

		35					40					45			
Gly	Asp	Ile	Phe	Pro	Gly	Gly	Asp	Tyr	Thr	Asn	Tyr	Ala	Glu	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys
				85					90					95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 102
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>
 <221> SITE
 <222> 31
 <223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
			20					25					30		
Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile
		35					40					45			
Tyr	Asn	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 103
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<400> 103

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Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Tyr
          20           25           30
Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile
          35           40           45
Tyr Asn Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu
          85           90           95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
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<210> 104

<211> 1193

<212> PRT

<213> Homo sapiens

<220>

<223> hCD45RC

<300>

<308> UniProt Accession P08575-10

<309> 2018 03 28

<400> 104

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Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
1           5           10           15
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
          20           25           30
Thr Asp Val Pro Gly Glu Arg Ser Thr Ala Ser Thr Phe Pro Thr Asp
          35           40           45
Pro Val Ser Pro Leu Thr Thr Thr Leu Ser Leu Ala His His Ser Ser
          50           55           60
Ala Ala Leu Pro Ala Arg Thr Ser Asn Thr Thr Ile Thr Ala Asn Thr
65           70           75           80
Ser Asp Ala Tyr Leu Asn Ala Ser Glu Thr Thr Thr Leu Ser Pro Ser
          85           90           95
Gly Ser Ala Val Ile Ser Thr Thr Thr Thr Ile Ala Thr Thr Pro Ser Lys
          100          105          110
Pro Thr Cys Asp Glu Lys Tyr Ala Asn Ile Thr Val Asp Tyr Leu Tyr
          115          120          125
Asn Lys Glu Thr Lys Leu Phe Thr Ala Lys Leu Asn Val Asn Glu Asn
          130          135          140
Val Glu Cys Gly Asn Asn Thr Cys Thr Asn Asn Glu Val His Asn Leu
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145					150					155				160	
Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys	Thr
				165					170					175	
Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu	Lys
			180					185					190		
Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr	Ile
		195					200					205			
Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln	Asn
	210				215						220				
Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys	Glu
225					230					235				240	
Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp	Ser
				245					250					255	
Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile	Ile
			260					265					270		
Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys	Arg
		275					280					285			
Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln	Arg
	290				295						300				
Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys	Asp
305					310					315				320	
Cys	Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn	Leu
				325					330					335	
Lys	Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile	Ala
			340					345					350		
Lys	Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr	Lys
		355					360					365			
Ser	Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr	Ser
	370				375						380				
Asp	Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn	Gly
385				390						395				400	
Pro	His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu	Val
				405					410					415	
Arg	Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu	Gln
			420					425					430		
Tyr	Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp	Tyr
		435					440					445			
Pro	Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn	Ser	Lys
	450				455						460				
Ala	Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile	Ala
465					470					475				480	
Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg	Ser
				485					490					495	
Cys	Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu	Lys
			500				505					510			
Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu	Thr
		515					520					525			
Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu	Phe
	530					535					540				
Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala	Arg

545					550					555				560
Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro Tyr
				565					570					575
Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly Ser
			580					585					590	
Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg Lys
		595					600					605		
Tyr	Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe Trp
	610					615					620			
Arg	Met	Ile	Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr Arg
625				630						635				640
Cys	Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser Met
				645					650					655
Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn Gln
			660					665					670	
His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val Asn
		675					680					685		
Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln	Phe Thr
	690					695					700			
Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu Lys
705				710					715					720
Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro Ile
				725					730					735
Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile Gly
			740					745					750	
Ile	Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val	Asp Val
		755				760						765		
Tyr	Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met	Val Gln
	770					775					780			
Val	Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu	Tyr Asn
785				790					795					800
Gln	Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro	Tyr Leu
				805					810					815
His	Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro	Leu Glu
			820					825					830	
Ala	Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr	Gln His
		835					840					845		
Ile	Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn Val
	850					855				860				
Ile	Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu Met
865					870				875					880
Ser	Lys	Glu	Ser	Glu	His	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp Ser
				885					890				895	
Asp	Ser	Glu	Glu	Pro	Ser	Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met Ser
		900						905					910	
Tyr	Trp	Lys	Pro	Glu	Val	Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys Glu
		915					920					925		
Thr	Ile	Gly	Asp	Phe	Trp	Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys Val
	930					935					940			
Ile	Val	Met	Leu	Thr	Glu	Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys Ala

945					950					955				960	
Gln	Tyr	Trp	Gly	Glu	Gly	Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val	Asp
				965					970					975	
Leu	Lys	Asp	Thr	Asp	Lys	Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe	Glu
			980					985					990		
Leu	Arg	His	Ser	Lys	Arg	Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr	Gln
		995					1000					1005			
Tyr	Thr	Asn	Trp	Ser	Val	Glu	Gln	Leu	Pro	Ala	Glu	Pro	Lys	Glu	Leu
	1010					1015					1020				
Ile	Ser	Met	Ile	Gln	Val	Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser
1025				1030					1035					1040	
Ser	Glu	Gly	Asn	Lys	His	His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys
			1045					1050					1055		
Arg	Asp	Gly	Ser	Gln	Gln	Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu
		1060					1065						1070		
Leu	Glu	Ser	Ala	Glu	Thr	Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val
		1075				1080					1085				
Lys	Ala	Leu	Arg	Lys	Ala	Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln
	1090					1095					1100				
Tyr	Gln	Phe	Leu	Tyr	Asp	Val	Ile	Ala	Ser	Thr	Tyr	Pro	Ala	Gln	Asn
1105				1110					1115					1120	
Gly	Gln	Val	Lys	Lys	Asn	Asn	His	Gln	Glu	Asp	Lys	Ile	Glu	Phe	Asp
			1125					1130					1135		
Asn	Glu	Val	Asp	Lys	Val	Lys	Gln	Asp	Ala	Asn	Cys	Val	Asn	Pro	Leu
		1140					1145				1150				
Gly	Ala	Pro	Glu	Lys	Leu	Pro	Glu	Ala	Lys	Glu	Gln	Ala	Glu	Gly	Ser
	1155					1160					1165				
Glu	Pro	Thr	Ser	Gly	Thr	Glu	Gly	Pro	Glu	His	Ser	Val	Asn	Gly	Pro
	1170				1175				1180						
Ala	Ser	Pro	Ala	Leu	Asn	Gln	Gly	Ser							
1185				1190											

<210> 105
 <211> 66
 <212> PRT
 <213> Homo sapiens

<220>
 <223> A determinant of hCD45

<400> 105
Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp Pro
1 5 10 15
Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg
20 25 30
Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr
35 40 45
Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe Asn
50 55 60

Thr Thr
65

<210> 106
<211> 47
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<220>
<223> B determinant of hCD45

<400> 106
Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His Ala Asp Ser
1 5 10 15
Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala
20 25 30
Ala Asn Ala Lys Leu Asn Pro Thr Pro Gly Ser Asn Ala Ile Ser
35 40 45

<210> 107
<211> 1211
<212> PRT
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<220>
<223> hCD45RA

<300>
<308> UniProt Accession P08575-8
<309> 2018 03 28

<400> 107
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
1 5 10 15
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
20 25 30
Thr Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp
35 40 45
Pro Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu
50 55 60
Arg Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn
65 70 75 80
Thr Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe
85 90 95
Asn Thr Thr Asp Ala Tyr Leu Asn Ala Ser Glu Thr Thr Thr Leu Ser
100 105 110
Pro Ser Gly Ser Ala Val Ile Ser Thr Thr Thr Ile Ala Thr Thr Pro
115 120 125

Ser	Lys	Pro	Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	Ile	Thr	Val	Asp	Tyr
130						135					140				
Leu	Tyr	Asn	Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	Lys	Leu	Asn	Val	Asn
145				150						155					160
Glu	Asn	Val	Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His
			165						170					175	
Asn	Leu	Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser
		180						185					190		
Cys	Thr	Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val
	195					200					205				
Glu	Lys	Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr
210						215				220					
Thr	Ile	Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr
225				230					235					240	
Gln	Asn	Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn
			245					250						255	
Lys	Glu	Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys
		260					265					270			
Asp	Ser	Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys
		275				280						285			
Ile	Ile	Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe
290						295				300					
Cys	Arg	Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro
305				310					315					320	
Gln	Arg	Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu
			325					330					335		
Lys	Asp	Cys	Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln
		340					345					350			
Asn	Leu	Lys	Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile
	355					360						365			
Ile	Ala	Lys	Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr
370						375					380				
Thr	Lys	Ser	Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met
385				390					395					400	
Thr	Ser	Asp	Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg
			405					410					415		
Asn	Gly	Pro	His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr
		420					425					430			
Leu	Val	Arg	Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp
	435					440					445				
Leu	Gln	Tyr	Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly
450					455						460				
Asp	Tyr	Pro	Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn
465				470					475					480	
Ser	Lys	Ala	Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser
			485					490					495		
Ile	Ala	Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys
		500					505					510			
Arg	Ser	Cys	Asn	Leu	Asp	Glu	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	
	515					520					525				

Glu	Lys	Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu
530						535					540				
Glu	Thr	Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala
545					550					555					560
Glu	Phe	Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu
				565					570					575	
Ala	Arg	Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu
			580					585					590		
Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala
		595					600					605			
Gly	Ser	Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro
610						615					620				
Arg	Lys	Tyr	Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp
625					630					635					640
Phe	Trp	Arg	Met	Ile	Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val
				645					650					655	
Thr	Arg	Cys	Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro
			660					665					670		
Ser	Met	Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile
		675					680					685			
Asn	Gln	His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile
690						695					700				
Val	Asn	Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln
705					710					715					720
Phe	Thr	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu
				725					730					735	
Leu	Lys	Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly
			740					745					750		
Pro	Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr
		755					760					765			
Ile	Gly	Ile	Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val
	770					775					780				
Asp	Val	Tyr	Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met
785					790					795					800
Val	Gln	Val	Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu
				805					810					815	
Tyr	Asn	Gln	Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro
			820					825					830		
Tyr	Leu	His	Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro
		835					840					845			
Leu	Glu	Ala	Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr
	850					855					860				
Gln	His	Ile	Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser
865					870					875					880
Asn	Val	Ile	Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu
				885					890					895	
Glu	Met	Ser	Lys	Glu	Ser	Glu	His	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp
			900					905					910		
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			20					25					30		
Thr	Gly	Val	Ser	Ser	Val	Gln	Thr	Pro	His	Leu	Pro	Thr	His	Ala	Asp
		35					40					45			
Ser	Gln	Thr	Pro	Ser	Ala	Gly	Thr	Asp	Thr	Gln	Thr	Phe	Ser	Gly	Ser
	50					55				60					
Ala	Ala	Asn	Ala	Lys	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Asn	Ala	Ile	Ser
65				70						75				80	
Asp	Ala	Tyr	Leu	Asn	Ala	Ser	Glu	Thr	Thr	Thr	Leu	Ser	Pro	Ser	Gly
			85					90						95	
Ser	Ala	Val	Ile	Ser	Thr	Thr	Thr	Ile	Ala	Thr	Thr	Pro	Ser	Lys	Pro
		100						105					110		
Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	Ile	Thr	Val	Asp	Tyr	Leu	Tyr	Asn
		115					120					125			
Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	Lys	Leu	Asn	Val	Asn	Glu	Asn	Val
	130					135					140				
Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His	Asn	Leu	Thr
145				150						155				160	
Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys	Thr	Ala
			165					170						175	
Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu	Lys	Phe
		180					185					190			
Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr	Ile	Cys
		195				200						205			
Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln	Asn	Ile
	210					215					220				
Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys	Glu	Ile
225				230						235				240	
Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp	Ser	Glu
			245					250						255	
Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile	Ile	Lys
		260						265					270		
Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys	Arg	Ser
	275					280						285			
Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln	Arg	Ser
	290				295					300					
Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys	Asp	Cys
305				310					315					320	
Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn	Leu	Lys
			325					330						335	
Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile	Ala	Lys
		340					345						350		
Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr	Lys	Ser
		355				360						365			
Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr	Ser	Asp
	370					375					380				
Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn	Gly	Pro

385					390					395				400
His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu	Val Arg
				405					410					415
Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu	Gln Tyr
			420					425					430	
Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp	Tyr Pro
		435					440					445		
Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn	Ser	Lys Ala
	450					455					460			
Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile	Ala Leu
465					470					475				480
Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg	Ser Cys
				485				490						495
Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu	Lys Gln
		500						505					510	
Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu	Thr Tyr
		515					520						525	
Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu	Phe Gln
	530					535						540		
Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala	Arg Lys
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Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr Asp
				565					570					575
Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser Asn
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Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp Arg
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Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met Glu
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Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln His
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Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn Lys
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Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu	Lys Leu
705					710					715				720
Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro	Ile Val
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Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	Gly Ile
			740					745					750	
Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val	Asp	Val Tyr
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Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met	Val	Gln Val
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Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu	Tyr	Asn Gln

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Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro	Tyr	Leu
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Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro	Leu	Glu
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Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr	Gln	His
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Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn	Val
	850					855				860				Ile
Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu	Met
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Lys	Glu	Ser	Glu	His	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp	Ser
			885					890					895	Asp
Ser	Glu	Glu	Pro	Ser	Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met	Ser
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	915						920					925		Thr
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Ser	Met	Ile	Gln	Val	Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser
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Glu	Gly	Asn	Lys	His	His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys
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		1060					1065					1070		Leu
Glu	Ser	Ala	Glu	Thr	Glu	Glu	Val	Asp	Ile	Phe	Gln	Val	Val	Lys
	1075				1080				1085					
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Gln	Phe	Leu	Tyr	Asp	Val	Ile	Ala	Ser	Thr	Tyr	Pro	Ala	Gln	Asn
1105				1110					1115					1120
Gln	Val	Lys	Lys	Asn	Asn	His	Gln	Glu	Asp	Lys	Ile	Glu	Phe	Asp
			1125					1130					1135	Asn
Glu	Val	Asp	Lys	Val	Lys	Gln	Asp	Ala	Asn	Cys	Val	Asn	Pro	Leu
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Ala	Pro	Glu	Lys	Leu	Pro	Glu	Ala	Lys	Glu	Gln	Ala	Glu	Gly	Ser
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Pro	Thr	Ser	Gly	Thr	Glu	Gly	Pro	Glu	His	Ser	Val	Asn	Gly	Pro
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Thr	Gly	Leu	Thr	Thr	Ala	Lys	Met	Pro	Ser	Val	Pro	Leu	Ser	Ser	Asp
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Pro	Leu	Pro	Thr	His	Thr	Thr	Ala	Phe	Ser	Pro	Ala	Ser	Thr	Phe	Glu
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Arg	Glu	Asn	Asp	Phe	Ser	Glu	Thr	Thr	Thr	Ser	Leu	Ser	Pro	Asp	Asn
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Thr	Ser	Thr	Gln	Val	Ser	Pro	Asp	Ser	Leu	Asp	Asn	Ala	Ser	Ala	Phe
			85					90						95	
Asn	Thr	Thr	Gly	Val	Ser	Ser	Val	Gln	Thr	Pro	His	Leu	Pro	Thr	His
			100					105					110		
Ala	Asp	Ser	Gln	Thr	Pro	Ser	Ala	Gly	Thr	Asp	Thr	Gln	Thr	Phe	Ser
		115					120					125			
Gly	Ser	Ala	Ala	Asn	Ala	Lys	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Asn	Ala
	130					135						140			
Ile	Ser	Asp	Ala	Tyr	Leu	Asn	Ala	Ser	Glu	Thr	Thr	Thr	Leu	Ser	Pro
145				150					155					160	
Ser	Gly	Ser	Ala	Val	Ile	Ser	Thr	Thr	Thr	Ile	Ala	Thr	Thr	Pro	Ser
			165					170						175	
Lys	Pro	Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	Ile	Thr	Val	Asp	Tyr	Leu
			180				185					190			
Tyr	Asn	Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	Lys	Leu	Asn	Val	Asn	Glu
		195					200					205			
Asn	Val	Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His	Asn
	210					215						220			
Leu	Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys
225				230						235				240	
Thr	Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu
			245						250					255	
Lys	Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr
		260						265					270		

Ile	Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln	275	280	285
Asn	Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys	290	295	300
Glu	Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp	305	310	315
Ser	Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile	325	330	335
Ile	Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys	340	345	350
Arg	Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln	355	360	365
Arg	Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys	370	375	380
Asp	Cys	Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn	385	390	395
Leu	Lys	Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile	405	410	415
Ala	Lys	Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr	420	425	430
Lys	Ser	Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr	435	440	445
Ser	Asp	Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn	450	455	460
Gly	Pro	His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu	465	470	475
Val	Arg	Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu	485	490	495
Gln	Tyr	Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp	500	505	510
Tyr	Pro	Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn	Ser	515	520	525
Lys	Ala	Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile	530	535	540
Ala	Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg	545	550	555
Ser	Cys	Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu	565	570	575
Lys	Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu	580	585	590
Thr	Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu	595	600	605
Phe	Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala	610	615	620
Arg	Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	625	630	635
Tyr	Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	645	650	655
Ser	Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	660	665	670

Lys	Tyr	Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	675	680	685
Trp	Arg	Met	Ile	Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	690	695	700
Arg	Cys	Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	705	710	715
Met	Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	725	730	735
Gln	His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	740	745	750
Asn	Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln	Phe	755	760	765
Thr	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu	770	775	780
Lys	Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro	785	790	795
Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	805	810	815
Gly	Ile	Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val	Asp	820	825	830
Val	Tyr	Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met	Val	835	840	845
Gln	Val	Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu	Tyr	850	855	860
Asn	Gln	Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro	Tyr	865	870	875
Leu	His	Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro	Leu	885	890	895
Glu	Ala	Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr	Gln	900	905	910
His	Ile	Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn	915	920	925
Val	Ile	Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu	930	935	940
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Ser	Tyr	Trp	Lys	Pro	Glu	Val	Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys	980	985	990
Glu	Thr	Ile	Gly	Asp	Phe	Trp	Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys	995	1000	1005
Val	Ile	Val	Met	Leu	Thr	Glu	Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys	1010	1015	1020
Ala	Gln	Tyr	Trp	Gly	Glu	Gly	Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val	1025	1030	1035
Asp	Leu	Lys	Asp	Thr	Asp	Lys	Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe	1045	1050	1055
Glu	Leu	Arg	His	Ser	Lys	Arg	Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr	1060	1065	1070

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 Asn Gly Gln Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe
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 Asp Asn Glu Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro
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 35 40 45
 Gly Ser Ala Val Ile Ser Thr Thr Thr Ile Ala Thr Thr Pro Ser Lys
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 Pro Thr Cys Asp Glu Lys Tyr Ala Asn Ile Thr Val Asp Tyr Leu Tyr
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 Asn Lys Glu Thr Lys Leu Phe Thr Ala Lys Leu Asn Val Asn Glu Asn

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Val	Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His	Asn	Leu	
			100					105					110			
Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys	Thr	
		115					120					125				
Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu	Lys	
	130					135					140					
Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr	Ile	
145				150						155					160	
Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln	Asn	
			165					170						175		
Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys	Glu	
			180					185					190			
Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp	Ser	
	195					200						205				
Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile	Ile	
	210					215					220					
Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys	Arg	
225				230						235					240	
Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln	Arg	
				245					250					255		
Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys	Asp	
			260					265					270			
Cys	Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn	Leu	
	275					280						285				
Lys	Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile	Ala	
	290					295					300					
Lys	Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr	Lys	
305					310					315					320	
Ser	Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr	Ser	
				325					330					335		
Asp	Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn	Gly	
			340					345					350			
Pro	His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu	Val	
	355						360					365				
Arg	Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu	Gln	
370						375					380					
Tyr	Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp	Tyr	
385				390						395					400	
Pro	Gly	Glu	Pro	Phe	Ile	Leu	His	His	Ser	Thr	Ser	Tyr	Asn	Ser	Lys	
				405					410					415		
Ala	Leu	Ile	Ala	Phe	Leu	Ala	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile	Ala	
			420					425					430			
Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg	Ser	
	435						440					445				
Cys	Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu	Lys	
	450					455					460					
Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu	Thr	
465				470						475					480	
Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu	Phe	

				485				490				495			
Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala	Arg
			500					505					510		
Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr
		515					520					525			
Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser
	530					535					540				
Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	Lys
545					550					555					560
Tyr	Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp
				565					570					575	
Arg	Met	Ile	Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	Arg
			580					585					590		
Cys	Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met
		595				600						605			
Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln
	610					615					620				
His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn
625					630					635					640
Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln	Phe	Thr
				645					650					655	
Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu	Lys
			660					665					670		
Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro	Ile
		675				680						685			
Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	Gly
	690					695					700				
Ile	Asp	Ala	Met	Leu	Glu	Gly	Leu	Glu	Ala	Glu	Asn	Lys	Val	Asp	Val
705					710					715					720
Tyr	Gly	Tyr	Val	Val	Lys	Leu	Arg	Arg	Gln	Arg	Cys	Leu	Met	Val	Gln
				725					730					735	
Val	Glu	Ala	Gln	Tyr	Ile	Leu	Ile	His	Gln	Ala	Leu	Val	Glu	Tyr	Asn
			740					745					750		
Gln	Phe	Gly	Glu	Thr	Glu	Val	Asn	Leu	Ser	Glu	Leu	His	Pro	Tyr	Leu
		755					760					765			
His	Asn	Met	Lys	Lys	Arg	Asp	Pro	Pro	Ser	Glu	Pro	Ser	Pro	Leu	Glu
	770					775					780				
Ala	Glu	Phe	Gln	Arg	Leu	Pro	Ser	Tyr	Arg	Ser	Trp	Arg	Thr	Gln	His
785					790					795					800
Ile	Gly	Asn	Gln	Glu	Glu	Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn	Val
				805					810					815	
Ile	Pro	Tyr	Asp	Tyr	Asn	Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu	Met
			820					825					830		
Ser	Lys	Glu	Ser	Glu	His	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp	Ser
		835					840					845			
Asp	Ser	Glu	Glu	Pro	Ser	Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met	Ser
	850					855					860				
Tyr	Trp	Lys	Pro	Glu	Val	Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys	Glu
865					870					875					880
Thr	Ile	Gly	Asp	Phe	Trp	Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys	Val

				885					890					895			
Ile	Val	Met	Leu	Thr	Glu	Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys	Ala		
			900					905					910				
Gln	Tyr	Trp	Gly	Glu	Gly	Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val	Asp		
		915					920					925					
Leu	Lys	Asp	Thr	Asp	Lys	Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe	Glu		
	930					935					940						
Leu	Arg	His	Ser	Lys	Arg	Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr	Gln		
945					950				955						960		
Tyr	Thr	Asn	Trp	Ser	Val	Glu	Gln	Leu	Pro	Ala	Glu	Pro	Lys	Glu	Leu		
			965						970						975		
Ile	Ser	Met	Ile	Gln	Val	Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser		
		980						985					990				
Ser	Glu	Gly	Asn	Lys	His	His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys		
	995						1000					1005					
Arg	Asp	Gly	Ser	Gln	Gln	Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu		
	1010					1015					1020						
Leu	Glu	Ser	Ala	Glu	Thr	Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val		
1025					1030					1035					1040		
Lys	Ala	Leu	Arg	Lys	Ala	Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln		
			1045						1050					1055			
Tyr	Gln	Phe	Leu	Tyr	Asp	Val	Ile	Ala	Ser	Thr	Tyr	Pro	Ala	Gln	Asn		
	1060							1065				1070					
Gly	Gln	Val	Lys	Lys	Asn	Asn	His	Gln	Glu	Asp	Lys	Ile	Glu	Phe	Asp		
	1075					1080					1085						
Asn	Glu	Val	Asp	Lys	Val	Lys	Gln	Asp	Ala	Asn	Cys	Val	Asn	Pro	Leu		
	1090					1095					1100						
Gly	Ala	Pro	Glu	Lys	Leu	Pro	Glu	Ala	Lys	Glu	Gln	Ala	Glu	Gly	Ser		
1105					1110					1115					1120		
Glu	Pro	Thr	Ser	Gly	Thr	Glu	Gly	Pro	Glu	His	Ser	Val	Asn	Gly	Pro		
			1125					1130						1135			
Ala	Ser	Pro	Ala	Leu	Asn	Gln	Gly	Ser									
			1140					1145									

<210> 111

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> VL-CDR2

<400> 111

Ala Thr Ser Asn Leu Pro Ser

1

5

<210> 112

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 112

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Xaa Tyr
          20          25          30
Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile
          35          40          45
Tyr Ala Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu
          85          90          95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

<210> 113

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 113

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
          20          25          30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
          35          40          45
Ala Thr Ser Asn Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
          50          55          60
Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65          70          75          80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
          85          90          95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
```

100

105

<210> 114

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Human HCCR

<400> 114

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5					10					15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75				80	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85						90					95	
Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
			100					105					110		
Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
			115				120					125			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
	130					135					140				
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
145					150					155					160
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			165						170					175	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			180					185					190		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195					200					205			
Lys	Ala	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	210					215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu
225					230					235					240
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			245						250					255	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			260					265					270		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		275					280					285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
	290					295					300				

Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
				325					330						

<210> 115
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human HCCR

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5				10						15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75				80	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90						95	
Arg	Val	Glu	Pro	Lys	Ser	Cys	Val	Ala	Ala	Ala	His	His	His	His	His
			100					105					110		

His

<210> 116
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH-CDR2

Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Ala	Asn	Tyr	Ala	Glu	Lys	Phe	Gln
1				5				10						15	
Gly															

<210> 117
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 117

Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	Ala	Glu	Lys	Phe	Lys
1				5					10					15	
Gly															

<210> 118

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 118

Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Gln
1				5					10					15	
Gly															

<210> 119

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 119

Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Ser	Ala	Glu	Lys	Phe	Gln
1				5					10					15	
Gly															

<210> 120

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> VL-CDR2

<400> 120

Asn Thr Ala Asn Leu Pro Ser

1 5

<210> 121

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized HCVR

<400> 121

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr

20 25 30

Tyr Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Asp Ile Phe Pro Gly Gly Gly Tyr Ala Asn Tyr Ala Glu Lys Phe

50 55 60

Gln Gly Arg Val Thr Leu Thr Ala Asp Thr Ser Ile Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Val Val Tyr Tyr Cys

85 90 95

Val Arg Arg Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

100 105 110

Ser Ser

<210> 122

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized HCVR

<400> 122

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr

20 25 30

Tyr Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Asp Ile Phe Pro Gly Gly Gly Tyr Thr Asn Tyr Ala Glu Lys Phe

50 55 60

Lys	Gly	Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys
				85					90					95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 123
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Tyr	Ile	Gly	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	Asp	Ile	Phe	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
	50				55					60					
Gln	Gly	Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Val	Val	Tyr	Tyr	Cys
				85					90					95	
Val	Arg	Arg	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 124
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized HCVR

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		

Tyr Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Phe Pro Gly Gly Gly Tyr Thr Asn Ser Ala Glu Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Leu Thr Ala Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Val Val Tyr Tyr Cys
 85 90 95
 Val Arg Arg Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110
 Ser Ser

<210> 125
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized LCVR

<220>
 <221> SITE
 <222> 31
 <223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<400> 125
 Gln Ile Val Leu Thr Gln Ser Pro Thr Ile Met Ser Ala Ser Pro Gly
 1 5 10 15
 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Xaa Tyr
 20 25 30
 Met His Trp Phe Gln Gln Lys Thr Gly Thr Ser Pro Arg Leu Trp Ile
 35 40 45
 Tyr Asn Thr Ala Asn Leu Pro Ser Gly Val Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Ser Phe Ser Leu Thr Ile Ser Arg Met Glu Ala
 65 70 75 80
 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu
 85 90 95
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 126
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Humanized LCVR

<400> 126

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Thr	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Thr	Gly	Thr	Ser	Pro	Arg	Leu	Trp	Ile	Tyr
		35					40					45			
Asn	Thr	Ala	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70					75				80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys						
			100					105							

<210> 127

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> 1

<223> Xaa is any amino acid but Ala (A) or Asn (N)

<220>

<223> VL-CDR2

<400> 127

Xaa	Thr	Ser	Asn	Leu	Pro	Ser
1			5			

<210> 128

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<220>

<221> SITE

<222> 31

<223> Xaa is selected from Asn (N), Ser (S) and Gly (G)

<220>

<221> SITE

<222> 50

<223> Xaa is any amino acid but Ala (A) or Asn (N)

<400> 128

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1			5						10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Xaa	Tyr
		20						25					30		
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile
		35					40					45			
Tyr	Xaa	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu
			85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> 129

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized LCVR

<220>

<221> SITE

<222> 49

<223> Xaa is any amino acid but Ala (A) or Asn (N)

<400> 129

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1			5						10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
		20						25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Xaa	Thr	Ser	Asn	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Gly	Ser	Gly	Thr	Glu	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
65				70					75					80	
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
			85					90						95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
		100						105							

