

SEQUENCE LISTING

<110> Vir Biotechnology, Inc.
Humabs BioMed SA

<120> ANTIBODIES AGAINST INFLUENZA A VIRUSES

<130> 930585.411W0

<140> PCT/US2021/060123

<141> 2021-11-19

<150> US 63/117,437

<151> 2020-11-23

<150> US 63/123,419

<151> 2020-12-09

<160> 58

<170> PatentIn version 3.5

<210> 1

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> FHF11 VH (wt-nt)

<400> 1

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acctgtggca tctccgggga cagtgtctct agtcacagtg ctgcttgga ctggatcagg 120

cagtcccat cgagaggcct tgagtggctg ggaaggacat attacaggtc caagtggat 180

aatgattatg cagtctctgt gaaaagtcga ataaccatca atccagacac atccaagaac 240

cagttctccc tacagttgat ctctgtgact cccgaggaca cggctgtcta ttactgtgca 300

agagtgggtg ctatgacttt tggacttctt acagggggta tggacgtctg gggccaaggg 360

accacgggtca ccgtctcctc a 381

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<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF11 VH (aa)

<400> 2

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

Thr Leu Ser Val Thr Cys Gly Ile Ser Gly Asp Ser Val Ser Ser His
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 3

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF11 CDR-H1 (aa)

<400> 3

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

<210> 4

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF11 CDR-H2 (aa)

<400> 4

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
1 5

<210> 5

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF11 CDR-H3 (aa)

<400> 5

Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly Gly Met Asp
1 5 10 15

Val

<210> 6

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> FHF11 VH (co-nt)

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acatgcggaa tctccggcga cagcgtgtcc agccactccg ccgcttgga ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagtggtag 180
aatgactatg ccgtgtctgt gaagtccagg atcaccatca accagatac atccaagaat 240
cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggag ctatgacatt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

<210> 7

<211> 328

<212> DNA

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<220>

<223> FHF11 Vk (wt-nt)

<400> 7

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ctctcctgca gggccagtca gagtctgagc cgcagctact tagcctggta ccagcagaga 120

cctggcaagc ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtggt gtctgggaca gacttcagtc tcaccatcag cagtctggag 240

cctgaagatt ctgcaatgta tttctgtcag tactatggtg attcacctct attcagtttc 300

ggcccaggga ccaaagtgga tatcaaac 328

<210> 8

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF11 Vk (aa)

<400> 8

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Arg Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Pro Glu Asp Ser Ala Met Tyr Phe Cys Gln Tyr Tyr Gly Asp Ser Pro
85 90 95

Leu Phe Ser Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11 CDR-L1 (aa)

<400> 9

Gln Ser Leu Ser Arg Ser Tyr
1 5

<210> 10
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11 CDR-L2 (aa)

<400> 10

Gly Ala Ser
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<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11 CDR-L3 (aa)

<400> 11

Gln Tyr Tyr Gly Asp Ser Pro Leu Phe Ser
1 5 10

<210> 12
<211> 327
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<220>
<223> FHF11 Vk (co-nt)

<400> 12

gagatcgtgc tgaccagtc tcctggcaca cagagcctgt ctccaggaga gagggccacc

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Val Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Ala Thr Phe Gly Ile Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 15
<211> 10
<212> PRT
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<220>
<223> FHF12 CDR-H1 (aa)

<400> 15

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

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF12 CDR-H2 (aa)

<400> 16

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
1 5

<210> 17
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> FHF12 CDR-H3 (aa)

<400> 17

Ala Arg Val Gly Ala Ala Thr Phe Gly Ile Leu Thr Gly Gly Met Asp
1 5 10 15

Val

<210> 18
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> FHF12 VH (co-nt)

<400> 18
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acatgcgcta tctccggcga cagcgtgtcc agccactccg ccgcttgga ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagtggtag 180
aatgactatg ccgtgtccgt gaagtccagg atcaccatca acccagatac atccaagaat 240
cagttcagcc tgcagctggt gtctgtgacc cccgaggaca cagccgtgta ctattgtgct 300
agagtgggcg ccgctacctt tggcatcctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

<210> 19
<211> 328
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<220>
<223> FHF12 Vk (wt-nt)

<400> 19
gaaattgtgt tgacgcagtc tccaggcacc cagtctttgt ctccagggga tagagccacc 60
ctctcctgca gggccagtca gagtctgagc agaagctact tagcctggta ccagcagaga 120
cctggcaagc ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcagtc tcaccatcag cagtctggag	240
cctgaagatt ctgctatgta tttctgtcag tactatggtg attcacctct attcagtttc	300
ggccctggga ccaaagtgga tatcaaac	328

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<220>
 <223> FHF12 Vk (aa)

<400> 20

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Gln	Ser	Leu	Ser	Pro	Gly
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Asp	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Ser	Arg	Ser
			20					25					30		

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

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				

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

Pro	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Gln	Tyr	Tyr	Gly	Asp	Ser	Pro
				85					90					95	

Leu	Phe	Ser	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys
				100				105				

<210> 21
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 <213> Artificial Sequence

<220>
 <223> FHF12 CDR-L1 (aa)

<400> 21

Gln Ser Leu Ser Arg Ser Tyr
1 5

<210> 22

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF12 CDR-L2 (aa)

<400> 22

Gly Ala Ser
1

<210> 23

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> FHF12 CDR-L3 (aa)

<400> 23

Gln Tyr Tyr Gly Asp Ser Pro Leu Phe Ser
1 5 10

<210> 24

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> FHF12 Vk (co-nt)

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ccaggcaagc cacctaggct gctgatctac ggagcttcca gcagggctac aggcatccct	180
gacagattca gcggctctgg ctccggcacc gatttttccc tgacaatctc ttccctggag	240
ccagaggact ccgcatgta tttctgtcag tactatggcg atagcccact gttctctttt	300
ggccccggca ccaaggtgga tatcaag	327

<210> 25
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<220>
<223> FHF11-VH W36F (nt)

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acatgcggaa tctccggcga cagcgtgtcc agccactccg ccgctttcaa ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagtgggtac 180
aatgactatg ccgtgtctgt gaagtccagg atcaccatca acccagatac atccaagaat 240
cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggcg ctatgacctt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

<210> 26
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11-VH W36F (aa)

<400> 26

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

Thr Leu Ser Val Thr Cys Gly Ile Ser Gly Asp Ser Val Ser Ser His
20 25 30

Ser Ala Ala Phe Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 27
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> FHF11-VH W59F (nt)

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acatgcggaa tctccggcga cagcgtgtcc agccactccg ccgcttgga ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagttctac 180
aatgactatg ccgtgtctgt gaagtccagg atcaccatca accagatac atccaagaat 240
cagtttagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggcg ctatgacctt cggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

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

<220>
<223> FHF11-VH W59F (aa)

<400> 28

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

Thr Leu Ser Val Thr Cys Gly Ile Ser Gly Asp Ser Val Ser Ser His
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Phe Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11-VH W59F CDRH2 (aa)

<400> 29

Thr Tyr Tyr Arg Ser Lys Phe Tyr Asn
1 5

<210> 30
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> FHF11v3 VH (nt)

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caggtgcagc tgcagcagtc tggaccagga ctggtgaagc ctagccagac cctgtctgtg 60
acatgcggca tctccggcga cagcgtgtcc agctactccg ccgcttggaa ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagtgttac 180

aatgactatg ccgtgtctgt gaagtccagg atcaccatca acccagatac atccaagaat 240
cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggcg ctatgacctt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

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

<220>
<223> FHF11v3 VH (aa)

<400> 31

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 32
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11v3 CDRH1 (aa)

<400> 32

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

<210> 33
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> FHF11v6 VH (nt)

<400> 33
caggtgcagc tgcagcagtc tggaccagga ctggtgaagc ctagccagac cctgtctgtg 60
acatgcggaa tctccggcga cagcgtgtcc agccactccg ccgcttgga ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag cggctggtac 180
aatgactatg ccgtgtctgt gaagtccagg atcaccatca accagatac atccaagaat 240
cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggcg ctatgacctt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

<210> 34
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11v6 VH (aa)

<400> 34

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

Thr Leu Ser Val Thr Cys Gly Ile Ser Gly Asp Ser Val Ser Ser His
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Gly Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11v6 CDRH2 (aa)

<400> 35

Thr Tyr Tyr Arg Ser Gly Trp Tyr Asn
1 5

<210> 36
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> FHF11v9 VH (nt)

<400> 36
caggtgcagc tgcagcagtc tggaccagga ctggtgaagc ctagccagac cctgtctgtg 60
acatgcggca tctccggcga cagcgtgtcc agctactccg ccgcttggaa ctggatcaga 120
cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag cggctggtac 180
aatgactatg ccgtgtctgt gaagtccagg atcaccatca accagatac atccaagaat 240

cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
agagtgggcg ctatgacctt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
accacagtga cagtgtcttc c 381

<210> 37
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF11v9 VH (aa)

<400> 37

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Gly Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 38
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<212> DNA
<213> Artificial Sequence

<220>

<223> FHF12-VH-W36F (nt)

<400> 38

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cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagtggtag      180
aatgactatg ccgtgtccgt gaagtccagg atcaccatca acccagatac atccaagaat      240
cagttcagcc tgcagctggt gtctgtgacc cccgaggaca cagccgtgta ctattgtgct      300
agagtgggcg ccgctacctt tggcatcctg acaggcgga tggacgtgtg gggacaggga      360
accacagtga cagtgtcttc c                                          381
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<210> 39

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<213> Artificial Sequence

<220>

<223> FHF12-VH-W36F (aa)

<400> 39

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

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 40
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<223> FHF12-VH-W59F (nt)

<400> 40
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cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag caagttctac 180
aatgactatg ccgtgtccgt gaagtccagg atcaccatca acccagatac atccaagaat 240
cagttcagcc tgcagctggg gtctgtgacc cccgaggaca cagccgtgta ctattgtgct 300
agagtgggcg ccgctacctt tggcatcctg acaggcggaa tggacgtgtg gggacagggg 360
accacagtga cagtgtcttc c 381

<210> 41
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF12-VH-W59F (aa)

<400> 41

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Phe Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Val Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Gly Ala Ala Thr Phe Gly Ile Leu Thr Gly
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FHF12-CDRH2-W59F (aa)

<400> 42

Thr Tyr Tyr Arg Ser Lys Phe Tyr Asn
1 5

<210> 43
<211> 128
<212> PRT
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<220>
<223> FM08 VH

<400> 43

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Gly Trp Tyr Asn Asp Tyr Ala
50 55 60

Glu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Asp Ala Phe Asp Met Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 44

<211> 103

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence FM08 VL

<400> 44

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

<210> 45

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> WT hIgG1 Fc

<400> 45

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 46
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric hinge sequence

<400> 46

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro

<210> 47
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence IgHG1*01, G1m3 CH1-CH3 with
M428L and N434S mutations and C-terminal lysine

<400> 47

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	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr		
305					310					315					320		
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
			325					330									

<210> 48

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence Kappa light chain CL

<400> 48

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> 49

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence IgHG1*01, G1m3 CH1-CH3 with
M428L and N434S mutations and without C-terminal
lysine

<400> 49

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	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly							
				325											

<210> 50

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence FHF11v9-MLNS heavy chain with
C-terminal lysine

<400> 50

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

Phe	Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr	Gln
		435					440					445			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		450				455									

<210> 51
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence FHF11v9-MLNS heavy chain
 without C-terminal lysine

<400> 51

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

305					310					315					320
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
				325					330					335	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
			340					345					350		
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met
	355						360					365			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
	370					375					380				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
385				390					395					400	
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
			405					410						415	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val
			420				425						430		
Phe	Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr	Gln
	435					440						445			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly								
	450					455									

<210> 52

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence FHF11v9-MLNS light chain

<400> 52

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Gln	Ser	Leu	Ser	Pro	Gly
1				5				10						15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Ser	Arg	Ser
			20					25				30			
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Lys	Pro	Pro	Arg	Leu	Leu
	35					40					45				
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50				55					60					
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu
65				70				75						80	
Pro	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Gln	Tyr	Tyr	Gly	Asp	Ser	Pro
			85					90					95		
Leu	Phe	Ser	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Thr	Val
			100				105						110		
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys
	115					120					125				
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
	130				135					140					
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn
145				150				155						160	
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser
			165				170						175		
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys
	180					185				190					
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr

	195		200		205
Lys	Ser	Phe	Asn	Arg	Gly
			Glu	Cys	
210			215		

<210> 53
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence - FHF11 and FHF12 CDRH1 with flanking Phe

<400> 53
 Gly Asp Ser Val Ser Ser His Ser Ala Ala Phe
 1 5 10

<210> 54
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence - FHF11v9 heavy chain nucleotide sequence

<400> 54
 cagggtgcagc tgcagcagtc tggaccagga ctggtgaagc ctagccagac cctgtctgtg 60
 acatgcggca tctccggcga cagcgtgtcc agctactccg ccgcttgga ctggatcaga 120
 cagagcccat ctaggggact ggagtggctg ggaaggacct actatcggag cggctggtac 180
 aatgactatg ccgtgtctgt gaagtccagg atcaccatca acccagatac atccaagaat 240
 cagttcagcc tgcagctgat ctctgtgacc cccgaggaca cagccgtgta ctattgtgcc 300
 agagtgggcg ctatgacctt tggcctgctg acaggcggaa tggacgtgtg gggacaggga 360
 accacagtga cagtgtcttc cgcacagacc aaggggcccat cggctcttccc cctggcacca 420
 agtagcaaga gcacatccgg tggcacagcc gccctggggt gtctggtgaa agattatttc 480
 cctgagcccg tgacagtctc ctggaactct ggcgccctga cctccggagt gcacacattc 540
 cctgtctgtc tgacgtccag cggcctgtac tccctgtctt ccgtggtgac cgtgccaagc 600
 tcttccctgg gcacccagac atatatctgc aacgtgaatc acaagccttc caatacaaag 660
 gtggacaaga ggggtggagcc aaagagctgt gataagacct atacatgccc accttgtcca 720
 gctccagagc tgctgggagg cccatccgtg ttcctgtttc caccgaagcc caaggacacc 780
 ctgatgatct ctagaacccc agaggtgaca tgcgtggtgg tggacgtgtc ccacgaggat 840
 cccgaggtga agtttaactg gtacgtggat ggcgtggagg tgcataatgc taagacaaag 900
 cccagggagg agcagtacaa cagcacctat cgggtggtgt ctgtgctgac agtgctgcat 960
 caggactggc tgaacggcaa ggagtataag tgcaaggtga gcaataaggc cctgcctgct 1020
 ccaatcgaga agaccatctc taaggccaag ggccagccca gagagcctca ggtgtacaca 1080
 ctgcctccaa gccgcgagga gatgaccaag aaccaggtgt ctctgacatg tctggtgaag 1140
 ggcttctatc cctctgacat cgctgtggag tgggagtcca atggccagcc tgagaacaat 1200
 tacaagacca caccctgtg gctggactcc gatggcagct tctttctgta ttccaagctg 1260
 accgtggata agagcagggtg gcagcagggc aacgtgttct cctgttctgt gatgcacgaa 1320
 gccctgcaca accattatac tcagaagtcc ctgtccctgt cccctggaaa a 1371

<210> 55
 <211> 649

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence - FHF11v9 light chain
nucleotide sequence

<400> 55
gaaattgtgt tgacgcagtc tccaggcacc cagtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtctgagc cgcagctact tagcctggta ccagcagaga 120
cctggcaagc ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcagtc tcaccatcag cagtctggag 240
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ggcccaggga ccaaagtgga tatcaaaccg tacggtggct gcaccatctg tcttcatctt 360
cccgccatct gatgagcaat tgaaatctgg aactgcctcc gtggtgtgcc tgctgaacaa 420
tttctacccc agggaggcca aggtgcagtg gaaggtggac aacgctctgc agagcggcaa 480
ttctcaggag tccgtgaccg agcaggacag caaggattct acatattccc tgtccagcac 540
cctgacactg agcaaggccg attacgagaa gcacaagggtg tatgcttgtg aggtgaccca 600
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<210> 56
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence - FHF11v9 heavy chain

<400> 56
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Val Thr Cys Gly Ile Ser Gly Asp Ser Val Ser Ser Tyr
20 25 30
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Gly Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Ile Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Val Gly Ala Met Thr Phe Gly Leu Leu Thr Gly
100 105 110
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
130 135 140
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr

				85					90					95		
Tyr	Tyr	Cys	Ala	Arg	Val	Gly	Ala	Met	Ile	Phe	Gly	Leu	Leu	Thr	Gly	
			100					105					110			
Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
		115					120					125				

<210> 58

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence - FHF-VL-UCA

<400> 58

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