

SEQUENCE LISTING

<110> InflaRx GmbH

<120> Humanized anti-C5a antibodies

<130> 680-10 PCT

<150> EP20173255.9

<151> 2020-05-06

<160> 25

<170> PatentIn version 3.5

<210> 1

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1

Thr	Leu	Gln	Lys	Lys	Ile	Glu	Glu	Ile	Ala	Ala	Lys	Tyr	Lys	His	Ser
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Val	Val	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys	Val	Asn	Asn	Asp	Glu
			20					25					30		

Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro	Arg	Cys	Ile
		35					40					45			

Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser	Gln	Leu	Arg	Ala	Asn
	50					55					60				

Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg
65					70				

<210> 2

<211> 9

<212> PRT

<213> Homo sapiens

<400> 2

Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala
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<210> 3

<211> 7
<212> PRT
<213> Homo sapiens

<400> 3

Ser His Lys Asp Met Gln Leu
1 5

<210> 4
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<212> PRT
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<400> 4

Asp Glu Thr Cys Glu Gln Arg
1 5

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

<400> 5

His Lys Asp Met Gln
1 5

<210> 6
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH0

<400> 6

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

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

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Arg Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 7
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH1

<400> 7

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

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

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Arg Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 8
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH2

<400> 8

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

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

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Arg Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 9
<211> 119
<212> PRT
<213> Artificial Sequence

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<223> VH3

<400> 9

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 Ser Phe Thr Thr Phe
20 25 30

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Arg Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 10

<211> 119

<212> PRT

<213> Artificial Sequence

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<223> VH4

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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 Ser Phe Thr Thr Phe
20 25 30

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Arg Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 11
<211> 119
<212> PRT
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<220>
<223> VH5

<400> 11

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 Ser Phe Thr Thr Phe
20 25 30

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

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 12
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> V_kappa_0

<400> 12

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

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

Gly Asp Ser Tyr Met Lys Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Ile Pro Ala
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 13
<211> 111

<212> PRT
<213> Artificial Sequence

<220>
<223> V_kappa_1

<400> 13

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

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

Gly Asp Ser Tyr Met Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Ile Pro Ser
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 14
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> V_kappa_2

<400> 14

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

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

Gly Asp Ser Tyr Met Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Ile Pro Ser
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 15
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> V_kappa_3

<400> 15

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

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

Gly Asp Ser Tyr Met Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Ile Pro Ser
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 16
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> V_kappa_4

<400> 16

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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 17
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence formed from the combination of VH1 to VH5

<220>
<221> MISC_FEATURE
<222> (9)..(9)

<223> Xaa9 is A or P

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa11 is L or P

<220>

<221> MISC_FEATURE

<222> (20)..(20)

<223> Xaa20 is I or V

<220>

<221> MISC_FEATURE

<222> (38)..(38)

<223> Xaa38 is K or R

<220>

<221> MISC_FEATURE

<222> (48)..(48)

<223> Xaa48 is I or M

<220>

<221> MISC_FEATURE

<222> (63)..(63)

<223> Xaa63 is K or R

<220>

<221> MISC_FEATURE

<222> (68)..(68)

<223> Xaa68 is A or V

<220>

<221> MISC_FEATURE

<222> (70)..(70)

<223> Xaa70 is L or M

<220>

<221> MISC_FEATURE

<222> (82)..(82)

<223> Xaa82 is E or Q

<220>

<221> MISC_FEATURE

<222> (86)..(86)

<223> Xaa86 is L or P

<220>

<221> MISC_FEATURE

<222> (87)..(87)

<223> Xaa87 is R or T

<220>

<221> MISC_FEATURE

<222> (91)..(91)

<223> Xaa91 is S or T

<400> 17

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

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

Trp Met Asp Trp Val Xaa Gln Ala Pro Gly Gln Gly Leu Glu Trp Xaa
35 40 45

Gly Arg Ile Asp Pro Ser Asp Ser Glu Ser Arg Leu Asp Gln Xaa Phe
50 55 60

Lys Asp Arg Xaa Thr Xaa Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Xaa Leu Ser Ser Xaa Xaa Ser Glu Asp Xaa Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Asp Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 18

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence formed from the combination of V_kappa_1 to
V_kappa_4

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa3 is V or Q

<220>

<221> MISC_FEATURE

<222> (4)..(4)
<223> Xaa4 is L or M

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa9 is A or S

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa12 is A or S

<220>
<221> MISC_FEATURE
<222> (62)..(62)
<223> Xaa62 is I or V

<220>
<221> MISC_FEATURE
<222> (84)..(84)
<223> Xaa84 is E or P

<400> 18

Asp	Ile	Xaa	Xaa	Thr	Gln	Ser	Pro	Xaa	Ser	Leu	Xaa	Ala	Ser	Val	Gly
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Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp
			20					25					30		

Gly	Asp	Ser	Tyr	Met	Lys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
		35					40					45			

Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Gln	Ser	Gly	Xaa	Pro	Ser
	50					55					60				

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

Ser	Leu	Gln	Xaa	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn
				85					90					95	

Glu	Asp	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110	

<210> 19

<211> 327
<212> PRT
<213> Homo sapiens

<400> 19

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

Ser Thr Ser Glu Ser 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 Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> IFX-1 CDR1 heavy chain

<400> 20

Cys Lys Ala Ser Gly Tyr Ser Phe Thr Thr Phe Trp Met Asp
1 5 10

<210> 21
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> IFX-1 CDR2 heavy chain

<400> 21

Ile	Asp	Pro	Ser	Asp	Ser	Glu	Ser	Arg	Leu	Asp	Gln
1				5					10		

<210> 22

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> IFX-1 CDR3 heavy chain

<400> 22

Cys	Ala	Arg	Gly	Asn	Asp	Gly	Tyr	Tyr	Gly	Phe	Ala	Tyr
1				5					10			

<210> 23

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> IFX-1 CDR1 light chain

<400> 23

Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Lys
1				5					10					15	

<210> 24

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> IFX-1 CDR2 light chain

<400> 24

Ile	Tyr	Ala	Ala	Ser	Asn	Leu
1				5		

<210> 25

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> IFX-1 CDR3 light chain

<400> 25

Cys	Gln	Gln	Ser	Asn	Glu	Asp	Pro	Tyr	Thr
1				5					10