

eolf-seql
SEQUENCE LISTING

<110> OSE IMMUNOTHERAPEUTICS

<120> NEW ANTI-SIRPa ANTIBODIES AND THEIR THERAPEUTIC APPLICATIONS

<130> F2173/8PCT

<150> US 62/322,707
<151> 2016-04-14

<150> EP 17305182.2
<151> 2017-02-17

<160> 73

<170> PatentIn version 3.5

<210> 1
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<213> Homo sapiens

<400> 1

Ser Leu Ile Pro Val Gly Pro
1 5

<210> 2
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<220>
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<223> Xaa = G or A

<400> 2

Xaa Arg Glu Leu Ile Tyr Asn Gln Lys Glu Gly His
1 5 10

<210> 3
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<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa = DV or T

<220>
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<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 3

Lys Phe Arg Lys Gly Ser Pro Asp Xaa Glu
1 5 10

<210> 4
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<213> Homo sapiens

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Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg
1 5 10 15

Asp Ile Thr Leu Lys Trp Phe
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Ile Cys Glu Val Ala His Val Thr Leu Gln Gly
1 5 10

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<213> Homo sapiens

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Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
1 5 10

<210> 7

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Gly Arg Glu Leu Ile Tyr Asn Gln Lys Glu Gly His
1 5 10

<210> 8

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Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu
1 5 10

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<400> 9

Ala Arg Glu Leu Ile Tyr Asn Gln Lys Glu Gly His
1 5 10

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<400> 10

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Lys Phe Arg Lys Gly Ser Pro Asp Thr Glu
1 5 10

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Gly Arg Glu Leu Ile Tyr Asn
1 5

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His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg Asp
1 5 10 15

Ile Thr Leu Lys Trp Phe
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<400> 13

Ala Arg Glu Leu Ile Tyr Asn
1 5

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<400> 14

Ser Tyr Trp Val His
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<400> 15

Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 16

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Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 17

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<400> 17

Gly	Gly	Thr	Gly	Thr	Met	Ala	Trp	Phe	Ala	Tyr
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Gly	Gly	Thr	Gly	Thr	Leu	Ala	Trp	Phe	Ala	Tyr
1				5					10	

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

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<400> 20

Gly	Gly	Thr	Gly	Thr	Leu	Ala	Tyr	Phe	Ala	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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1	5	10

<210> 21
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<400> 21

Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Tyr	Gly	Asn	Thr	Tyr	Leu	Tyr
1				5					10					15	

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<400> 22

Arg	Val	Ser	Asn	Arg	Phe	Ser
1				5		

<210> 23
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<400> 23

Phe	Gln	Gly	Thr	His	Val	Pro	Tyr	Thr
1				5				

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<400> 24

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Val Arg Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 25

<211> 120

<212> PRT

<213> Artificial Sequence

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<223> Heavy chain variable domain

<400> 25

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 26

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<400> 26

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

Ser Leu Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr

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20

25

30

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 27

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<400> 27

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

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

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

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Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 28

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val Asp Lys Ser Ile Ser Thr Ala Tyr

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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	Gly	Gly	Thr	Gly	Thr	Leu	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	Gln					
				100					105					110						
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser													
				115					120											
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<400> 29																				
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu					
1					5					10					15					
Ser	Leu	Arg	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr					
				20					25					30						
Trp	Val	His	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met					
				35					40					45						
Gly	Asn	Ile	Asp	Pro	Ser	Asp	Ser	Asp	Thr	His	Tyr	Ser	Pro	Ser	Phe					
				50					55					60						
Gln	Gly	His	Val	Thr	Leu	Ser	Val	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						

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Val Arg Gly Gly Thr Gly Thr Met Ala Tyr Phe Ala Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 30
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<400> 30

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
 50 55 60

Gln Gly His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Leu Ala Tyr Phe Ala Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser

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115

120

<210> 31
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<400> 31

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln Gly
 85 90 95

Thr His Val Pro Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 32
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 <223> Light chain variable domain

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<400> 32

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Tyr Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 33

<211> 112

<212> PRT

<213> Artificial Sequence

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<223> Light chain variable domain

<400> 33

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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Tyr Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 34

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<213> Artificial Sequence

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<400> 34

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

eolf-seql																		
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	Pro	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			

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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 Pro Gly Lys
325

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<213> Artificial Sequence

<220>
<223> Light chain constant domain-CLkappa

<400> 35

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

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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

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<211> 447
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<213> Artificial Sequence

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<223> Heavy chain sequence 18D5

<400> 36

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Val Arg Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val

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115

120

125

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

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

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Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

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Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 38

<211> 447

<212> PRT

<213> Artificial Sequence

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<223> Heavy chain sequence HB

<400> 38

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln

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100

105

110

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser

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290

295

300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 39

<211> 447

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<213> Artificial Sequence

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<223> Heavy chain sequence HC

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eolf-seql

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

eolf-seql

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

eolf-seql

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 40

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain sequence HE

<400> 40

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val 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

eolf-seql

85

90

95

Val Arg Gly Gly Thr Gly Thr Leu Ala Trp Phe Ala Tyr Trp Gly Gln
 100 105 110

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

eolf-seql

275

280

285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 41

<211> 447

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Heavy chain sequence HF

<400> 41

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val 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 Gly Gly Thr Gly Thr Met Ala Tyr Phe Ala Tyr Trp Gly Gln
100 105 110

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

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

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

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

eolf-seql

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

eolf-seql

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 42
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain sequence HEF

<400> 42

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Leu Ser Val Asp Lys Ser Ile Ser Thr Ala Tyr

eolf-seql

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	Gly	Gly	Thr	Gly	Thr	Leu	Ala	Tyr	Phe	Ala	Tyr	Trp	Gly	Gln
			100					105						110	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120					125		
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
			130					135					140		
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145						150					155				160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170						175
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180						185					190	
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
			195				200						205		
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
			210			215						220			
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225						230					235				240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
					245				250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu

eolf-seql

260

265

270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 43

eolf-seql

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain sequence 18D5

<400> 43

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

eolf-seql

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 44
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain sequence LA

<400> 44

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Tyr Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln Gly

eolf-seql

85

90

95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 45

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain sequence LB

<400> 45

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

eolf-seql

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

eolf-seql

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 46
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence coding the heavy chain variable domain 18D5

<400> 46
caggtgcagc tgcagcagcc aggagctgag ctggtgaggc ctggctccag cgtgaagctg 60
tcctgcaagg ctagcggcta caccttcaca agctattggg tgacttgggt gaagcagcgg 120
ccaatccagg gcctggagtg gatcggcaac atcgaccca gcgactctga taccattac 180
aatcagaagt ttaaggacaa ggcctctctg accgtggata agtcttcag cacagcttat 240
atgcagctgt cttccctgac attcaggat tccgccgtgt actattgcgt gaggggagga 300
accggaacaa tggcttggtt tgcttactgg ggccaggga ccctgggtgac agtgtctgct 360

<210> 47
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence coding the heavy chain variable domain HA

<400> 47
gaggtgcagc tgggtgcagag cggagctgag gtgaagaagc caggcgagtc tctgaggatc 60
tcctgcaagg ctagcggcta caccttcaca tcttattggg tgacttgggt gcggcagatg 120
ccaggcaagg gcctggagtg gatcggcaac atcgacccta gcgactctga taccactac 180
aatcagaagt ttaaggacca tgtgacctg tctgtggata agtccatcag cacagcctat 240
ctgcagctgt ccagcctgaa ggcctccgat acagctatgt actattgcgt gaggggagga 300
accggaacaa tggcttggtt cgcttactgg ggccaggga ccctgggtgac agtgtcttcc 360

eolf-seql

<210> 48
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence coding the heavy chain variable domain HB

<400> 48
 gaggtgcagc tgggtgcagtc cggagctgag gtgaagaagc caggcgagtc tctgaggatc 60
 tcctgcaagg cttctggcta ctctttcacc agctattggg tgcactgggt gcggcagatg 120
 ccaggcaagg gcctggagtg gatgggcaac atcgacccta gcgactctga tacacactac 180
 aatcagaagt ttaaggacca tgtgaccctg agcgtggata agtccatcag cacagcctat 240
 ctgcagctgt ccagcctgaa ggccctctgat accgctatgt actattgcgt gaggggagga 300
 accggaacaa tggcttggtt cgcttactgg ggccagggca ccctggtgac agtgtcttcc 360

<210> 49
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence coding the heavy chain variable domain HC

<400> 49
 gaggtgcagc tgggtgcagtc tggcgccgag gtgaagaagc caggcgagag cctgaggatc 60
 tcttgcaagg ctagcggcta ctctttcacc tcctattggg tgcactgggt gcggcagatg 120
 ccaggcaagg gcctggagtg gatgggcaac atcgaccca gcgactctga tacacactac 180
 tcccctagct ttcagggccca tgtgaccctg tccgtggaca agtctatctc cacagcctat 240
 ctgcagctgt ccagcctgaa ggccagcgat accgctatgt actattgcgt gaggggagga 300
 accggaacaa tggcttggtt cgcttactgg ggccagggca ccctggtgac agtgtcttcc 360

<210> 50
 <211> 360
 <212> DNA

eolf-seql

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence coding the heavy chain variable domain HE

<400> 50

```
gaggtgcagc tgggtgcagtc tggcgccgag gtgaagaagc caggcgagag cctgaggatc      60
tcttgcaagg ctagcggcta ctctttcacc tcctattggg tgcactgggt gcggcagatg      120
ccaggcaagg gcctggagtg gatgggcaac atcgacccca gcgactctga tacacactac      180
ttccctagct ttcagggccca tgtgaccctg tccgtggaca agtctatctc cacagcctat      240
ctgcagctgt ccagcctgaa ggccagcgat accgctatgt actattgcgt gaggggagga      300
accggcacac tggcttggtt cgcttactgg ggccagggca ccctggtgac agtgtcttcc      360
```

<210> 51

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence coding the heavy chain variable domain HF

<400> 51

```
gaggtgcagc tgggtgcagtc tggcgccgag gtgaagaagc caggcgagag cctgaggatc      60
tcttgcaagg ctagcggcta ctctttcacc tcctattggg tgcactgggt gcggcagatg      120
ccaggcaagg gcctggagtg gatgggcaac atcgacccca gcgactctga tacacactac      180
ttccctagct ttcagggccca tgtgaccctg tccgtggaca agtctatctc cacagcctat      240
ctgcagctgt ccagcctgaa ggccagcgat accgctatgt actattgcgt gaggggagga      300
accggaacaa tggcttactt cgcttattgg ggccagggca ccctggtgac agtgtcttcc      360
```

<210> 52

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence coding the heavy chain variable domain HEF

eolf-seql

<400> 52
gaggtgcagc tgggtgcagtc tggcgccgag gtgaagaagc caggcgagag cctgaggatc 60
tcttgcaagg ctagcggcta ctctttcacc tcctattggg tgcactgggt gcggcagatg 120
ccaggcaagg gcctggagtg gatgggcaac atcgaccca gcgactctga tacacactac 180
tcccctagct ttcaggcca tgtgaccctg tccgtggaca agtctatctc cacagcctat 240
ctgcagctgt ccagcctgaa ggccagcgat accgctatgt actattgcgt gaggggagga 300
accggcacac tggcttactt cgcttattgg ggccaggga ccctggtgac agtgtcttcc 360

<210> 53
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence coding the light chain variable domain 18D5

<400> 53
gacgtggtca tgacccagac accactgagc ctgcccgtgt ccctgggcga tcaggcctct 60
atctcctgca ggtccagcca gtccctgggtg cacagctatg gcaacacata cctgtattgg 120
tacctgcaga agccaggcca gtccccaag ctgctgatct acagggtgtc taatcggttc 180
tccggcgtgc ctgacagggt ctccggctct ggctccggca ccgatttcac actgaagatc 240
agcagggtgg aggctgagga cctgggcgtg tatttctgtt ttcagggcac ccatgtgcc 300
tacacatttg gctctggcac caagctggag atcaag 336

<210> 54
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence coding the light chain variable domain LA

<400> 54
gacgtggtca tgacacagag cccactgtct ctgcctgtga ccctgggaca gccagcctct 60

eolf-seql

atctcctgca ggtccagcca gtccctgggtg cacagctatg gcaacacata cctgtattgg 120
taccagcaga ggcccggaca gagcccaagg ctgctgatct acagggtgtc taatcggttc 180
tccggcgtgc ctgacagggt tagcggctct ggctccggca ccgatttcac actgaagatc 240
tctagagtgg aggctgagga tgtgggcgtg tatttctgtt ttcagggcac ccatgtgcca 300
tacacatttg gcggcggcac caaggtggag atcaag 336

<210> 55

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence coding the light chain variable domain LB

<400> 55

gacgtggtca tgacacagag cccactgtct ctgcctgtga ccctgggaca gccagcctct 60
atctcctgca ggtccagcca gtccctgggtg cacagctacg gcaacacata cctgtattgg 120
ttccagcaga ggcccggaca gagcccaagg ctgctgatct atagggtgtc taatcggttc 180
tccggcgtgc ctgacagggt tagcggatct ggatccggaa ccgacttcac cctgaagatc 240
tctagagtgg aggctgagga tgtgggcgtg tactattgtt tccagggcac ccatgtgcca 300
tacacatttg gcggcggcac caaggtggag atcaag 336

<210> 56

<211> 456

<212> PRT

<213> Mus musculus

<400> 56

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

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

eolf-seql

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Val Arg Gly Gly Thr Gly Thr Met Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

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

Tyr Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
130 135 140

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

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

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

Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala
195 200 205

Ser Ser Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser
210 215 220

eolf-seq1

Thr Ile Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala
225 230 235 240

Pro Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile
245 250 255

Lys Asp Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val
260 265 270

Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
275 280 285

Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
290 295 300

Tyr Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Gln His Gln
305 310 315 320

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp
325 330 335

Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val
340 345 350

Arg Ala Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser
355 360 365

Arg Lys Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly
370 375 380

Asp Ile Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr
385 390 395 400

Lys Asp Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr
405 410 415

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Ser Lys Leu Asn Met Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe
420 425 430

Ser Cys Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys
435 440 445

Thr Ile Ser Arg Ser Pro Gly Lys
450 455

<210> 57
<211> 219
<212> PRT
<213> Mus musculus

<400> 57

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu

eolf-seql

115

120

125

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 58

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence coding HCDR1

<400> 58

agctattggg tgcac

15

<210> 59

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence coding HCDR1

<400> 59

tcctattggg tgcac 15

<210> 60
 <211> 15
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<220>
 <223> Sequence coding HCDR1

<400> 60
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<210> 61
 <211> 51
 <212> DNA
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<220>
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 aacatcgacc ccagcgactc tgatacccat tacaatcaga agtttaagga c 51

<210> 62
 <211> 51
 <212> DNA
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<220>
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<400> 62
 aacatcgacc ccagcgactc tgatacacac tactccccta gctttcaggg c 51

<210> 63
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence coding HCDR3

<400> 63

ggaggaaccg gaacaatggc ttggtttgct tac eolf-seql 33

<210> 64
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<212> DNA
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<400> 64
ggaggaaccg gcacactggc ttggttcgct tac 33

<210> 65
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<400> 65
ggaggaaccg gaacaatggc ttacttcgct tat 33

<210> 66
<211> 33
<212> DNA
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<223> Sequence coding HCDR3

<400> 66
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<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 67

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agggtccagcc agtccctggt gcacagctat ggcaacacat acctgtat 48

<210> 68
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<220>
 <223> Sequence coding LCDR2

<400> 68
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<210> 69
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 <212> DNA
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<400> 69
 tttcagggca cccatgtgcc atacaca 27

<210> 70
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 70

Glu	Leu	Ile	Tyr	Asn	Gln	Lys	Glu	Gly	His	Phe	Pro	Arg
1				5					10			

<210> 71
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 71

Arg	Asn	Asn	Met	Asp	Phe	Ser	Ile	Arg	Ile	Gly	Asn
1				5						10	

eolf-seql

<210> 72
<211> 9
<212> PRT
<213> Homo sapiens

<400> 72

Ser Pro Arg Asp Ile Thr Leu Lys Trp
1 5

<210> 73
<211> 4
<212> PRT
<213> Homo sapiens

<400> 73

Tyr Asn Gln Lys
1