

eolf-seq1
SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
<120> Therapeutic fusion protein
<130> 31238 WO
<150> EP13179056.0
<151> 2013-08-02
<160> 13
<170> PatentIn version 3.5
<210> 1
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<212> PRT
<213> Homo sapiens
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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
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Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
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Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

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

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Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu
 115 120 125
 Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile
 130 135 140
 Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu
 145 150 155 160
 Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln
 165 170 175
 Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn
 180 185 190
 Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp
 195 200 205
 Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu
 210 215 220
 Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu
 225 230 235 240
 Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile
 245 250 255
 Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu
 260 265 270
 Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala
 275 280 285
 Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr
 290 295 300
 Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro
 305 310 315 320
 Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile
 325 330 335
 Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu
 340 345 350
 Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln
 355 360 365
 Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser
 370 375 380

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Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly
385 390 395 400

Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn
405 410 415

Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe
420 425 430

Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg
435 440 445

Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu
450 455 460

Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile
465 470 475 480

Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu
485 490 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
500 505 510

Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
515 520 525

Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
530 535 540

Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
545 550 555 560

Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
565 570 575

Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
580 585 590

Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr
595 600 605

Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
610 615 620

Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
625 630 635 640

Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
645 650 655

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Gln Ala Tyr Arg 660 Ala Tyr Gln Asn Tyr 665 Ile Lys Lys Asn Gly 670 Glu Glu

Lys Leu 675 Leu Pro Gly Leu Asp 680 Leu Asn His Lys Gln 685 Leu Phe Phe Leu

Asn Phe 690 Ala Gln Val Trp Cys 695 Gly Thr Tyr Arg Pro 700 Glu Tyr Ala Val

Asn Ser 705 Ile Lys Thr Asp 710 Val His Ser Pro Gly 715 Asn Phe Arg Ile 720 Ile

Gly Thr Leu Gln 725 Asn Ser Ala Glu Phe Ser 730 Glu Ala Phe His Cys 735 Arg

Lys Asn Ser 740 Tyr Met Asn Pro Glu Lys 745 Lys Cys Arg Val Trp 750

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<213> Homo sapiens

<400> 3

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

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

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

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

Ala Arg Gly 100 Lys Gly Asn Thr His Lys 105 Pro Tyr Gly Tyr Val 110 Arg Tyr

Phe Asp Val 115 Trp Gly Gln Gly Thr 120 Leu Val Thr Val Ser 125 Ser

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

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Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
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<212> PRT

<213> Homo sapiens

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

Gly

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<211> 17

<212> PRT

<213> Homo sapiens

<400> 7

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 1 5 10 15

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val

<210> 8
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Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
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<210> 9
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Leu Gln Ile Tyr Asn Met Pro Ile
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 <213> Artificial Sequence

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 <223> Heavy chain antibody construct

<400> 11

Gln Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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90

85

95

Ala Arg Gly Lys₁₀₀ Gly Asn Thr His Lys₁₀₅ Pro Tyr Gly Tyr Val₁₁₀ Arg Tyr
Phe Asp Val₁₁₅ Trp Gly Gln Gly Thr₁₂₀ Leu Val Thr Val Ser₁₂₅ Ser Ala Ser
Thr Lys₁₃₀ Gly Pro Ser Val Phe₁₃₅ Pro Leu Ala Pro Ser₁₄₀ Ser Lys Ser Thr
Ser Gly Gly Thr Ala Ala₁₅₀ Leu Gly Cys Leu Val₁₅₅ Lys Asp Tyr Phe Pro₁₆₀
Glu Pro Val Thr Val₁₆₅ Ser Trp Asn Ser Gly₁₇₀ Ala Leu Thr Ser Gly₁₇₅ Val
His Thr Phe Pro₁₈₀ Ala Val Leu Gln Ser₁₈₅ Ser Gly Leu Tyr Ser₁₉₀ Leu Ser
Ser Val Val₁₉₅ Thr Val Pro Ser Ser₂₀₀ Ser Leu Gly Thr Gln₂₀₅ Thr Tyr Ile
Cys Asn Val Asn His Lys Pro₂₁₅ Ser Asn Thr Lys Val₂₂₀ Asp Lys Lys Val
Glu Pro Lys Ser Cys Asp₂₃₀ Lys Thr His Thr Cys₂₃₅ Pro Pro Cys Pro Ala₂₄₀
Pro Glu Leu Leu Gly₂₄₅ Gly Pro Ser Val Phe₂₅₀ Leu Phe Pro Pro Lys₂₅₅ Pro
Lys Asp Thr Leu₂₆₀ Met Ile Ser Arg Thr₂₆₅ Pro Glu Val Thr Cys₂₇₀ Val Val
Val Asp Val₂₇₅ Ser His Glu Asp Pro₂₈₀ Glu Val Lys Phe Asn₂₈₅ Trp Tyr Val
Asp Gly Val Glu Val His Asn₂₉₅ Ala Lys Thr Lys Pro₃₀₀ Arg Glu Glu Gln
Tyr Asn Ser Thr Tyr Arg₃₁₀ Val Val Ser Val Leu₃₁₅ Thr Val Leu His Gln₃₂₀
Asp Trp Leu Asn Gly₃₂₅ Lys Glu Tyr Lys Cys₃₃₀ Lys Val Ser Asn Lys₃₃₅ Ala
Leu Pro Ala Pro₃₄₀ Ile Glu Lys Thr Ile₃₄₅ Ser Lys Ala Lys Gly₃₅₀ Gln Pro
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr

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

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625					630												640
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
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Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Asn	Ser		
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Leu	Thr	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr	Gly		
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Met	His	Trp	Ile	Arg	Gln	Ala	Pro	Lys	Lys	Gly	Leu	Glu	Trp	Ile	Ala		
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Met	Ile	Tyr	Tyr	Asp	Ser	Ser	Lys	Met	Asn	Tyr	Ala	Asp	Thr	Val	Lys		
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Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu		
785					790				795						800		
Glu	Met	Asn	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala		
				805					810					815			
Val	Pro	Thr	Ser	His	Tyr	Val	Val	Asp	Val	Trp	Gly	Gln	Gly	Val	Ser		
			820					825					830				
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu		
		835					840					845					
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys		
	850					855					860						
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser		
865					870					875					880		
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser		
				885					890					895			
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser		

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900

905

910

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
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Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
930 935 940

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<211> 1168

<212> PRT

<213> Artificial Sequence

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<223> Heavy chain antibody construct

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

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

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

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

Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
100 105 110

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

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

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Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
195 200 205

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225 230 235 240

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
245 250 255

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
275 280 285

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

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

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
325 330 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
340 345 350

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

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
370 375 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385 390 395 400

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
420 425 430

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
435 440 445

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
450 455 460

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Gly Gly Gly Gly Ser Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys
465 470 475 480

Ile Lys Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu
485 490 495

Pro Cys Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg
500 505 510

Asn Val Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu
515 520 525

Arg Asp Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys
530 535 540

Thr Glu Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser
545 550 555 560

Cys Ile Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu
565 570 575

Lys Leu Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp
580 585 590

Glu Gln Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln
595 600 605

Leu Asn Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly
610 615 620

Thr Asp Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro
625 630 635 640

Arg Leu Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr
645 650 655

Lys Glu Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg
660 665 670

Leu Ile Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala
675 680 685

Leu Glu Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala
690 695 700

Thr Ala Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys
705 710 715 720

Met Thr Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly
725 730 735

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Lys Pro Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val
 740 745 750
 Asn Ile Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu
 755 760 765
 Tyr Leu Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp
 770 775 780
 Leu Gln Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser
 785 790 795 800
 Leu Ser Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu
 805 810 815
 Tyr Gly Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr
 820 825 830
 Val Asn Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala
 835 840 845
 Ala Phe Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln
 850 855 860
 Ile Arg Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp
 865 870 875 880
 Ala Glu Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu
 885 890 895
 Arg Ile Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn
 900 905 910
 Asn Glu Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn
 915 920 925
 Ile Ile Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu
 930 935 940
 Arg Glu Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val
 945 950 955 960
 Asn Ala Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly
 965 970 975
 Ile Leu Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn
 980 985 990
 Tyr Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe
 995 1000 1005

eo1f-seq1

Asp Asp Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp
 1010 1015 1020
 Trp Trp Thr Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln
 1025 1030 1035
 Cys Met Val Tyr Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly
 1040 1045 1050
 Gly Gln His Leu Asn Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala
 1055 1060 1065
 Asp Asn Gly Gly Leu Gly Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr
 1070 1075 1080
 Ile Lys Lys Asn Gly Glu Glu Lys Leu Leu Pro Gly Leu Asp Leu
 1085 1090 1095
 Asn His Lys Gln Leu Phe Phe Leu Asn Phe Ala Gln Val Trp Cys
 1100 1105 1110
 Gly Thr Tyr Arg Pro Glu Tyr Ala Val Asn Ser Ile Lys Thr Asp
 1115 1120 1125
 Val His Ser Pro Gly Asn Phe Arg Ile Ile Gly Thr Leu Gln Asn
 1130 1135 1140
 Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg Lys Asn Ser Tyr
 1145 1150 1155
 Met Asn Pro Glu Lys Lys Cys Arg Val Trp
 1160 1165

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 <213> Artificial Sequence

<220>
 <223> Light chain antibody construct

<400> 13

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser 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 Val Pro Ala Arg Phe Ser
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50						55				eolf-seq1 60					
Gly 65	Ser	Gly	Ser	Gly	Thr 70	Asp	Phe	Thr	Leu	Thr 75	Ile	Ser	Ser	Leu	Glu 80
Pro	Glu	Asp	Phe	Ala 85	Thr	Tyr	Tyr	Cys	Leu 90	Gln	Ile	Tyr	Asn	Met 95	Pro
Ile	Thr	Phe	Gly 100	Gln	Gly	Thr	Lys	Val 105	Glu	Ile	Lys	Arg	Thr 110	Val	Ala
Ala	Pro	Ser 115	Val	Phe	Ile	Phe	Pro 120	Pro	Ser	Asp	Glu	Gln 125	Leu	Lys	Ser
Gly	Thr 130	Ala	Ser	Val	Val	Cys 135	Leu	Leu	Asn	Asn	Phe 140	Tyr	Pro	Arg	Glu
Ala 145	Lys	Val	Gln	Trp	Lys 150	Val	Asp	Asn	Ala	Leu 155	Gln	Ser	Gly	Asn	Ser 160
Gln	Glu	Ser	Val	Thr 165	Glu	Gln	Asp	Ser	Lys 170	Asp	Ser	Thr	Tyr	Ser 175	Leu
Ser	Ser	Thr	Leu 180	Thr	Leu	Ser	Lys	Ala 185	Asp	Tyr	Glu	Lys	His 190	Lys	Val
Tyr	Ala	Cys 195	Glu	Val	Thr	His	Gln 200	Gly	Leu	Ser	Ser	Pro 205	Val	Thr	Lys
Ser	Phe 210	Asn	Arg	Gly	Glu	Cys 215									