

SEQUENCE LISTING

<110> BOEHRINGER INGELHEIM INTERNATIONAL GMBH

<120> BIPARATOPIC POLYPEPTIDES ANTAGONIZING WNT SIGNALING IN TUMOR CELLS

<130> P12-0401/WO/1

<160> 47

<170> BiSSAP 1.2

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<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of Wnt1-333E06mod

<400> 1

Thr	Tyr	Thr	Val	Gly
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<211> 17

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<213> Artificial Sequence

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<223> CDR2 of Wnt1-333E06mod

<400> 2

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

<210> 3

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<223> CDR3 of Wnt1-333E06mod

<400> 3

Asp	Thr	Arg	Thr	Val	Ala	Leu	Leu	Gln	Tyr	Arg	Tyr	Asp	Tyr
1				5					10				

<210> 4

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<223> CDR1 of Wnt1-333G06

<400> 4

Ser Tyr Ala Met Gly
1 5

<210> 5

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<220>

<223> CDR2 of Wnt1-333G06

<400> 5

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

<210> 6

<211> 19

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<213> Artificial Sequence

<220>

<223> CDR3 of Wnt1-333G06

<400> 6

Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr Trp Trp
1 5 10 15
Trp Glu Tyr

<210> 7

<211> 5

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<213> Artificial Sequence

<220>

<223> CDR1 of Wnt1-332D03mod

<400> 7

Arg Tyr Thr Met Gly
1 5

<210> 8

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of Wnt1-332D03mod

<400> 8

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

<210> 9

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of Wnt1-332D03mod

<400> 9

Asp	Arg	Arg	Gly	Arg	Gly	Glu	Asn	Tyr	Ile	Leu	Leu	Tyr	Ser	Ser	Gly
1				5					10					15	
Arg	Tyr	Glu	Tyr												
			20												

<210> 10

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of Wnt3a-093A01

<400> 10

Ser	Tyr	Ala	Met	Gly
1				5

<210> 11

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of Wnt3a-093A01

<400> 11

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

<210> 12

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of Wnt3a-093A01

<400> 12

Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn Tyr Asp
 1 5 10 15
 Tyr

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of Wnt3a-367B10

<400> 13

Ser Tyr Ala Met Gly
 1 5

<210> 14

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of Wnt3a-367B10

<400> 14

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

<210> 15

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of Wnt3a-367B10

<400> 15

Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr
 1 5 10 15

<210> 16

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of Alb11

<400> 16

Ser Phe Gly Met Ser
1 5

<210> 17

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of Alb11

<400> 17

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

<210> 18

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of Alb11

<400> 18

Gly Gly Ser Leu Ser Arg
1 5

<210> 19

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain Wnt1-333E06mod

<400> 19

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

		100						105				110
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					

<210> 20
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<220>
 <223> VHH domain Wnt1-333G06

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

<210> 21
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain Wnt1-332D03mod

<400> 21
 Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Arg Tyr
 20 25 30
 Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45
 Ala Ala Ile Val Arg Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ile Leu Leu Tyr Ser

100 105 110
 Ser Gly Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125
 Ser

<210> 22
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain Wnt3a-093A01

<400> 22
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45
 Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn
 100 105 110
 Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 23
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain Wnt3a-367B10

<400> 23
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45
 Ala Ala Ile Ser Trp Arg Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr

			100					105					110
Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
			115				120					125	

<210> 24

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain Alb11

<400> 24

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

<210> 25

<211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500575

<400> 25

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

<210> 26
<211> 439
<212> PRT
<213> Artificial Sequence

<400> 26
Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr

[illegible]

<210> 27
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500720

<400>	27														
Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Leu	Thr	Phe	Ser	Arg	Tyr
			20					25					30		
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val
		35				40						45			
Ala	Ala	Ile	Val	Arg	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Ala	Asp	Arg	Arg	Gly	Arg	Gly	Glu	Asn	Tyr	Ile	Leu	Leu	Tyr	Ser
			100					105					110		
Ser	Gly	Arg	Tyr	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
145					150				155						160
Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val
				165					170					175	
Gln	Pro	Gly	Asn	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
			180					185					190		
Phe	Ser	Ser	Phe	Gly	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
		195					200					205			
Leu	Glu	Trp	Val	Ser	Ser	Ile	Ser	Gly	Ser	Gly	Ser	Asp	Thr	Leu	Tyr
	210					215					220				
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
225					230				235					240	
Thr	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala
				245					250					255	
Val	Tyr	Tyr	Cys	Thr	Ile	Gly	Gly	Ser	Leu	Ser	Arg	Ser	Ser	Gln	Gly
			260					265					270		
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		275					280					285			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	290					295					300				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu
305					310				315					320	
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
				325					330					335	

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          355          360          365
Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
   370          375          380
Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
385          390          395          400
Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly
          405          410          415
Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly
          420          425          430
Thr Leu Val Thr Val Ser Ser Ala
          435          440

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<210> 28

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain F0129093A01

<400> 28

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

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<210> 29

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain F0130333G06

<400> 29

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr

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			20					25					30				
Ala	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val		
		35					40					45					
Ala	Ala	Ile	Arg	Arg	Ser	Gly	Arg	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	Val	Tyr		
65					70				75						80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85					90					95				
Ala	Ala	Ala	Arg	Arg	Val	Arg	Ser	Ser	Thr	Arg	Tyr	Asn	Thr	Gly	Thr		
		100					105					110					
Trp	Trp	Trp	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
	115					120						125					
Ala	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala		
	130					135					140						
Ala	His	His	His	His	His	His											
145					150												

<210> 30

<211> 148

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain F0129093A03

<400> 30

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly		
1				5				10					15				
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	Ser	Thr	Tyr		
		20					25					30					
Val	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val		
	35					40					45						
Ala	Ala	Ile	Asn	Trp	Ser	Gly	Ser	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	Val	Tyr		
65				70				75						80			
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85					90					95				
Ala	Ala	Ser	Arg	Ser	Ser	Tyr	Ala	Gly	Arg	Thr	Tyr	Tyr	Glu	Leu	Tyr		
		100					105					110					
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala		
	115					120						125					
Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His		
	130					135					140						
His	His	His	His														
145																	

<210> 31

<211> 146

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain F0130333E06

<400> 31

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

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<210> 32

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH domain F0130332D03

<400> 32

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

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<210> 33
 <211> 148
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain F0130367B10

<400> 33
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45
 Ala Ala Ile Ser Trp Arg Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Gly Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr
 100 105 110
 Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ala Ala
 115 120 125
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His
 130 135 140
 His His His His
 145

<210> 34
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain F0130378B05

<400> 34
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Arg Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45
 Ala Ala Ile Ser Arg Ser Gly Gly 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 Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Asp Arg Arg Val Tyr Ser Thr Leu Pro Pro Thr Thr Ser Arg
 100 105 110
 Tyr Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala

	115		120		125										
Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His
	130					135					140				
His	His	His	His	His											
145															

<210> 35
 <211> 147
 <212> PRT
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<220>
 <223> VHH domain F0130378A04

<400> 35															
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val
		35					40					45			
Ala	Ala	Ile	Thr	Arg	Thr	Gly	Arg	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	Val	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90				95		
Ala	Ala	Asp	Arg	Arg	Gly	Tyr	Tyr	Tyr	Tyr	Asp	Ser	Ser	Phe	Tyr	Asp
			100					105					110		
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Glu
		115					120						125		
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His	His
	130					135					140				
His	His	His													
145															

<210> 36
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH domain F0130372C08

<400> 36															
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	Ser	Asp	Tyr
			20					25					30		
Gly	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val
		35					40					45			
Ala	Ala	Ile	Ser	Trp	Ser	Gly	Gly	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	Val	Tyr

65					70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95
Ala	Ala	Lys	Arg	Arg	Gly	Arg	Gly	Ser	Val	Ser	Pro	Asn	Ser	Ser
			100					105					110	
Arg	Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120					125		Ala
Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala
	130					135					140			
His	His	His	His	His	His									
145					150									

<210> 37

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500016

<400> 37

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

			260					265					270				
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
			275					280					285				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
			290					295					300				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu		
305							310					315			320		
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys		
				325					330						335		
Ala	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Gly	Trp	Phe	Arg		
			340					345					350				
Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Ser	Trp	Arg		
			355					360					365				
Ser	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile		
			370				375					380					
Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu		
385						390					395				400		
Arg	Pro	Glu	Gly	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Asp	Pro	Arg	Gly		
				405					410						415		
Tyr	Gly	Val	Ala	Tyr	Val	Ser	Ala	Tyr	Tyr	Glu	Tyr	Trp	Gly	Gln	Gly		
			420					425					430				
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser		
			435				440					445					
Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His	His	His	His	His				
			450				455					460					

<210> 38

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500018

<400> 38

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

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

<210> 39

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500021

<400> 39

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

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

<210> 40
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VHH construct F013500026

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

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

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<210> 41

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500030

<400> 41

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

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				245					250				255			
Cys	Thr	Ile	Gly	Gly	Ser	Leu	Ser	Arg	Ser	Ser	Gln	Gly	Thr	Leu	Val	
			260					265					270			
Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
		275					280					285				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
	290					295					300					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	
305				310					315						320	
Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
			325					330					335			
Gly	Arg	Thr	Phe	Ser	Asp	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	
		340					345					350				
Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Ser	Trp	Ser	Gly	Gly	Arg	
	355					360					365					
Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
370						375					380					
Asn	Ser	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	
385				390					395						400	
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Lys	Arg	Arg	Gly	Arg	Gly	Ser	
			405					410					415			
Val	Ser	Pro	Asn	Ser	Ser	Ser	Arg	Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	
		420					425					430				
Leu	Val	Thr	Val	Ser	Ser	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	
	435					440					445					
Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His	His	His	His	His				
	450					455					460					

<210> 42

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500032

<400> 42

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

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

<210> 43

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500033

<400> 43

Glu Val Gln Leu Val	Glu Ser Gly Gly	Gly Leu Val Gln Pro	Gly Gly
1	5	10	15
Ser Leu Arg Leu Ser	Cys Val Ala Ser	Gly Arg Thr Phe	Ser Ser Tyr

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

450

455

460

<210> 44

<211> 456

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> VHH construct F013500039

<400> 44

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

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

<210> 45

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500046

<400> 45

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly		
1				5				10					15				
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Leu	Thr	Phe	Ser	Arg	Tyr		
		20					25					30					
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val		
		35				40						45					
Ala	Ala	Ile	Asn	Arg	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ser	Asp	Ser	Val		
		50			55					60							
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr		
65				70				75							80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85				90						95				
Ala	Ala	Asp	Arg	Arg	Gly	Arg	Gly	Glu	Asn	Tyr	Ser	Leu	Leu	Tyr	Ser		
		100					105					110					
Ser	Asn	Arg	Tyr	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser		
		115				120						125					
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
		130				135					140						
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly		
145				150				155						160			
Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val		
			165					170						175			
Gln	Pro	Gly	Asn	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr		
		180					185						190				
Phe	Ser	Ser	Phe	Gly	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly		
		195				200						205					
Leu	Glu	Trp	Val	Ser	Ser	Ile	Ser	Gly	Ser	Gly	Ser	Asp	Thr	Leu	Tyr		
		210				215				220							
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys		

225					230					235					240
Thr	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala
				245					250					255	
Val	Tyr	Tyr	Cys	Thr	Ile	Gly	Gly	Ser	Leu	Ser	Arg	Ser	Ser	Gln	Gly
			260					265					270		
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		275					280				285				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	290					295				300					
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu
305					310				315					320	
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
				325				330						335	
Ala	Ala	Ser	Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Gly	Trp	Phe	Arg
			340				345						350		
Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Ser	Trp	Ser
		355					360					365			
Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
	370					375					380				
Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu
385					390				395						400
Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Ser	Pro	Ile	Pro
				405					410					415	
Tyr	Gly	Ser	Leu	Leu	Arg	Arg	Arg	Asn	Asn	Tyr	Asp	Tyr	Trp	Gly	Gln
			420				425						430		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile
		435				440					445				
Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His	His	His	His	His	
	450					455					460				

<210> 46

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH construct F013500047

<400> 46

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

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

<210> 47

<211> 462

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> VHH construct F013500053

<400> 47

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

		435					440				445			
Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala	His	His	His	His	His	His	His
	450					455					460			