

<110> ABL bio
 <120> A METHOD FOR PURIFYING OF BIOACTIVE PEPTIDE USING PROTEIN A
 AFFINITY CHROMATOGRAPHY
 <130> PX210081PCT
 <150> KR 10-2020-0173808
 <151> 2020-12-11
 <150> US 62/953,687
 <151> 2019-12-26
 <150> US 62/953,685
 <151> 2019-12-26
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 <213> Artificial Sequence
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<400> 1
 Glu Val Gln Leu Leu 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
 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Tyr Asp Asn Ala Asn 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 Lys Gly Val Leu Thr Thr Leu Met Asn Trp Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 2
<211> 110
<212> PRT
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<220>
<223> L Variable region 1564

<400> 2
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30
Asp Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Ala Asn Val Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Asp Ser Leu
85 90 95
Asn Ala Tyr Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 3
<211> 121
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<213> Artificial Sequence

<220>
<223> H Variable region F06

<400> 3
Glu Val Gln Leu Leu 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 Phe Thr Phe Ser Ser Tyr
20 25 30
Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Tyr Asp Asn Ala Asn 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 Lys Gly Val Leu Thr Thr Leu Met Asn Trp Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 4
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<220>
<223> L Variable region F06

<400> 4
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Asp Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Ala Gly Ser Leu
85 90 95

Asn Ala Tyr Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 5
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<220>

<223> H Variable region VH5

<400> 5

Glu Val Gln Leu Leu 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 Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Asp Asn Ala 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 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 Lys Gly Val Leu Thr Thr Leu Met Asn Trp Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<220>

<223> L Variable region VH5

<400> 6

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Asp Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg

65		70		75		80									
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	Ala	Trp	Asp	Asp	Ser	Leu
				85					90					95	

Asn	Ala	Tyr	Val	Phe	Gly	Cys	Gly	Thr	Lys	Leu	Thr	Val	Leu
			100					105					110

<210> 7
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<220>
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<400>	7														
Glu	Val	Gln	Leu	Leu	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	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		

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

Ser	Ala	Ile	Ser	Gly	Ser	Asn	Ala	Asn	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	Lys	Gly	Val	Leu	Thr	Thr	Leu	Met	Asn	Trp	Phe	Asp	Tyr	Trp	Gly
			100				105						110		

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120	

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

<220>
 <223> L Variable region VH16

<400> 8
 Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Asp Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Ala Asn Val Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Asp Ser Leu
 85 90 95
 Asn Ala Tyr Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
 100 105 110

<210> 9
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H Variable region VH9

<400> 9
 Glu Val Gln Leu Leu 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 Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Asp Asn 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 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 Lys Gly Val Leu Thr Thr Leu Met Asn Trp Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 10
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> L Variable region VH9

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

<210> 11
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
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<400> 11
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

<210> 12
 <211> 716
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> hu11F11(ver.2)(M428L)-F06(de2)(StoP)

 <400> 12

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	Thr	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Phe	20	25	30	
Tyr	Met	Glu	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Arg	Leu	Glu	Trp	Ile	35	40	45	
Ala	Ala	Ser	Arg	Asn	Lys	Ala	Asn	Asp	Tyr	Thr	Thr	Glu	Tyr	Ser	Ala	50	55	60	
Ser	Val	Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	65	70	75	80
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Ile	Tyr	85	90	95	
Tyr	Cys	Ala	Arg	Asp	Ala	His	Gly	Lys	Pro	Phe	Ala	Tyr	Trp	Gly	Gln	100	105	110	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	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	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	195	200	205	
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	210	215	220	
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	225	230	235	240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	245	250	255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	260	265	270	
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	275	280	285	

Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
290						295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305					310					315					320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
				325					330					335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			340					345					350		
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu
		355					360					365			
Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	370					375					380				
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
385					390					395					400
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp
				405					410					415	
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Leu	His
			420					425					430		
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
		435					440					445			
Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
	450					455					460				
Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly
465					470					475					480
Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Ser
				485					490					495	
Asn	Asp	Val	Ser	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu
			500					505					510		
Leu	Ile	Tyr	Ala	Asn	Val	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe
		515					520					525			
Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu
	530					535					540				
Arg	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	Thr	Trp	Ala	Gly	Ser
545					550					555					560
Leu	Asn	Ala	Tyr	Val	Phe	Gly	Cys	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly

565					570					575						
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			580						585					590		
Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
		595					600					605				
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	
	610					615					620					
Ser	Ser	Tyr	Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Cys	Leu	
625					630					635					640	
Glu	Trp	Val	Ser	Ala	Ile	Ser	Tyr	Asp	Asn	Ala	Asn	Thr	Tyr	Tyr	Ala	
				645					650						655	
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
			660					665					670			
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
		675					680					685				
Tyr	Tyr	Cys	Ala	Lys	Gly	Val	Leu	Thr	Thr	Leu	Met	Asn	Trp	Phe	Asp	
	690					695					700					
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
705					710					715						

<210> 13
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu11F11(ver.2)(M428L)

<400> 13																
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Thr	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Phe	
			20					25					30			
Tyr	Met	Glu	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Arg	Leu	Glu	Trp	Ile	
		35					40					45				
Ala	Ala	Ser	Arg	Asn	Lys	Ala	Asn	Asp	Tyr	Thr	Thr	Glu	Tyr	Ser	Ala	
	50					55					60					
Ser	Val	Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	

65					70					75					80
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Ile	Tyr
				85					90					95	
Tyr	Cys	Ala	Arg	Asp	Ala	His	Gly	Lys	Pro	Phe	Ala	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	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	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				245					250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			260					265					270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	275						280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305					310					315					320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
				325					330					335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			340					345					350		

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

<210> 14
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (G4S)3

<400> 14
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 15
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F06(de2)(StoP) VL

<400> 15
 Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30

Asp Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

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

<210> 16
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (G4S)4

<400> 16
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser
 20

<210> 17
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F06(de2)(StoP) VH

<400> 17
 Glu Val Gln Leu Leu 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 Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Tyr Asp Asn Ala Asn 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 Lys Gly Val Leu Thr Thr Leu Met Asn Trp Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 18

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> ch1E4 VH

<400> 18

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

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

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

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Ser Gly Asn Tyr Asp Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 19

<211> 112

<212> PRT

<213> Artificial Sequence

<220>
<223> ch1E4 VL

<400> 19
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
Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Leu Leu Ile Tyr Lys 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
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Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
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<220>
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