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<110> Glaxo Group Limited

<120> Novel antigen binding proteins

<130> PB63376

<150> US61/138980

<151> 2008-12-19

<160> 111

<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> Mus musculus

<400> 1

Gly Tyr Phe Met His

1 5

<210> 2

<211> 17

<212> PRT

<213> Mus musculus

<400> 2

Asn Ile Tyr Pro Tyr Asn Gly Val Ser Asn Tyr Asn Gln Arg Phe Lys

1 5 10 15

Ala

<210> 3

<211> 15

<212> PRT

<213> Mus musculus

<400> 3

Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp Val

1 5 10 15

<210> 4

<211> 11

<212> PRT

<213> Mus musculus

<400> 4

Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser

1 5 10

<210> 5

<211> 7

<212> PRT
<213> Mus musculus

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Arg Ala Asn Arg Leu Val Asp
1 5

<210> 6
<211> 9
<212> PRT
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<400> 6
Leu Gln Cys Asp Glu Phe Pro Leu Thr
1 5

<210> 7
<211> 124
<212> PRT
<213> Mus musculus

<400> 7
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Phe Met His Trp Val Lys Gln Ser His Gly Asn Ile Leu Asp Trp Ile
35 40 45
Gly Asn Ile Tyr Pro Tyr Asn Gly Val Ser Asn Tyr Asn Gln Arg Phe
50 55 60
Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp
100 105 110
Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 8
<211> 107
<212> PRT
<213> Mus musculus

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

<210> 9
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial signal sequence

<400> 9
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser

<210> 10
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human acceptor framework for VH

<221> VARIANT
 <222> (99)...(108)
 <223> Xaa is any amino acid

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

<210> 11
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 <213> Artificial Sequence

<220>
 <223> human acceptor framework for VL

<221> VARIANT
 <222> (89)...(98)
 <223> Xaa is any amino acid

<400> 11

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

<210> 12

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised VH: H0

<400> 12

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

<210> 13

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised VH: H1

<400> 13

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr
		20						25					30		
Phe	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35					40						45			
Gly	Asn	Ile	Tyr	Pro	Tyr	Asn	Gly	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe
	50				55					60					

Lys	Ala	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90						95	
Ala	Arg	Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Phe	Asp
			100					105					110		
Val	Trp	Gly	Thr	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
		115					120								

<210> 14

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised VH: H2

<400> 14

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

<210> 15

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised VL: L0

<400> 15

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

<210> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised VL: L1

<400> 16
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Arg
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Cys Asp Glu Phe Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 17
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised VL: L2

<400> 17
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Cys Asp Glu Phe Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 18
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised VL: L3

<400> 18
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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

<210> 19
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10B3 chimera VH: N54D

<400> 19																
Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	
			20					25					30			
Phe	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Asn	Ile	Leu	Asp	Trp	Ile	
		35					40					45				
Gly	Asn	Ile	Tyr	Pro	Tyr	Asp	Gly	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe	
	50					55					60					
Lys	Ala	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
65					70					75					80	
Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Phe	Asp	
			100					105						110		
Val	Trp	Gly	Thr	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
			115					120								

<210> 20
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10B3 chimera VH: N54Q

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

Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Phe	Asp
			100					105					110		
Val	Trp	Gly	Thr	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
		115					120								

<210> 21
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10B3 chimera VL: C91S

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

<210> 22
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanised VH: H2 N54D

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

<210> 23

<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised VH: H2 N54Q

<400> 23
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Tyr Pro Tyr Gln Gly Val Ser Asn Tyr Asn Gln Arg Phe
50 55 60
Lys Ala Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp
100 105 110
Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 24
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised VL: L2 C91S

<400> 24
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Ser Asp Glu Phe Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 25
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> 10B3 chimera VH

<400> 25
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

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

<210> 26

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> 10B3 chimera heavy chain

<400> 26

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


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<210> 28
<211> 454
<212> PRT
<213> Artificial Sequence
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<220>
<223> humanised heavy chain: H0
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<400> 28

Gln 1	Val	Gln	Leu	Val 5	Gln	Ser	Gly	Ala	Glu 10	Val	Lys	Lys	Pro	Gly 15	Ala
Ser	Val	Lys	Val 20	Ser	Cys	Lys	Ala 25	Ser	Gly	Tyr	Thr	Phe	Thr 30	Gly	Tyr
Phe	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Gln	Gly	Leu 45	Glu	Trp	Met
Gly	Asn 50	Ile	Tyr	Pro	Tyr	Asn 55	Gly	Val	Ser	Asn 60	Tyr	Asn	Gln	Arg	Phe
Lys 65	Ala	Arg	Val	Thr	Met 70	Thr	Thr	Asp	Thr	Ser 75	Thr	Ser	Thr	Ala	Tyr 80
Met	Glu	Leu	Arg	Ser 85	Leu	Arg	Ser	Asp	Asp	Thr 90	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Arg 100	Tyr	Tyr	Gly	Thr	Gly 105	Pro	Ala	Asp	Trp	Tyr 110	Phe	Asp	
Val	Trp 115	Gly	Gln	Gly	Thr	Leu 120	Val	Thr	Val	Ser 125	Ser	Ala	Ser	Thr	Lys
Gly	Pro 130	Ser	Val	Phe	Pro	Leu 135	Ala	Pro	Ser	Ser 140	Lys	Ser	Thr	Ser	Gly
Gly 145	Thr	Ala	Ala	Leu 150	Gly	Cys	Leu	Val	Lys	Asp 155	Tyr	Phe	Pro	Glu	Pro 160
Val	Thr	Val	Ser 165	Trp	Asn	Ser	Gly	Ala 170	Leu	Thr	Ser	Gly	Val	His 175	Thr
Phe	Pro	Ala 180	Val	Leu	Gln	Ser	Ser 185	Gly	Leu	Tyr	Ser	Leu 190	Ser	Ser	Val
Val	Thr 195	Val	Pro	Ser	Ser	Ser 200	Leu	Gly	Thr	Gln 205	Thr	Tyr	Ile	Cys	Asn
Val	Asn 210	His	Lys	Pro	Ser	Asn 215	Thr	Lys	Val	Asp 220	Lys	Lys	Val	Glu	Pro
Lys 225	Ser	Cys	Asp	Lys 230	Thr	His	Thr	Cys	Pro 235	Pro	Cys	Pro	Ala	Pro	Glu 240
Leu	Leu	Gly	Gly 245	Pro	Ser	Val	Phe	Leu 250	Phe	Pro	Pro	Lys	Pro	Lys 255	Asp
Thr	Leu	Met	Ile 260	Ser	Arg	Thr	Pro 265	Glu	Val	Thr	Cys 270	Val	Val	Val	Asp
Val	Ser 275	His	Glu	Asp	Pro	Glu 280	Val	Lys	Phe	Asn 285	Trp	Tyr	Val	Asp	Gly
Val	Glu 290	Val	His	Asn 295	Ala	Lys	Thr	Lys	Pro 300	Arg	Glu	Glu	Gln	Tyr	Asn
Ser 305	Thr	Tyr	Arg	Val 310	Val	Ser	Val	Leu	Thr 315	Val	Leu	His	Gln	Asp	Trp 320
Leu	Asn	Gly	Lys 325	Glu	Tyr	Lys	Cys	Lys 330	Val	Ser	Asn	Lys	Ala	Leu	Pro
Ala	Pro	Ile 340	Glu	Lys	Thr	Ile	Ser 345	Lys	Ala	Lys	Gly	Gln 350	Pro	Arg	Glu
Pro	Gln 355	Val	Tyr	Thr	Leu	Pro 360	Pro	Ser	Arg	Asp 365	Glu	Leu	Thr	Lys	Asn
Gln	Val 370	Ser	Leu	Thr 375	Cys	Leu	Val	Lys	Gly 380	Phe	Tyr	Pro	Ser	Asp	Ile
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr

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

<210> 29

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H1

<400> 29

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

				325					330				335				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu		
			340					345					350				
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn		
		355					360					365					
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
	370					375					380						
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr		
385					390					395					400		
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys		
			405					410						415			
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gly	Asn	Val	Phe	Ser	Cys			
		420						425				430					
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu		
	435					440						445					
Ser	Leu	Ser	Pro	Gly	Lys												
	450																

<210> 30

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H2

<400> 30

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

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

<210> 31

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised light chain: L0

<400> 31

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

195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 32
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised light chain: L1

<400> 32
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Arg
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Cys Asp Glu Phe Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 33
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> humanised light chain: L2

<400> 33
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

<210> 35
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10B3 chimera N54D heavy chain

<400> 35
 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30
 Phe Met His Trp Val Lys Gln Ser His Gly Asn Ile Leu Asp Trp Ile
 35 40 45
 Gly Asn Ile Tyr Pro Tyr Asp Gly Val Ser Asn Tyr Asn Gln Arg Phe
 50 55 60
 Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp
 100 105 110
 Val Trp Gly Thr Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 165 170 175
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 180 185 190
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 195 200 205
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 210 215 220
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 225 230 235 240
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 245 250 255
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 260 265 270
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 275 280 285
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 290 295 300
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 305 310 315 320
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 325 330 335
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 340 345 350
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 355 360 365
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 405 410 415

Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
			420					425					430		
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
		435					440					445			
Ser	Leu	Ser	Pro	Gly	Lys										
		450													

<210> 36

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> 10B3 chimera N54Q heavy chain

<400> 36

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

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

<210> 37

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10B3 chimera C91S light chain

<400> 37

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

<210> 38

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

[illegible]

<210> 39
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanised heavy chain: H2 N54Q

<400> 39

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	1	5	10	15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	20	25	30	
Phe	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	35	40	45	
Gly	Asn	Ile	Tyr	Pro	Tyr	Gln	Gly	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe	50	55	60	
Lys	Ala	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	65	70	75	80
Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Phe	Asp	100	105	110	
Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	115	120	125	
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	130	135	140	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	145	150	155	160
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	165	170	175	
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	180	185	190	
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	195	200	205	
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	210	215	220	
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	225	230	235	240
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	245	250	255	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	260	265	270	
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	275	280	285	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	290	295	300	
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	305	310	315	320
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	325	330	335	
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	340	345	350	
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	355	360	365	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	370	375	380	
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	385	390	395	400

Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys
				405					410					415	
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
			420					425					430		
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
		435					440					445			
Ser	Leu	Ser	Pro	Gly	Lys										
	450														

<210> 40

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised light chain: L2 C91S

<400> 40

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

<210> 41

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> 10B3 chimera heavy chain

<400> 41

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gttcagctgc agcagtctgg acctgaactg gtgaagcctg gggcttcagt gaagatatcc 120
tgcaaggctt ctggttactc attcactggc tacttcatgc actgggtgaa gcagagccat 180

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cagagattca	aggccaaggc	cacattgact	gtagacaagt	cctctagtag	agcctacatg	300
gagctccgca	gccttacatc	tgaggactct	gcagtctatt	actgtgcaag	acgctattac	360
tacggtagcg	gaccggctga	ttggtagctt	gatgtctggg	gcactgggac	actagtgacc	420
gtgtccagcg	ccagcaccaa	gggccccagc	gtgttcccc	tggccccag	cagcaagagc	480
accagcgcg	gcacagccgc	cctgggctgc	ctgggtgaagg	actacttccc	cgaaccgggtg	540
accgtgtcct	ggaacagcgg	agccctgacc	agcggcgtgc	acaccttccc	cgcctgtctg	600
cagagcagcg	gcctgtacag	cctgagcagc	gtgggtgaccg	tggccagcag	cagcctgggc	660
acccagacct	acatctgtaa	cgtgaaccac	aagcccagca	acaccaaggt	ggacaagaag	720
gtggagccca	agagctgtga	caagaccac	acctgcccc	cctgccctgc	ccccgagctg	780
ctgggagggc	ccagcgtgtt	cctgttcccc	cccaagccta	aggacacct	gatgatcagc	840
agaaccccc	aggtgacctg	tgtgggtggtg	gatgtgagcc	acgaggacc	tgaggtgaag	900
ttcaactgg	acgtggacgg	cgtggaggtg	cacaatgcc	agaccaagcc	cagggaggag	960
cagtacaaca	gcacctaccg	ggtgggtgtcc	gtgctgaccg	tgctgcacca	ggattggctg	1020
aacggcaagg	agtacaagtg	taaggtgtcc	aacaaggccc	tgcctgcccc	tatcgagaaa	1080
accatcagca	aggccaagg	ccagcccaga	gagccccagg	tgtacacct	gccccctagc	1140
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agcgacatcg	ccgtggagt	ggagagcaac	ggccagcccc	agaacaacta	caagaccacc	1260
ccccctgtgc	tggacagcga	tggcagcttc	ttcctgtaca	gcaagctgac	cgtggacaag	1320
agcagatggc	agcagggcaa	cgtgttcagc	tgtccgtga	tgcacgaggc	cctgcacaat	1380
cactacacc	agaagagcct	gagcctgtcc	cctggcaagt	ga		1422

<210> 42

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> 10B3 chimera light chain

<400> 42

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atcaagatga	cccagtctcc	atcttccatg	tatgcattct	tacgagagag	agtcactatc	120
acttgcaagg	cgagtcagga	cattaatagc	tatttaagct	ggttccagca	gaaaccagg	180
aatctccta	agacccta	ctatcgtgca	aacagattgg	tagatgggg	cccatcaagg	240
ttcagtggca	gtggatctgg	gcaagattat	tctctcacca	tcagcagcct	ggagtatgaa	300
gatatgggaa	tttattattg	tctacagtgt	gatgaatttc	cgctcacgtt	cgggtgctgg	360
accaagctgg	agctgaaacg	tacgggtggc	gccccagc	tgttcatctt	cccccccagc	420
gatgagcagc	tgaagagcgg	caccgccagc	gtgggtgtgt	tgtgaacaa	cttctacccc	480
cgggaggcca	aggtgcagt	gaaggtggac	aatgccctgc	agagcggcaa	cagccaggag	540
agcgtgaccg	agcaggacag	caaggactcc	acctacagcc	tgagcagcac	cctgaccctg	600
agcaaggccg	actacgagaa	gcacaaggtg	tacgctgtg	aggtgaccca	ccagggcctg	660
tccagccccg	tgaccaagag	cttcaaccgg	ggcgagtgt	ga		702

<210> 43

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H0

<400> 43

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tgcaaggcca	gcggctacac	cttcaccggc	tacttcatgc	actgggtgag	gcaggctccc	180
ggccaggggc	tggagtggat	gggcaacatc	tacccttaca	acggcgtcag	caactacaac	240
cagaggttca	aggccagggt	gacctgacc	accgacacct	ctaccagcac	cgcctacatg	300
gaactgagga	gcctgaggag	cgacgacacc	gccgtgtact	actgcgccag	gaggtactat	360
tacggcaccg	gacccgccga	ttggtacttc	gacgtgtggg	gacaggggac	actagtgacc	420
gtgtccagcg	ccagcaccaa	gggccccagc	gtgttcccc	tggccccag	cagcaagagc	480

accagcggcg	gcacagccgc	cctgggctgc	ctggtgaagg	actacttccc	cgaaccggtg	540
accgtgtcct	ggaacagcgg	agccctgacc	agcggcgtgc	acaccttccc	cgccgtgctg	600
cagagcagcg	gcctgtacag	cctgagcagc	gtggtgaccg	tgccagcag	cagcctgggc	660
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ctgggaggcc	ccagcgtgtt	cctgttcccc	cccaagccta	aggacaccct	gatgatcagc	840
agaacccccg	aggtgacctg	tgtggtggtg	gatgtgagcc	acgaggaccc	tgaggtgaag	900
ttcaactgg	acgtggacgg	cgtggaggtg	cacaatgcc	agaccaagcc	cagggaggag	960
cagtacaaca	gcacctaccg	ggtggtgtcc	gtgctgaccg	tgctgcacca	ggattggctg	1020
aacggcaagg	agtacaagt	taaggtgtcc	aacaaggccc	tgctgcccc	tatcgagaaa	1080
accatcagca	aggccaaggg	ccagcccaga	gagccccagg	tgtacacct	gccccctagc	1140
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agcgacatcg	ccgtggagtg	ggagagcaac	ggccagccc	agaacaacta	caagaccacc	1260
ccccctgtgc	tggacagcga	tggcagcttc	ttcctgtaca	gcaagctgac	cgtggacaag	1320
agcagatggc	agcagggcaa	cgtgttcagc	tgctccgtga	tgacagaggc	cctgcacaat	1380
cactacaccc	agaagagcct	gagcctgtcc	cctggcaagt	ga		1422

<210> 44

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H1

<400> 44

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gtgcagctgg	tgacagcgg	cgacagaggtg	aagaagcccc	gcgccagcgt	gaaagtgagc	120
tgcaaggcca	gcggctacac	cttcaccggc	tacttcatgc	actgggtgag	gcaggtccc	180
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tacggcaccg	gacccgccga	ttggtacttc	gacgtgtggg	gaacggggac	actagtgacc	420
gtgtccagcg	ccagcaccaa	gggccccagc	gtgttcccc	tgccccccag	cagcaagagc	480
accagcggcg	gcacagccgc	cctgggctgc	ctggtgaagg	actacttccc	cgaaccggtg	540
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ttcaactgg	acgtggacgg	cgtggaggtg	cacaatgcc	agaccaagcc	cagggaggag	960
cagtacaaca	gcacctaccg	ggtggtgtcc	gtgctgaccg	tgctgcacca	ggattggctg	1020
aacggcaagg	agtacaagt	taaggtgtcc	aacaaggccc	tgctgcccc	tatcgagaaa	1080
accatcagca	aggccaaggg	ccagcccaga	gagccccagg	tgtacacct	gccccctagc	1140
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agcgacatcg	ccgtggagtg	ggagagcaac	ggccagccc	agaacaacta	caagaccacc	1260
ccccctgtgc	tggacagcga	tggcagcttc	ttcctgtaca	gcaagctgac	cgtggacaag	1320
agcagatggc	agcagggcaa	cgtgttcagc	tgctccgtga	tgacagaggc	cctgcacaat	1380
cactacaccc	agaagagcct	gagcctgtcc	cctggcaagt	ga		1422

<210> 45

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H2

<400> 45

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tgcaaggcca	gcggctactc	cttcaccggc	tactttcatgc	actgggtgag	gcaggctccc	180
ggccagggcc	tggagtggat	gggcaacatc	tacccttaca	acggcgtcag	caactacaac	240
cagaggttca	aggccagggg	gaccatgacc	accgacacct	ctaccagcac	cgcctacatg	300
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tacggcaccg	gacccgccga	ttggtacttc	gacgtgtggg	gacaggggac	actagtgacc	420
gtgtccagcg	ccagcaccaa	gggccccagc	gtgttcccc	tggccccag	cagcaagagc	480
accagcggcg	gcacagccgc	cctgggctgc	ctggtgaagg	actacttccc	cgaaccgggtg	540
accgtgtcct	ggaacagcgg	agccctgacc	agcggcgctgc	acaccttccc	cgcctgtctg	600
cagagcagcg	gcctgtacag	cctgagcagc	gtggtgaccg	tgccagcag	cagcctgggc	660
accagacct	acatctgtaa	cgtgaaccac	aagcccagca	acaccaaggt	ggacaagaag	720
gtggagccca	agagctgtga	caagaccac	acctgcccc	cctgcctgc	ccccgagctg	780
ctgggagccc	ccagcgtgtt	cctgttcccc	cccaagccta	aggacacct	gatgatcagc	840
agaacccccg	aggtgacctg	tgtggtggtg	gatgtgagcc	acgaggacct	tgaggtgaag	900
ttcaactggg	acgtggacgg	cgtggaggtg	cacaatgcc	agaccaagcc	cagggaggag	960
cagtacaaca	gcacctaccg	ggtggtgtcc	gtgctgaccg	tgctgcacca	ggattggctg	1020
aacggcaagg	agtacaagtg	taaggtgtcc	aacaaggccc	tgcctgcccc	tatcgagaaa	1080
accatcagca	aggccaaggg	ccagcccaga	gagccccagg	tgtacacct	gccccctagc	1140
agagatgagc	tgaccaagaa	ccaggtgtcc	ctgacctgcc	tggagaagg	cttctacccc	1200
agcgacatcg	ccgtggagtg	ggagagcaac	ggccagcccc	agaacaacta	caagaccacc	1260
ccccctgtgc	tggacagcga	tggcagcttc	ttcctgtaca	gcaagctgac	cgtggacaag	1320
agcagatggc	agcagggcaa	cgtgttcagc	tgctccgtga	tgcacgaggc	cctgcacaat	1380
cactacaccc	agaagagcct	gagcctgtcc	cctggcaagt	ga		1422

<210> 46

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised light chain: L0

<400> 46

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acctgcaagg	ccagccagga	catcaacagc	tacctgagct	ggttccagca	gaagcccggc	180
aaggctccca	agagcctgat	ctacagggcc	aacaggctcg	tggacggcgt	gcctagcaag	240
tttagcggca	gcggaagcgg	cacagacttc	accctgacca	tcagctccct	gcagcccagag	300
gacttcgcca	cctactactg	cctgcagtgc	gacgagttcc	ccctgacctt	cggccagggc	360
accaaactgg	agatcaagcg	tacgggtggc	gccccagcg	tgttcatctt	cccccccagc	420
gatgagcagc	tgaagagcgg	caccgccagc	gtggtgtgtc	tgctgaacaa	cttctacccc	480
cgggaggcca	aggtgcagtg	gaaggtggac	aatgccttgc	agagcggcaa	cagccaggag	540
agcgtgaccg	agcaggacag	caaggactcc	acctacagcc	tgagcagcac	cctgaccttg	600
agcaaggccg	actacgagaa	gcacaagggt	tacgcctgtg	aggtgaccca	ccagggcctg	660
tccagccccg	tgaccaagag	cttcaaccgg	ggcgagtgtc	ga		702

<210> 47

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised light chain: L1

<400> 47

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agcaaggccg actacgagaa gcacaaggtg tacgcctgtg aggtgaccca ccagggcctg 660
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<210> 48

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised light chain: L2

<400> 48

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acctgcaagg ccagccagga catcaacagc tacctgagct ggttccagca gaagcccggc 180
aaggctccca agagcctgat ctacagggcc aacaggctcg tggacggcgt gcctagcaag 240
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gacttcgcca cctactactg cctgcagtgc gacgagttcc ccctgacctt cggccagggc 360
accaaactgg agatcaagcg tacggtggcc gccccagcg tgttcattct cccccccagc 420
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agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 600
agcaaggccg actacgagaa gcacaaggtg tacgcctgtg aggtgaccca ccagggcctg 660
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<210> 49

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised light chain: L3

<400> 49

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acctgcaagg ccagccagga catcaacagc tacctgagct ggttccagca gaagcccggc 180
aaggctccca agagcctgat ctacagggcc aacaggctcg tggacggcgt gcctagcaag 240
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gacttcgcca cctactactg cctgcagtgc gacgagttcc ccctgacctt cggcgcgggc 360
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gatgagcagc tgaagagcgg caccgccagc gtggtgtgtc tgctgaacaa cttctacccc 480
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agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 600
agcaaggccg actacgagaa gcacaaggtg tacgcctgtg aggtgaccca ccagggcctg 660
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<210> 50

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> 10B3 chimera N54D heavy chain

<400> 50

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ggcaatatcc	tcgattggat	tggaaatatt	tatccttacg	atggtgtttc	taactacaac	240
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cagtacaaca	gcacctaccg	ggtggtgtcc	gtgctgaccg	tgctgcacca	ggattggctg	1020
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agcagatggc	agcagggcaa	cgtgttcagc	tgctccgtga	tgacagaggc	cctgcacaat	1380
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<210> 51

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> 10B3 chimera N54Q heavy chain

<400> 51

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ggcaatatcc	tcgattggat	tggaaatatt	tatccttacc	aaggtgtttc	taactacaac	240
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gagctccgca	gccttacatc	tgaggactct	gcagtctatt	actgtgcaag	acgctattac	360
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gtgtccagcg	ccagcaccaa	gggccccagc	gtgttcccc	tggccccagc	cagcaagagc	480
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<210> 52

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> 10B3 chimera C91S light chain

<400> 52

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ttcagtggca gtggatctgg gcaagattat tctctcacca tcagcagcct ggagtatgaa 300
gatatgggaa tttattattg tctacagtct gatgaatttc cgctcacgtt cgggtgctggg 360
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gatgagcagc tgaagagcgg caccggcagc gtgggtgtgtc tgctgaacaa cttctacccc 480
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agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 600
agcaaggccg actacgagaa gcacaagggtg tacgcctgtg aggtgaccca ccagggcctg 660
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<210> 53

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H2 N54D

<400> 53

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agcagatggc agcagggcaa cgtgttcagc tgctcctgta tgcacgagge cctgcacaa 1380
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<210> 54

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H2 N54Q

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<210> 55

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> humanised light chain: L2 C91S

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aaggctccca agagcctgat ctacagggcc aacaggctcg tggacggcgt gcctagcaag 240
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gacttcgcca cctactactg cctgcagagc gacgagttcc ccctgacctt cggccaggggc 360
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agcaaggccg actacgagaa gcacaagggt tacgcctgtg aggtgaccca ccagggcctg 660
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<210> 56

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial myostatin linear peptide 1

<400> 56

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Gly

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<210> 57
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<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 3

<400> 57
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Arg Tyr

<210> 58
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 5

<400> 58
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1 5 10 15
Thr Val

<210> 59
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 7

<400> 59
Ser Gly Ser Gly Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe
1 5 10 15
Glu Ala

<210> 60
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 9

<400> 60
Ser Gly Ser Gly Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly
1 5 10 15
Trp Asp

<210> 61
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 11

<400> 61
Ser Gly Ser Gly Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
1 5 10 15
Ile Ala

<210> 62
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 13

<400> 62
Ser Gly Ser Gly Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys
1 5 10 15
Arg Tyr

<210> 63
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 15

<400> 63
Ser Gly Ser Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala
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Asn Tyr

<210> 64
<211> 18
<212> PRT
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<220>
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<400> 64
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1 5 10 15
Gly Glu

<210> 65
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 19

<400> 65
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1 5 10 15
Phe Val

<210> 66
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 21

<400> 66
Ser Gly Ser Gly Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu
1 5 10 15
Gln Lys

<210> 67
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 23

<400> 67
Ser Gly Ser Gly Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro
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His Thr

<210> 68
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 25

<400> 68
Ser Gly Ser Gly Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu
1 5 10 15
Val His

<210> 69

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 27

<400> 69
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Asn Pro

<210> 70
<211> 18
<212> PRT
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<220>
<223> artificial myostatin linear peptide 29

<400> 70
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1 5 10 15
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<210> 71
<211> 18
<212> PRT
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<220>
<223> artificial myostatin linear peptide 31

<400> 71
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Cys Cys

<210> 72
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 33

<400> 72
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1 5 10 15
Thr Lys

<210> 73
<211> 18

<212> PRT
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<220>
<223> artificial myostatin linear peptide 35

<400> 73
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<210> 74
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 74
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<210> 75
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 39

<400> 75
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Gly Lys

<210> 76
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial myostatin linear peptide 41

<400> 76
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Ile Ile

<210> 77
<211> 18
<212> PRT

<213> Artificial Sequence

<220>

<223> artificial myostatin linear peptide 43

<400> 77

Ser Gly Ser Gly Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
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Lys Ile

<210> 78

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial myostatin linear peptide 45

<400> 78

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Met Val

<210> 79

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial myostatin linear peptide 47

<400> 79

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<210> 80

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial myostatin linear peptide 49

<400> 80

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Cys Ser

<210> 81

<211> 14

<212> PRT

<213> Homo sapien

<400> 81
Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
1 5 10

<210> 82
<211> 15
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<220>
<223> CDRH3 variant Y96L

<400> 82
Arg Leu Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp Val
1 5 10 15

<210> 83
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 variant G99D

<400> 83
Arg Tyr Tyr Tyr Asp Thr Gly Pro Ala Asp Trp Tyr Phe Asp Val
1 5 10 15

<210> 84
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 variant G99S

<400> 84
Arg Tyr Tyr Tyr Ser Thr Gly Pro Ala Asp Trp Tyr Phe Asp Val
1 5 10 15

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 variant G100A_K

<400> 85
Arg Tyr Tyr Tyr Gly Thr Lys Pro Ala Asp Trp Tyr Phe Asp Val
1 5 10 15

<210> 86
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 variant P100B_F

<400> 86

Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Phe	Ala	Asp	Trp	Tyr	Phe	Asp	Val
1				5					10					15

<210> 87

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 variant P100B_I

<400> 87

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

<210> 88

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 variant W100E_F

<400> 88

Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Phe	Tyr	Phe	Asp	Val
1				5					10					15

<210> 89

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 variant F100G_N

<400> 89

Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Asn	Asp	Val
1				5					10					15

<210> 90

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 variant F100G_Y

<400> 90

Arg	Tyr	Tyr	Tyr	Gly	Thr	Gly	Pro	Ala	Asp	Trp	Tyr	Tyr	Asp	Val
1				5					10					15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 variant V102N

<400> 91
Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp Asn
1 5 10 15

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 variant V102S

<400> 92
Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Phe Asp Ser
1 5 10 15

<210> 93
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2 variant G55D

<400> 93
Asn Ile Tyr Pro Tyr Asn Asp Val Ser Asn Tyr Asn Gln Arg Phe Lys
1 5 10 15
Ala

<210> 94
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2 variant G55L

<400> 94
Asn Ile Tyr Pro Tyr Asn Leu Val Ser Asn Tyr Asn Gln Arg Phe Lys
1 5 10 15
Ala

<210> 95
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> CDRH2 variant G55S

<400> 95

Asn	Ile	Tyr	Pro	Tyr	Asn	Ser	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe	Lys
1				5					10					15	

Ala

<210> 96

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH2 variant G55T

<400> 96

Asn	Ile	Tyr	Pro	Tyr	Asn	Thr	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe	Lys
1				5					10					15	

Ala

<210> 97

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH2 variant G55V

<400> 97

Asn	Ile	Tyr	Pro	Tyr	Asn	Val	Val	Ser	Asn	Tyr	Asn	Gln	Arg	Phe	Lys
1				5					10					15	

Ala

<210> 98

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> humanised heavy chain: H2_F100G_Y Fc disabled

<400> 98

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

<220>

<223> human acceptor framework for VL

<221> VARIANT

<222> (96)...(105)

<223> Xaa is any amino acid

<400> 100

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
          20          25          30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Xaa
          85          90          95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Gly Gln Gly Thr Lys Leu
          100          105          110
Glu Ile Lys
          115
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<210> 101

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> HexaHisGB1Tev/(D76A) mouse myostatin polyprotein

<400> 101

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


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

<210> 104

<211> 109

<212> PRT

<213> Homo sapien

<400> 104

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

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

<210> 105
 <211> 603
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Furin expression construct

<400> 105

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

145					150					155				160
Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu
				165					170					175
Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro
			180					185					190	
Glu	Ser	Asp	Phe	Leu	Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys
		195					200				205			
Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala
	210					215					220			
Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe
	225				230					235				240
Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr
			245					250					255	
Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile
		260					265					270		Trp
Gln	Ser	Ile	Asp	Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln
	275						280					285		Pro
Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly
	290				295				300					
Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn
	305				310				315					320
Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg
			325				330						335	

<210> 107

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Tev protease expression construct

<400> 107

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

210		215		220
Val Phe Met Val Lys Pro	Glu Glu Pro Phe Gln	Pro Val Lys Glu Ala		
225		230		240
Thr Gln Leu Met Asn Glu		235		
	245			

<210> 108
 <211> 242
 <212> PRT
 <213> Homo sapien

<400> 108

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

<210> 109
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRL3 variant C91S

<400> 109

Leu Gln Ser Asp Glu Phe Pro Leu Thr
1 5

<210> 110

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

<220>
<223> CDRH3 variant Y100G_S

<400> 110
Arg Tyr Tyr Tyr Gly Thr Gly Pro Ala Asp Trp Tyr Ser Asp Val
1 5 10 15

<210> 111
<211> 803
<212> PRT
<213> Artificial Sequence

<220>
<223> BMP-1 expression construct

<400> 111
Met Pro Gly Val Ala Arg Leu Pro Leu Leu Leu Gly Leu Leu Leu Leu
1 5 10 15
Pro Arg Pro Gly Arg Pro Leu Asp Leu Ala Asp Tyr Thr Tyr Asp Leu
20 25 30
Ala Glu Glu Asp Asp Ser Glu Pro Leu Asn Tyr Lys Asp Pro Cys Lys
35 40 45
Ala Ala Ala Phe Leu Gly Asp Ile Ala Leu Asp Glu Glu Asp Leu Arg
50 55 60
Ala Phe Gln Val Gln Gln Ala Val Asp Leu Arg Arg His Thr Ala Arg
65 70 75 80
Lys Ser Ser Ile Lys Ala Ala Val Pro Gly Asn Thr Ser Thr Pro Ser
85 90 95
Cys Gln Ser Thr Asn Gly Gln Pro Gln Arg Gly Ala Cys Gly Arg Trp
100 105 110
Arg Gly Arg Ser Arg Ser Arg Arg Ala Ala Thr Ser Arg Pro Glu Arg
115 120 125
Val Trp Pro Asp Gly Val Ile Pro Phe Val Ile Gly Gly Asn Phe Thr
130 135 140
Gly Ser Gln Arg Ala Val Phe Arg Gln Ala Met Arg His Trp Glu Lys
145 150 155 160
His Thr Cys Val Thr Phe Leu Glu Arg Thr Asp Glu Asp Ser Tyr Ile
165 170 175
Val Phe Thr Tyr Arg Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg
180 185 190
Gly Gly Gly Pro Gln Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe
195 200 205
Gly Ile Val Val His Glu Leu Gly His Val Val Gly Phe Trp His Glu
210 215 220
His Thr Arg Pro Asp Arg Asp Arg His Val Ser Ile Val Arg Glu Asn
225 230 235 240
Ile Gln Pro Gly Gln Glu Tyr Asn Phe Leu Lys Met Glu Pro Gln Glu
245 250 255
Val Glu Ser Leu Gly Glu Thr Tyr Asp Phe Asp Ser Ile Met His Tyr
260 265 270
Ala Arg Asn Thr Phe Ser Arg Gly Ile Phe Leu Asp Thr Ile Val Pro
275 280 285
Lys Tyr Glu Val Asn Gly Val Lys Pro Pro Ile Gly Gln Arg Thr Arg
290 295 300
Leu Ser Lys Gly Asp Ile Ala Gln Ala Arg Lys Leu Tyr Lys Cys Pro
305 310 315 320

Ala	Cys	Gly	Glu	Thr	Leu	Gln	Asp	Ser	Thr	Gly	Asn	Phe	Ser	Ser	Pro
				325					330					335	
Glu	Tyr	Pro	Asn	Gly	Tyr	Ser	Ala	His	Met	His	Cys	Val	Trp	Arg	Ile
				340				345						350	
Ser	Val	Thr	Pro	Gly	Glu	Lys	Ile	Ile	Leu	Asn	Phe	Thr	Ser	Leu	Asp
				355			360					365			
Leu	Tyr	Arg	Ser	Arg	Leu	Cys	Trp	Tyr	Asp	Tyr	Val	Glu	Val	Arg	Asp
						375					380				
Gly	Phe	Trp	Arg	Lys	Ala	Pro	Leu	Arg	Gly	Arg	Phe	Cys	Gly	Ser	Lys
385					390					395					400
Leu	Pro	Glu	Pro	Ile	Val	Ser	Thr	Asp	Ser	Arg	Leu	Trp	Val	Glu	Phe
				405					410					415	
Arg	Ser	Ser	Ser	Asn	Trp	Val	Gly	Lys	Gly	Phe	Phe	Ala	Val	Tyr	Glu
				420				425					430		
Ala	Ile	Cys	Gly	Gly	Asp	Val	Lys	Lys	Asp	Tyr	Gly	His	Ile	Gln	Ser
				435			440					445			
Pro	Asn	Tyr	Pro	Asp	Asp	Tyr	Arg	Pro	Ser	Lys	Val	Cys	Ile	Trp	Arg
						455					460				
Ile	Gln	Val	Ser	Glu	Gly	Phe	His	Val	Gly	Leu	Thr	Phe	Gln	Ser	Phe
465					470					475					480
Glu	Ile	Glu	Arg	His	Asp	Ser	Cys	Ala	Tyr	Asp	Tyr	Leu	Glu	Val	Arg
				485					490					495	
Asp	Gly	His	Ser	Glu	Ser	Ser	Thr	Leu	Ile	Gly	Arg	Tyr	Cys	Gly	Tyr
				500				505					510		
Glu	Lys	Pro	Asp	Asp	Ile	Lys	Ser	Thr	Ser	Ser	Arg	Leu	Trp	Leu	Lys
							520					525			
Phe	Val	Ser	Asp	Gly	Ser	Ile	Asn	Lys	Ala	Gly	Phe	Ala	Val	Asn	Phe
						535					540				
Phe	Lys	Glu	Val	Asp	Glu	Cys	Ser	Arg	Pro	Asn	Arg	Gly	Gly	Cys	Glu
545					550					555					560
Gln	Arg	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Tyr	Lys	Cys	Ser	Cys	Asp	Pro
				565					570					575	
Gly	Tyr	Glu	Leu	Ala	Pro	Asp	Lys	Arg	Arg	Cys	Glu	Ala	Ala	Cys	Gly
				580				585					590		
Gly	Phe	Leu	Thr	Lys	Leu	Asn	Gly	Ser	Ile	Thr	Ser	Pro	Gly	Trp	Pro
							600					605			
Lys	Glu	Tyr	Pro	Pro	Asn	Lys	Asn	Cys	Ile	Trp	Gln	Leu	Val	Ala	Pro
						615					620				
Thr	Gln	Tyr	Arg	Ile	Ser	Leu	Gln	Phe	Asp	Phe	Phe	Glu	Thr	Glu	Gly
625					630					635					640
Asn	Asp	Val	Cys	Lys	Tyr	Asp	Phe	Val	Glu	Val	Arg	Ser	Gly	Leu	Thr
				645					650					655	
Ala	Asp	Ser	Lys	Leu	His	Gly	Lys	Phe	Cys	Gly	Ser	Glu	Lys	Pro	Glu
				660				665					670		
Val	Ile	Thr	Ser	Gln	Tyr	Asn	Asn	Met	Arg						

