

SEQUENCE LISTING

<110> LIU, Yue
 NIJJAR, Tarlochan
 CHAKRABARTTY, Avijit

<120> ANTI-TRANSTHYRETIN ANTIBODIES

<130> 057450/473373

<150> 62/109,002

<151> 2015-01-28

<150> 62/266,556

<151> 2015-12-11

<160> 118

<170> FastSEQ for Windows Version 4.0

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<212> PRT

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<223> m9D5VH

<400> 1

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

<210> 2

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<213> Artificial Sequence

<220>

<223> 1SEQ_H

<400> 2

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

50		55		60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr				
65		70		75
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Tyr Tyr Cys				
		85		90
Ala Arg Gly Ala Met Phe Gly Asn Asp Phe Lys Tyr Pro Met Asp Arg				
		100		105
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser				
		115		120

<210> 3
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BAC02114

<400> 3
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 Phe Thr Phe Ser Ser Tyr
20 25 30
Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Ile Thr Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Gln Gly Ser Arg Tyr Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 4
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AAX82494

<400> 4
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Leu Tyr Tyr Gly Tyr Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 5
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5VHv1

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

<210> 6
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5VHv2

<400> 6
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 Phe Thr Phe Ser Ser Tyr
20 25 30
Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val
35 40 45
Ala Glu Ile Ser Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60
Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Ser Asn Leu Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe Phe Asp
100 105 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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

<220>
<223> Hu9D5VHv2b

<400> 7

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

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

<220>
 <223> Hu9D5VHv3

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

<210> 9
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 <213> Artificial Sequence

<220>
 <223> Hu9D5VHv3b

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

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

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<220>
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<400>	10														
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1			5					10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		20					25						30		
Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40						45			
Ser	Glu	Ile	Ser	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50			55							60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65				70					75					80	
Leu	Gln	Ser	Asn	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95		
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	Phe	Asp
		100				105							110		
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115					120								

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 <223> Hu9D5VHv4b

<400>	11														
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		20					25						30		
Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Arg	Leu	Glu	Leu	Val
	35					40						45			
Ala	Glu	Ile	Ser	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50			55							60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
65				70					75					80	
Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	Phe	Asp
		100				105							110		
Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
		115					120								

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<212> PRT
<213> Artificial Sequence

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<223> Hu9D5VHv5

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

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 9D5 CDRH1 - Kabat

<400> 13
Ser Tyr Thr Met Ser
1 5

<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 9D5 CDRH2 - Kabat

<400> 14
Glu Ile Ser Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val Lys
1 5 10 15
Gly

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

<220>
<223> 9D5 CDRH3 - Kabat

<400> 15
His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe Phe Asp Val
1 5 10 15

<210> 16
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> m9D5VL

<400> 16
Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro Val Thr Pro Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Leu Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95
Leu Glu Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 17
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 1MJU_L

<400> 17
Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro Val Thr Pro Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln His
85 90 95
Leu Glu Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 18
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> ABC66952

<400> 18
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ser Leu Leu Tyr Ser

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

<210> 19
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5VLv1

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

<210> 20
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5VLv2

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

<210> 21

<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5VLv3

<400> 21
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Leu Ala Ser Gly Val Pro
50 55 60
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95
Leu Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 22
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5VLv4

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

<210> 23
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5VLv5

<400> 23
Asp Ile Val Met Thr Gln Ser Ala Pro Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45

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

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

<220>
 <223> 9D5 CDRL1 - Kabat

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

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 9D5 CDRL2 - Kabat

Arg	Val	Ser	Asn	Leu	Ala	Ser
1				5		

<210> 26
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 9D5 CDRL3 - Kabat

Met	Gln	His	Leu	Glu	Tyr	Pro	Leu	Thr
1			5					

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

<220>
 <223> Hu9D5 H1 heavy chain

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	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Leu	Val
			35				40					45			

Ala	Glu	Ile	Ser	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
50						55				60					
Lys	Gly	Arg	Phe	Thr	Phe	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70				75						80
Leu	Gln	Ser	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	Phe	Asp
			100					105					110		
Val	Trp	Gly	Gln	Gly	Thr	Thr	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	Arg	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	Glu	Glu	Met	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> 28

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu9D5 H2 heavy chain

<400> 28

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 Phe Thr Phe Ser Ser Tyr			
Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val			
Ala Glu Ile Ser Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val			
Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr			
Leu Gln Ser Asn Leu Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe Phe Asp			
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys			
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly			
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro			
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr			
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val			
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn			
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro			
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro			
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu			
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn			
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile			
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr			
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys			
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys			
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu			
Ser Leu Ser Pro Gly Lys			

<210> 29

<211> 454

<212> PRT

<213> Artificial Sequence

<223> Hu9D5 H2b heavy chain

[illegible]

<210> 30
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5 H3 heavy chain

<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 Phe Thr Phe Ser Ser Tyr
 20 25 30
 Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Glu Ile Ser Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Ser Asn Leu Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe Phe Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Thr 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 Arg 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 Glu Glu Met 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
Ser Leu Ser Pro Gly Lys
450

440

445

<210> 31
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Hu9D5 H3b heavy chain

<400> 31
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Thr Met Ser Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Leu Val
35 40 45
Ala Glu Ile Ser Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe 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 Arg 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 Glu Glu Met 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> 32
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5 H4 heavy chain

<400>	32														
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	Phe	Thr	Phe	Ser	Ser	Tyr
		20					25					30			
Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40						45			
Ser	Glu	Ile	Ser	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50				55						60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65				70					75						80
Leu	Gln	Ser	Asn	Leu	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	Phe	Asp
		100					105					110			
Val	Trp	Gly	Gln	Gly	Thr	Thr	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	Arg	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	Glu	Glu	Met	Thr	Lys	Asn

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	Glu	Glu	Met	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> 34

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu9D5 H5 heavy chain

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

<210> 36
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5 L2 light chain

<400> 36
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Leu Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
 85 90 95
 Leu Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 37
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu9D5 L3 light chain

<400> 37
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Leu Ala Ser Gly Val Pro
 50 55 60
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
 85 90 95
 Leu Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
130						135					140				
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150					155					160
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185					190		
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
	195						200					205			
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
	210					215									

<210> 38

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu9D5 L4 light chain

<400> 38

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

<210> 39

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu9D5 L5 light chain

<400> 39

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

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

<210> 42
 <211> 396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> m9D5VL with signal peptide

<400> 42
 atgaggtgcc tagctgagtt cctggggcctg cttgtgctct ggatccctgg agccattggg 60
 gatattgtga tgactcaggc tgcaccctct gtacctgtca ctccctggaga gtcagtatcc 120
 atctcctgca ggtctagtaa gagtctcctg catagtaatg gcaacactta cttgtattgg 180
 ttccctgcaga ggccaggcca gtctcctcaa ctccctgatat atcgggtgtc caaccttgcc 240
 tcaggagtcc cagacaggtt cagtggcagt gggtcaggaa ctgctttcac actgagaatc 300
 agtagagtgg aggctgagga tgtgggtgtt tattactgta tgcaacattt agaatatccg 360
 ctcacgttcg gtgctgggac caagctggag ctgaaa 396

<210> 43
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> m9D5VL with signal peptide

<400> 43
 Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
 1 5 10 15
 Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro
 20 25 30
 Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 40 45
 Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Leu Ala
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe
 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110
 Cys Met Gln His Leu Glu Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 120 125
 Leu Glu Leu Lys
 130

<210> 44
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu9D5VHv1

<400> 44
gaggtgcagc tgggtggagtc cggcgggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc tcctacacca tgtcctgggt gcgccaggcc 120
cccggaagg gcctggagct ggtggccgag atctccaaact ccggcgacac cacctactac 180
cccgacaccg tgaagggccg cttcaccttc tcccgcgaca acgccaagaa ctccctgtac 240
ctgcagtcca actccctgaa ggccgaggac accgccgtgt actactgcgc ccgccactac 300
tactacggcg gcggctacgg cggctggttc ttcgacgtgt ggggccaggg caccaccgtg 360
accgtgtcct ca 372

<210> 45
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VHv2

<400> 45
gaggtgcagc tgggtggagtc cggcgggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc tcctacacca tgtcctgggt gcgccaggcc 120
cccggaagg gcctggagct ggtggccgag atctccaaact ccggcgacac cacctactac 180
cccgacaccg tgaagggccg cttcaccttc tcccgcgaca acgccaagaa ctccctgtac 240
ctgcagtcca acctgctgcg cgccgaggac accgccgtgt actactgcgc ccgccactac 300
tactacggcg gcggctacgg cggctggttc ttcgacgtgt ggggccaggg caccaccgtg 360
accgtgtcct ca 372

<210> 46
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VHv2b

<400> 46
gaggtgcaac tgggtggagtc tggcgggcggc ttggtgcaac ctggcggctc cctgaagctg 60
tcctgtgccg cctccggctt caccttcagc agctatacca tgtcttgggt gcgccaaacc 120
cccgagaaga ggctggagtt ggtggctgag attagtaata gcggcgatac cacctactat 180
cccgataccg tgaagggccg cttcaccatt tccagagata atgctaagaa taccctgtat 240
ctgcaaatga gtagcctgaa gtctgaggat accgctatgt attattgtgc tagacattat 300
tattatggcg gcggctatgg cggctggttc ttcgatgtgt ggggccaagg caccctggtc 360
accgtgtcct ca 372

<210> 47
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VHv3

<400> 47
gaggtgcagc tgggtggagtc cggcgggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc tcctacacca tgtcctgggt gcgccaggcc 120
cccggaagg gcctggagtg ggtgtccgag atctccaaact ccggcgacac cacctactac 180
cccgacaccg tgaagggccg cttcaccttc tcccgcgaca acgccaagaa ctccctgtac 240
ctgcagtcca acctgctgcg cgccgaggac accgccgtgt actactgcgc ccgccactac 300
tactacggcg gcggctacgg cggctggttc ttcgacgtgt ggggccaggg caccaccgtg 360
accgtgtcct ca 372

<210> 48
<211> 372
<212> DNA

<213> Artificial Sequence

<220>

<223> Hu9D5VHv3b

<400> 48

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gaggtgcaac  tgggtggagtc  tggcgggcggc  ttggtgcaac  ctggcgggctc  cctgaagctg  60
tcctgtgccg  cctccggctt  caccttcagc  agctatacca  tgtcctgggt  gcgccaaacc  120
cccgggaaga  ggctggagtt  ggtggctgag  attagtaata  gcggcgatac  cacctactat  180
cccgataccg  tgaagggccg  cttcaccatt  tccagagata  atgctaagaa  taccctgtat  240
ctgcaaatga  gtagcctgaa  gtctgaggat  accgctatgt  attattgtgc  tagacattat  300
tattatggcg  gcggctatgg  cggctggttc  ttcgatgtgt  ggggccaagg  caccctggtc  360
accgtgtcct  ca                                     372
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<210> 49

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Hu9D5VHv4

<400> 49

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gaggtgcagc  tgggtggagtc  cggcgggcggc  ctggtgcagc  ccggcgggctc  cctgcgcctg  60
tcctgcgccg  cctccggctt  caccttctcc  tcctacacca  tgtcctgggt  gcgccaggcc  120
cccggcaagg  gcctggagtg  ggtgtccgag  atctccaact  ccggcgacac  cacctactac  180
cccgacaccg  tgaagggccg  cttcaccatc  tcccgcgaca  acgccaagaa  ctccctgtac  240
ctgcagtcca  acctgctgcg  cgccgaggac  accgccgtgt  actactgcgc  ccgccactac  300
tactacggcg  gcggctacgg  cggctggttc  ttcgacgtgt  ggggccaagg  caccaccgtg  360
accgtgtcct  ca                                     372
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<210> 50

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Hu9D5VHv4b

<400> 50

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gaggtgcaac  tgggtggagtc  tggcgggcggc  ttggtgcaac  ctggcgggctc  cctgaagctg  60
tcctgtgccg  cctccggctt  caccttcagc  agctatacca  tgtcctgggt  gcgccaaacc  120
cccgggaaga  ggctggagtt  ggtggctgag  attagtaata  gcggcgatac  cacctactat  180
cccgataccg  tgaagggccg  cttcaccatt  tccagagata  atgctaagaa  taccctgtat  240
ctgcaaatga  gtagcctgaa  gtctgaggat  accgctatgt  attattgtgc  tagacattat  300
tattatggcg  gcggctatgg  cggctggttc  ttcgatgtgt  ggggccaagg  caccctggtc  360
accgtgtcct  ca                                     372
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<210> 51

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Hu9D5VHv5

<400> 51

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gaggtgcagc  tgggtggagtc  cggcgggcggc  ctggtgcagc  ccggcgggctc  cctgcgcctg  60
tcctgcgccg  cctccggctt  caccttctcc  tcctacacca  tgtcctgggt  gcgccagacc  120
cccgagaagc  gcctggagct  ggtggccgag  atctccaact  ccggcgacac  cacctactac  180
cccgacaccg  tgaagggccg  cttcaccatc  tcccgcgaca  acgccaagaa  caccctgtac  240
ctgcagatga  acctgctgcg  cgccgaggac  accgccgtgt  actactgcgc  ccgccactac  300
tactacggcg  gcggctacgg  cggctggttc  ttcgacgtgt  ggggccaagg  caccaccgtg  360
accgtgtcct  ca                                     372
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<210> 52
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VLv1

<400> 52
gacatcgtga tgaccagtc cccctgtcc ctgccgtga ccccggcga gccgcctcc 60
atctcctgcc gtcctccaa gtccctgctg cactccaacg gcaacaccta cctgtactgg 120
ttcctgcaga agcccgcca gtccccccag ctgctgatct accgctgtgc caacctggcc 180
tccggcgtgc ccgaccgctt ctccggctcc ggctccggca ccgacttcac cctgaagatc 240
tcccgcgtgg aggccgagga cgtgggcgtg tactactgca tgcagcacct ggagtacccc 300
ctgaccttcg gccagggcac caagctggag atcaaa 336

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

<220>
<223> Hu9D5VLv2

<400> 53
gacatcgtga tgaccagtc cccctgtcc ctgccgtga ccccggcga gccgcctcc 60
atctcctgcc gtcctccaa gtccctgctg cactccaacg gcaacaccta cctgtactgg 120
tacctgcaga agcccgcca gtccccccag ctgctgatct accgctgtgc caacctggcc 180
tccggcgtgc ccgaccgctt ctccggctcc ggctccggca ccgacttcac cctgaagatc 240
tcccgcgtgg aggccgagga cgtgggcgtg tactactgca tgcagcacct ggagtacccc 300
ctgaccttcg gccagggcac caagctggag atcaaa 336

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

<220>
<223> Hu9D5VLv3

<400> 54
gacatcgtga tgaccagtc cccctgtcc ctgccgtga ccccggcga gccgcctcc 60
atctcctgcc gtcctccaa gtccctgctg cactccaacg gcaacaccta cctgtactgg 120
tacctgcaga agcccgcca gtccccccag ctgctgatct accgctgtgc caacctggcc 180
tccggcgtgc cctcccgctt ctccggctcc ggctccggca ccgacttcac cctgaagatc 240
tcccgcgtgg aggccgagga cgtgggcgtg tactactgca tgcagcacct ggagtacccc 300
ctgaccttcg gccagggcac caagctggag atcaaa 336

<210> 55
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VLv4

<400> 55
gacatcgtga tgaccagtc cccccctcc ctgccgtga ccccggcga gccgtgtcc 60
atctcctgcc gtcctccaa gtccctgctg cactccaacg gcaacaccta cctgtactgg 120
ttcctgcagc gcccgcca gtccccccag ctgctgatct accgctgtgc caacctggcc 180
tccggcgtgc cctcccgctt ctccggctcc ggctccggca ccgccttcac cctgcgcata 240
tcccgcgtgg aggccgagga cgtgggcgtg tactactgca tgcagcacct ggagtacccc 300
ctgaccttcg gccagggcac caagctggag atcaaa 336

<210> 56
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Hu9D5VLv5

<400> 56
gacatcgtga tgaccagtc cgccccctcc ctgcccgtga cccccggcga gtccgtgtcc 60
atctcctgcc gctcctccaa gtccctgctg cactccaacg gcaacaccta cctgtactgg 120
ttcctgcagc gccccggcca gtccccccag ctgctgatct accgcgtgtc caacctggcc 180
tccggcgtgc cctcccgttt ctccggctcc ggctccggca ccgccttcac cctgcgcata 240
tcccgcgtgg aggccgagga cgtgggcgtg tactactgca tgcagcacct ggagtacccc 300
ctgaccttcg gccaaaggcac caagctggag atcaaa 336

<210> 57
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 9D5VH Signal Peptide

<400> 57
Met Asp Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
1 5 10 15
Val Leu Cys

<210> 58
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> 9D5VH Signal Peptide

<400> 58
atggactttg ggctcagctt gattttcctt gtccttgttt taaaagggtg cctgtgt 57

<210> 59
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 9D5VL Signal Peptide

<400> 59
Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ala Ile Gly
20

<210> 60
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> 9D5VL Signal Peptide

<400> 60

atgaggtgcc tagctgagtt cctggggctg cttgtgctct ggatccctgg agccattggg 60

<210> 61

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> m14G8VH

<400> 61

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

<210> 62

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> 1MQK_H

<400> 62

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

<210> 63

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> AAD30410

<400> 63

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

<210> 64

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Hui4G8VHv1

<400> 64

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

<210> 65

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Hui4G8VHv2

<400> 65

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

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

<210> 66
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu14G8VHv3

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

<210> 67
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRH1 - Kabat

<400> 67
Ser Tyr Thr Met Ser
1 5

<210> 68
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRH2 - Kabat

<400> 68
Glu Ile Asn Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val Lys
1 5 10 15

Gly

<210> 69
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G8 CDRH3 - Kabat

<400> 69
His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe Phe Asp Val
1 5 10 15

<210> 70
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> m14G8VL

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

<210> 71
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> MJU_L

<400> 71
Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro Val Thr Pro Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln His

				85					90					95			
Leu	Glu	Tyr	Pro	Phe	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys		
			100					105					110				

Arg

<210> 72
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ABA71374

<400> 72

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

Arg

<210> 73
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ABC66952

<400> 73

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

Arg

<210> 74
 <211> 113
 <212> PRT

<213> Artificial Sequence

<220>

<223> Hu14G8VLv1

<400> 74

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

<210> 75

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu14G8VLv2

<400> 75

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

<210> 76

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu14G8VLv3

<400> 76

```
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1           5           10           15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
          20          25          30
```

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

Arg

<210> 77
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRL1 (mouse, HuVLv1, HuVLv2) - Kabat

<400> 77
 Arg Ser Asn Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr
 1 5 10 15

<210> 78
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRL2 - Kabat

<400> 78
 Arg Val Ser Asn Leu Ala Ser
 1 5

<210> 79
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRL3 - Kabat

<400> 79
 Met Gln His Leu Glu Tyr Pro Leu Thr
 1 5

<210> 80
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G8 CDRL1 (HuVLv3) - Kabat

<400> 80
 Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr
 1 5 10 15

<210> 81
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu14G8 H1 heavy chain

<400> 81
 Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Leu Val
 35 40 45
 Ala Glu Ile Asn Asn Ser Gly Asp Thr Thr Tyr Tyr Pro Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp Phe 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 Arg 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 Glu Glu Met 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> 82
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HUL4G8 H2 heavy chain

<400> 82

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10					15		
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		20						25					30		
Thr	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Lys	Arg	Leu	Glu	Leu	Val
	35						40					45			
Ala	Glu	Ile	Asn	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	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	Arg	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	Glu	Glu	Met	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> 83

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu14G8 H3 heavy chain

<400> 83

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Thr	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Lys	Arg	Leu	Glu	Leu	Val
		35					40					45			
Ala	Glu	Ile	Asn	Asn	Ser	Gly	Asp	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Arg	His	Tyr	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Trp	Phe	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	Arg	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	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	Glu	Glu	Met	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		
						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> 84
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu14G8 L1 light chain

<400> 84

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

<210> 85
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu14G8 L2 light chain

<400> 85

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

<210> 86

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Hu14G8 L3 light chain

<400> 86

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 87
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> m14G8VH with signal peptide

<400> 87
atgaatttcg ggctcagctt gatttttcctt gtccttggtt taaaagggtg cctgtgtgaa 60
gtgaagctgg tggagtctgg gggagggtta gtgcagcctg gagggtcctt gaaactctcc 120
tgtgcagcct ccggaattcac ttccagtagc tataccatgt cttgggttcg ccagactcca 180
gaaaagagggc tggagttggg cgcagaaatt aataatagtg gtgataccac ctactatcca 240
gacactgtaa agggccgatt caccatctcc agagacaatg ccaagaacac cctgtacctg 300
caaatgagca gtctgaagtc tgaggacacg gccatgtatt actgtgcaag acattattac 360
tatggtggtg gctacggggg gtggttcttc gatgtctggg gcacaggac cacggtcacc 420
gtctcctca 429

<210> 88
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> m14G8VH with signal peptide

<400> 88
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
1 5 10 15
Val Leu Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45
Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
50 55 60
Glu Leu Val Ala Glu Ile Asn Asn Ser Gly Asp Thr Thr Tyr Tyr Pro
65 70 75 80
Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110
Tyr Tyr Cys Ala Arg His Tyr Tyr Tyr Gly Gly Gly Tyr Gly Gly Trp
115 120 125
Phe Phe Asp Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
130 135 140

<210> 89
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> m14G8VL with signal peptide

<400> 89
atgagggtgcc tagctgagtt cctggggctg cttgtgctct ggatccctgg agccattggg 60
gatattgtga tgactcaggc tgcaccctct gtacctgtca ctcctggaga gtcagtatcc 120

```

atctcctgca ggtctaataa gagtctcctg catagtaatg gcaacactta cttgtattgg 180
ttcctgcaga ggccaggcca gtctcctcaa ctccctgatat atcgggtgtc caaccttgcc 240
tcaggagttc cagacaggtt cagtggcagt gggtcaggaa ctgctttcac actgagaatc 300
agtagagtgg aggctgagga tgtgggtgtt tattactgta tgcaacattt agaatatccg 360
ctcacgttcg gtgctgggac caagctggag ctgaaacgt 399

```

<210> 90
 <211> 133
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> m14G8VL with signal peptide

```

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

```

<210> 91
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VHv1

```

<400> 91
gaggtgaagc tgggtggagtc tggcgggcggc ttggtgcaac ctggcggctc cctgaagctg 60
tcctgtgccg cctccggctt caccttcagc agctatacca tgtcttgggt gcgccaaacc 120
cccgagaaga ggctggagtt ggtggctgag attaataata gcggcgatac cacctactat 180
cccgataccg tgaagggccg cttcaccatt tccagagata atgctaagaa taccctgtat 240
ctgcaaatga gtagcctgaa gtctgaggat accgctatgt attattgtgc tagacattat 300
tattatggcg gcggctatgg cggctgggtc ttcgatgtgt ggggcaccgg caccctggtc 360
accgtgtcct ca 372

```

<210> 92
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VHv2

```

<400> 92
gaggtgcaac tgggtggagtc tggcgggcggc ttggtgcaac ctggcggctc cctgaagctg 60
tcctgtgccg cctccggctt caccttcagc agctatacca tgtcttgggt gcgccaaacc 120
cccgagaaga ggctggagtt ggtggctgag attaataata gcggcgatac cacctactat 180

```

cccgataccg	tgaagggccg	cttcaccatt	tccagagata	atgctaagaa	taccctgtat	240
ctgcaaatga	gtagcctgaa	gtctgaggat	accgctatgt	attattgtgc	tagacattat	300
tattatggcg	gcggctatgg	cggctggttc	ttcgatgtgt	ggggccaagg	caccctggtc	360
accgtgtcct	ca					372

<210> 93
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VHv3

<400> 93						
gaggtgcaac	tgggtggagtc	tggcggcggc	ttggtgcaac	ctggcggctc	cctgaagctg	60
tcctgtgccc	cctccggctt	caccttcagc	agctatacca	tgtcttgggt	gcgcaaacc	120
cccgagaaga	ggctggagtt	ggtggctgag	attaataata	gcggcgatac	cacctactat	180
cccgataccg	tgaagggccg	cttcaccatt	tccagagata	atgctaagaa	taccctgtat	240
ctgcaaatga	atagcctgag	ggctgaggat	accgctgtgt	attattgtgc	tagacattat	300
tattatggcg	gcggctatgg	cggctggttc	ttcgatgtgt	ggggccaagg	caccctggtc	360
accgtgtcct	ca					372

<210> 94
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VLv1

<400> 94						
gatatcgtga	tgaccagtc	tgccccctcc	ctgcctgtga	cccctggcga	gtccgtgtcc	60
atctcctgcc	ggtccaacaa	gagcctgctg	cacagcaacg	gcaacaccta	cctgtactgg	120
ttcctgcaaa	agcccggcca	atccccctcaa	ctgctgatct	accgggtgtc	caacctggcc	180
tccggcgtgc	ccgatagggt	ctccggaagc	ggctccggca	ccgccttcac	cctgaagatt	240
agtagagtcg	aggccgagga	tgtgggcgtg	tactactgta	tgcaaacactt	ggagtacccc	300
ctgacgttcg	gccaaggcac	caagctggag	atcaagcgt			339

<210> 95
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VLv2

<400> 95						
gatatcgtga	tgaccagtc	tcccctgtcc	ctgcctgtga	cccctggcga	gcccgcctcc	60
atctcctgcc	ggtccaacaa	gagcctgctg	cacagcaacg	gcaacaccta	cctgtactgg	120
ttcctgcaaa	agcccggcca	atccccctcaa	ctgctgatct	accgggtgtc	caacctggcc	180
tccggcgtgc	ccgatagggt	ctccggaagc	ggctccggca	ccgatttcac	cctgaagatt	240
agtagagtcg	aggccgagga	tgtgggcgtg	tactactgta	tgcaaacactt	ggagtacccc	300
ctgacgttcg	gccaaggcac	caagctggag	atcaagcgt			339

<210> 96
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu14G8VLv3

<400> 96						
gatatcgtga	tgaccagtc	tcccctgtcc	ctgcctgtga	cccctggcga	gcccgcctcc	60

```

atctcctgcc ggtccagcaa gagcctgctg cacagcaacg gcaacaccta cctgtactgg 120
ttcctgcaaaa agcccggcca atccccctcaa ctgctgatct accgggtgtc caacctggcc 180
tccggcgtgc ccagtaggtt ctccggaagc ggctccggca ccgatttcac cctgaagatt 240
agtagagtcg aggccgagga tgtgggctg tactactgta tgcaacactt ggagtacccc 300
ctgacgttcg gccaaaggcac caagctggag atcaagcgt 339

```

```

<210> 97
<211> 19
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 14G8VH Signal Peptide

```

```

<400> 97
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
  1             5             10             15
Val Leu Cys

```

```

<210> 98
<211> 57
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> 14G8VH Signal Peptide

```

```

<400> 98
atgaatttcg gcctgagctt gattttcctg gtgctggtgt tgaagggcgt gctgtgt 57

```

```

<210> 99
<211> 20
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 14G8VL Signal Peptide

```

```

<400> 99
Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
  1             5             10             15
Gly Ala Ile Gly
             20

```

```

<210> 100
<211> 60
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> 14G8VL Signal Peptide

```

```

<400> 100
atgaggtgcc tggccgagtt cctgggcctg ctggtgctgt ggatccctgg cgccatcggc 60

```

```

<210> 101
<211> 330
<212> PRT
<213> Artificial Sequence

```

<220>

<223> Human IgG1 heavy chain constant region

<400> 101

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

<210> 102

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG1 heavy chain constant region of IgG1
Glm3 allotype

<400> 102

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5				10						15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			

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

<210> 103

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG1 heavy chain constant region of IgG1
Glm3 allotype

<400> 103

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

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

<210> 104

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Human kappa light chain constant region

<400> 104

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

<210> 105

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Human kappa light chain constant region

<400> 105

Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
1				5					10					15	

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

<210> 106
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IgG1 heavy chain constant region of IgG1
 G1m3 allotype

<400> 106

gcctccacca	agggtccatc	ggtcttcccc	ctggcaccct	cctccaagag	cacctctggg	60
ggcacagcgg	ccctgggctg	cctgggtcaag	gactacttcc	ccgaaccggg	gacgggtgtcg	120
tggaactcag	gcgccctgac	cagcggcgtg	cacaccttcc	cggctgtcct	acagtcctca	180
ggactctact	ccctcagcag	cgtgggtgacc	gtgccttcca	gcagcttggg	caccagacc	240
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagag	agttgagccc	300
aaatcttgtg	acaaaactca	cacatgccca	ccgtgcccag	cacctgaact	cctggggggga	360
ccgtcagttc	tcctcttccc	cccaaaaacc	aaggacaccc	tcattgatctc	ccggaccctc	420
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	480
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgcggggagga	gcagtacaac	540
agcacgtacc	gtgtgggtcag	cgtcctcacc	gtcctgcacc	aggactgggt	gaatggcaag	600
gagtacaagt	gcaaggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	660
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccgggaggag	720
atgaccaaga	accaggtcag	cctgacctgc	ctgggtcaaag	gcttctatcc	cagcgacatc	780
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	840
ctggactccg	acggctcctt	cttcctctat	agcaagctca	ccgtggacaa	gagcaggtgg	900
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	960
cagaagagcc	tctccctgtc	cccgggtaaa				990

<210> 107
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human kappa light chain constant region

<400> 107

cgaactgttg	ctgcaccatc	tgtcttcatc	ttcccgccat	ctgatgagca	gttgaaatct	60
ggaactgcct	ctgttgtgtg	cctgctgaat	aacttctatc	ccagagaggc	caaagtacag	120
tggaagggtg	ataacgccct	ccaatcgggt	aactcccagg	agagtgtcac	agagcaggac	180
agcaaggaca	gcacctacag	cctcagcagc	accctgacgc	tgagcaaagc	agactacgag	240
aaacacaaag	tctacgcctg	cgaagtcacc	catcagggcc	tgagctcgcc	cgtcacaaag	300
agcttcaaca	gggagagtg	t				321

<210> 108
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Human kappa light chain constant region

<400> 108

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aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 180
aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 240
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 300
ttcaacaggg gagagtgt                                     318
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<210> 109

<211> 147

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Ser His Arg Leu Leu Leu Leu Cys Leu Ala Gly Leu Val Phe
 1           5           10           15
Val Ser Glu Ala Gly Pro Thr Gly Thr Gly Glu Ser Lys Cys Pro Leu
 20           25           30
Met Val Lys Val Leu Asp Ala Val Arg Gly Ser Pro Ala Ile Asn Val
 35           40           45
Ala Val His Val Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu Pro Phe
 50           55           60
Ala Ser Gly Lys Thr Ser Glu Ser Gly Glu Leu His Gly Leu Thr Thr
 65           70           75           80
Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val Glu Ile Asp Thr Lys
 85           90           95
Ser Tyr Trp Lys Ala Leu Gly Ile Ser Pro Phe His Glu His Ala Glu
100          105          110
Val Val Phe Thr Ala Asn Asp Ser Gly Pro Arg Arg Tyr Thr Ile Ala
115          120          125
Ala Leu Leu Ser Pro Tyr Ser Tyr Ser Thr Thr Ala Val Val Thr Asn
130          135          140
Pro Lys Glu
145
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<210> 110

<211> 127

<212> PRT

<213> Homo sapiens

<400> 110

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Gly Pro Thr Gly Thr Gly Glu Ser Lys Cys Pro Leu Met Val Lys Val
 1           5           10           15
Leu Asp Ala Val Arg Gly Ser Pro Ala Ile Asn Val Ala Val His Val
 20           25           30
Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu Pro Phe Ala Ser Gly Lys
 35           40           45
Thr Ser Glu Ser Gly Glu Leu His Gly Leu Thr Thr Glu Glu Gln Phe
 50           55           60
Val Glu Gly Ile Tyr Lys Val Glu Ile Asp Thr Lys Ser Tyr Trp Lys
 65           70           75           80
Ala Leu Gly Ile Ser Pro Phe His Glu His Ala Glu Val Val Phe Thr
 85           90           95
Ala Asn Asp Ser Gly Pro Arg Arg Tyr Thr Ile Ala Ala Leu Leu Ser
100          105          110
Pro Tyr Ser Tyr Ser Thr Thr Ala Val Val Thr Asn Pro Lys Glu
115          120          125
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<210> 111

<211> 127

<212> PRT

<213> Homo sapiens

<400> 111

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

<210> 112

<211> 138

<212> PRT

<213> Homo sapiens

<400> 112

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

<210> 113

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Transthyretin residues 89-97

<400> 113

Glu	His	Ala	Glu	Val	Val	Phe	Thr	Ala
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<210> 114

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Potential transthyretin immunogen

<400> 114

Gly Gly Glu His Ala Glu Val Val Phe Thr Ala Gly Gly Lys Gly
1 5 10 15

<210> 115

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Potential transthyretin immunogen

<400> 115

Cys Gly Gly Glu His Ala Glu Val Val Phe Thr Ala
1 5 10

<210> 116

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Potential transthyretin immunogen

<400> 116

Glu His Ala Glu Val Val Phe Thr Ala Cys Gly Gly
1 5 10

<210> 117

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 9D5 CDRH1 - Composite Chothia-Kabat

<400> 117

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

<210> 118

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 14G8 CDRH1 - Composite Chothia-Kabat

<400> 118

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