

Sequence Listing

<110> SHANGHAI JUNSHI BIOSCIENCES CO., LTD.
SUZHOU JUNMENG BIOSCIENCES CO., LTD.

<120> ANTI-IL-17A ANTIBODY AND USE THEREOF

<130> 199971PCWO

<150> CN 201811515045.7

<151> 2018-12-12

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Gly Tyr Ile Phe Thr Asn Tyr Gly
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Ile Asn Asp His Thr Gly Glu Pro
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Ala Asn Tyr Gly Phe Gly Tyr Phe Asp Tyr

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

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Asp Tyr Tyr Gly Ser Ser Leu Leu Asp Tyr
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Ser Asp Tyr Ala Trp
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Phe Ile Ser Tyr Ser Gly Pro Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

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Gly Gly Asp Gly Asp Ser Phe Asp Tyr
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Gln Ser Leu Val His Ser Asn Gly Asn Ser Tyr
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<400> 14
Lys Val Ser
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Ser Gln Ser Thr His Val Pro Tyr Thr
1 5

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Arg Ser Gly Gln Ser Leu Val His Ser Asn Gly His Thr Tyr Phe His
1 5 10 15

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

1 5

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<223> LCDR3

<400> 21

Leu Gln Tyr Glu Met Leu Pro Leu Thr

1 5

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<400> 22

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Asp

1 5 10 15

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<223> LCDR2

<400> 23

Lys Val Ser Asn Arg Phe Ser

1 5

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<223> LCDR3

<400> 24

Phe Gln Gly Ser His Phe Pro Thr
1 5

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<211> 117

<212> PRT

<213> Artificial Sequence

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<223> VH

<400> 25

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

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<400> 26

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

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

<210> 27
 <211> 119
 <212> PRT
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<220>
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<400>	27														
Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr
			20					25					30		
Tyr	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	Arg	Ile	Asp	Pro	Ala	Asn	Gly	Asn	Thr	Lys	Tyr	Asp	Pro	Lys	Phe
	50					55					60				
Gln	Gly	Lys	Ala	Thr	Ile	Thr	Gly	Asp	Lys	Ser	Ser	Asn	Ala	Ala	Tyr
65					70				75						80
Leu	Gln	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Val	Thr	Asp	Tyr	Tyr	Gly	Ser	Ser	Leu	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Thr	Leu	Thr	Val	Ser	Ser									
			115												

<210> 28
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<220>
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<400>	28														
Asp	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1			5						10					15	
Ser	Leu	Ser	Leu	Thr	Cys	Thr	Val	Thr	Gly	Tyr	Ser	Ile	Thr	Ser	Asp
			20					25					30		
Tyr	Ala	Trp	Ser	Trp	Ile	Arg	Gln	Phe	Pro	Gly	Asn	Lys	Leu	Glu	Trp
		35				40						45			
Met	Ala	Phe	Ile	Ser	Tyr	Ser	Gly	Pro	Thr	Ser	Tyr	Asn	Pro	Ser	Leu

50		55		60	
Lys	Ser	Arg	Val	Ser	Ile
65				70	
Leu	Gln	Leu	Lys	Ser	Val
			85		
Ala	Arg	Gly	Gly	Asp	Gly
		100			
Thr	Leu	Thr	Val	Ser	Ser
		115			

<210> 29
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<220>
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<400> 29	
Asp	Val
1	
Val	Met
	5
Thr	Gln
	10
Pro	Leu
	15
Ser	Leu
	20
Pro	Val
	25
Ser	Leu
	30
Val	Ser
	35
Leu	Gly
	40
Gln	Lys
	45
Pro	Gly
	50
Val	Pro
	55
Ser	Val
	60
Asn	Arg
	65
Phe	Thr
	70
Leu	Lys
	75
Val	Ile
	80
Ser	Gln
	85
Thr	Ser
	90
His	Gln
	95
Val	Leu
	100
Pro	Glu
	105
Tyr	Ile
	110
Thr	Lys

<210> 30
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

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

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	Leu	Gly	Ile	Tyr	Phe	Cys	Ser	Gln	Ser
			85					90					95		
Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100				105					110			

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<220>
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<400> 31
Asp Val Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser His 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 Gly 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 Val Tyr Tyr Cys Leu Gln Tyr Glu Met Leu Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 32
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 <212> PRT
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<400> 32
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Phe Thr Leu Lys Ile

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

<210> 33
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<400>	33														
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	Ile	Phe	Thr	Asn	Tyr
			20				25						30		
Gly	Met	Asn	Trp	Met	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Asp	His	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90						95	
Ala	Asn	Tyr	Gly	Phe	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												

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

<220>
 <223> VL

<400>	34														
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1			5						10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20				25						30		
Asn	Gly	Asn	Ser	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile

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

<210> 35
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<400>	35														
Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Thr	Asn	Tyr
			20					25					30		
Gly	Met	Asn	Trp	Met	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Asp	His	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90					95		
Ala	Asn	Tyr	Gly	Phe	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												

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<220>
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<400>	36														
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20					25					30		
Asn	Gly	Asn	Ser	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile

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

<210> 37
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<400>	37														
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Thr	Gly	Tyr	Ser	Ile	Ser	Ser	Asp
			20					25					30		
Tyr	Ala	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp
		35					40					45			
Ile	Gly	Phe	Ile	Ser	Tyr	Ser	Gly	Pro	Thr	Ser	Tyr	Asn	Pro	Ser	Leu
	50					55					60				
Lys	Ser	Arg	Val	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser
65					70				75					80	
Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Gly	Gly	Asp	Gly	Asp	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser										
															115

<210> 38
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<220>
 <223> VL

<400>	38														
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser
			20					25					30		
Asn	Gly	Asn	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Lys	Ser
		35					40					45			
Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile

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

<210> 39
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<220>
 <223> VL

<400>	39														
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser
			20					25					30		
Asn	Gly	Asn	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Phe	Thr	Leu	Lys	Ile
65					70				75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly
				85				90						95	
Ser	His	Phe	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
			100					105					110		

<210> 40
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<220>
 <223> VH

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

				85					90					95			
Ala	Arg	Gly	Gly	Asp	Gly	Asp	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr		
			100					105					110				
Thr	Val	Thr	Val	Ser	Ser												
			115														

<210> 41
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<400> 41																	
Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Thr	Pro	Gly		
1				5					10					15			
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Ile	Val	His	Ser		
			20					25					30				
Asn	Gly	Asn	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser		
		35					40					45					
Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro		
	50					55					60						
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile		
65					70					75					80		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly		
				85					90					95			
Ser	His	Phe	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys			
			100					105					110				

<210> 42
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<220>
 <223> HC

<400> 42																	
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	Ile	Phe	Thr	Asn	Tyr		
			20					25					30				
Gly	Met	Asn	Trp	Met	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met		
		35					40					45					
Gly	Trp	Ile	Asn	Asp	His	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Lys	Phe		
	50					55					60						
Gln	Gly	Arg	Val	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr		
65					70					75					80		
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		

				85					90					95			
Ala	Asn	Tyr	Gly	Phe	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu		
			100					105					110				
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu		
		115					120					125					
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys		
		130				135					140						
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser		
145					150					155					160		
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser		
			165					170					175				
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser		
		180						185					190				
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn		
		195					200					205					
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro		
		210				215					220						
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe		
225					230					235					240		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val		
				245					250					255			
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe		
		260					265					270					
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro		
		275					280				285						
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr		
		290				295					300						
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val		
305					310					315					320		
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala		
			325					330						335			
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln		
		340						345						350			
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly		
		355					360					365					
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro		
		370				375					380						
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser		
385					390					395					400		
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu		
			405					410						415			
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His		
		420						425					430				
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
		435					440										

<210> 43
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>

<223> LC

<400> 43

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1			5						10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
		20					25						30		
Asn	Gly	Asn	Ser	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70						75					80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Ser	Gln	Ser
			85					90						95	
Thr	His	Val	Pro	Tyr	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> 44

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> HC

<400> 44

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

	50				55				60							
Gln 65	Gly	Arg	Val	Thr	Phe 70	Thr	Leu	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr 80	
Met	Glu	Leu	Ser	Arg 85	Leu	Arg	Ser	Asp	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Asn	Tyr	Gly 100	Phe	Gly	Tyr	Phe	Asp 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Leu	
Val	Thr	Val 115	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
Ala	Pro 130	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	
Leu 145	Val	Lys	Asp	Tyr	Phe 150	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser 160	
Gly	Ala	Leu	Thr	Ser 165	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser 175	
Ser	Gly	Leu	Tyr 180	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
Leu	Gly 195	Thr	Lys	Thr	Tyr	Thr	Cys 200	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	
Thr	Lys 210	Val	Asp	Lys	Arg	Val 215	Glu	Ser	Lys	Tyr	Gly 220	Pro	Pro	Cys	Pro	
Pro 225	Cys	Pro	Ala	Pro	Glu 230	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe 240	
Pro	Pro	Lys	Pro	Lys 245	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val 255	
Thr	Cys	Val	Val 260	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe 270	
Asn	Trp 275	Tyr	Val	Asp	Gly	Val	Glu 280	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
Arg	Glu 290	Glu	Gln	Phe	Asn 295	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
Val 305	Leu	His	Gln	Asp	Trp 310	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val 320	
Ser	Asn	Lys	Gly 325	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala 335	
Lys	Gly	Gln	Pro 340	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	
Glu	Glu	Met 355	Thr	Lys	Asn	Gln	Val 360	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
Phe	Tyr 370	Pro	Ser	Asp	Ile	Ala 375	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
Glu 385	Asn	Asn	Tyr	Lys	Thr 390	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser 400	
Phe	Phe	Leu	Tyr	Ser 405	Arg	Leu	Thr	Val	Asp 410	Lys	Ser	Arg	Trp	Gln	Glu 415	
Gly	Asn	Val	Phe 420	Ser	Cys	Ser	Val	Met 425	His	Glu	Ala	Leu	His 430	Asn	His	
Tyr	Thr	Gln 435	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					

<210> 45
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> LC

<400> 45
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asn Gly Asn Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95
Thr His Val Pro Tyr 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> 46
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> HC

<400> 46
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Ser Ser Asp

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

			420					425					430
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
			435				440					445	

<210> 47
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC

<400> 47
 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Lys Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95
 Ser His Phe Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 48
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC

<400> 48

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

<210> 49

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> HC

<400> 49

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

				85				90					95				
Ala	Arg	Gly	Gly	Asp	Gly	Asp	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr		
			100					105					110				
Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro		
		115					120					125					
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly		
		130				135					140						
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn		
145				150					155						160		
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln		
			165					170						175			
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser		
		180					185						190				
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser		
		195					200				205						
Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys		
		210				215					220						
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu		
225				230					235						240		
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu		
			245					250						255			
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln		
		260					265						270				
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys		
		275				280					285						
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu		
		290				295					300						
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys		
305				310					315						320		
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys		
			325					330						335			
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser		
		340						345					350				
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys		
		355					360					365					
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln		
		370				375					380						
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly		
385				390					395					400			
Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln		
			405					410						415			
Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn		
		420						425					430				
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
		435					440					445					

<210> 50

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> LC

<400> 50

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

<210> 51

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> HC

<400> 51

caggtgcagc	tggtgcagag	cggcgccgag	gtgaagaagc	ccggcgccag	cgtgaagggtg	60
agctgcaagg	ccagcggcta	catcttcacc	aactacggca	tgaactggat	gagacaggcc	120
cccggccagg	gcctggagtg	gatgggctgg	atcaacgacc	acaccggcga	gcccacctac	180
gccgacaagt	tccagggcag	agtgaccttc	accctggaca	ccagcatcag	caccgcctac	240
atggagctga	gcagactgag	aagcgacgac	accgccgtgt	actactgcgc	caactacggc	300
ttcggctact	tcgactactg	gggccagggc	accctgggtga	ccgtgagcag	cgctagcacc	360
aagggcccca	gcgtgttccc	cctggcccct	tgcagcagaa	gcaccagcga	gagcacagcc	420

gccctgggct	gcctggtgaa	ggactacttc	cccagagccc	tgaccgtgtc	ctggaacagc	480
ggcgctctga	ccagcggcgt	gcataccttc	cccgccgtgc	tccagagcag	cggactgtac	540
tccctgagca	gcgtgggtgac	cgtgccttcc	agcagcctgg	gcaccaagac	ctacacctgc	600
aacgtggacc	acaagcccag	caacaccaag	gtggacaaga	gagtggagag	caagtacggc	660
cctccctgcc	ccccttgccc	tgcccccgag	ttcctgggcg	gacctagcgt	gttcctgttc	720
ccccccaagc	ccaaggacac	cctgatgatc	agcagaaccc	ccgagggtgac	ctgcgtgggtg	780
gtggacgtgt	cccaggagga	ccccgaggtc	cagtttaatt	ggtacgtgga	cggcgtggaa	840
gtgcataacg	ccaagaccaa	gcccagagag	gagcagttca	acagcaccta	cagagtgggtg	900
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tccaacaagg	gcctgcctag	cagcatcgag	aagaccatca	gcaaggccaa	gggccagcca	1020
cgggagcccc	aggtctacac	cctgccacct	agccaagagg	agatgaccaa	gaaccagggtg	1080
tccctgacct	gtctggtgaa	aggcttctat	cccagcgata	tcgccgtgga	gtgggagagc	1140
aacggccagc	ccgagaacaa	ctacaagacc	acccccctg	tgctggacag	cgacggcagc	1200
ttcttctgt	actccagact	gaccgtggac	aagtccagat	ggcaggagggg	caacgtcttc	1260
agctgctccg	tgatgcacga	ggccctgcac	aaccactaca	cccagaagtc	cctgagcctg	1320
agcctgggca	agtga					1335

<210> 52
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LC

<400> 52	
gacgtggtga	tgacccagag cccccctgagc ctgcccgtga ccctggggcca gcccgccagc 60
atcagctgca	gaagcagcca gagcctgggtg cacagcaacg gcaacagcta cctgcactgg 120
tacctgcaga	agcccgccca gagccccag ctgctgatct acaagggtgag caacagattc 180
agcggcgtgc	ccgacagatt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240
agcagagtgg	aggccgagga cgtgggcgtg tactactgca gccagagcac ccacgtgccc 300
tacaccttcg	gccagggcac caagctggag atcaagcgaa ctgtggctgc accatctgtc 360
ttcatcttcc	cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
ctgaataact	tctatcccag agaggccaaa gtacagtggga aggtggataa cgccctccaa 480
tcgggtaact	cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
agcagcacc	tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
gtcacccatc	agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttag 660

<210> 53
 <211> 1335
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HC

<400> 53	
cagatccagc	tggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaagatc 60
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cccggccagg	gcctggagtg gatgggctgg atcaacgacc acaccggcga gcccacctac 180

gccgacaagt	tccagggcag	agtgaccttc	accctggaca	ccagcgccag	caccgcctac	240
atggagctga	gcagactgag	aagcgacgac	accgccgtgt	actactgcgc	caactacggc	300
ttcggctact	tcgactactg	gggccagggc	accctgggtga	ccgtgagcag	cgctagcacc	360
aagggcccca	gcgtgttccc	cctggccctt	tgtagcagaa	gcaccagcga	gagcacagcc	420
gccctgggct	gcctggtgaa	ggactacttc	cccagagccc	tgaccgtgtc	ctggaacagc	480
ggcgctctga	ccagcggcgt	gcataaccttc	cccgccgtgc	tccagagcag	cggactgtac	540
tccctgagca	gcgtggtgac	cgtgccttcc	agcagcctgg	gcaccaagac	ctacacctgc	600
aacgtggacc	acaagcccag	caacaccaag	gtggacaaga	gagtggagag	caagtacggc	660
cctccctgcc	ccccttgccc	tgcccccag	ttcctgggcg	gacctagcgt	gttcctgttc	720
ccccccaagc	ccaaggacac	cctgatgatc	agcagaaccc	ccgaggtgac	ctgcgtggtg	780
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tccaacaagg	gcctgcctag	cagcatcgag	aagaccatca	gcaaggccaa	gggccagcca	1020
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tccctgacct	gtctggtgaa	aggcttctat	cccagcgata	tcgccgtgga	gtgggagagc	1140
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ttcttctgt	actccagact	gaccgtggac	aagtccagat	ggcaggaggg	caacgtcttc	1260
agctgctccg	tgatgcacga	ggccctgcac	aaccactaca	cccagaagtc	cctgagcctg	1320
agcctgggca	agtga					1335

<210> 54
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LC

<400> 54	
gacgtggtga	tgacccagag cccctgagc ctgcccgtga ccctgggcca gcccgccagc 60
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tacctgcaga	agcccggcca gagccccag ctgctgatct acaagggtgag caacagattc 180
agcggcggtg	ccgacagatt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240
agcagagtgg	aggccgagga cgtgggcgtg tacttctgca gccagagcac ccacgtgccc 300
tacaccttcg	gccagggcac caagctggag atcaagcgaa ctgtggctgc accatctgtc 360
ttcatcttcc	cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
ctgaataact	tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
tcgggtaact	cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
agcagcacc	tgacgtgtag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 600
gtcacccatc	agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttag 660

<210> 55
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HC

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<400> 55
cagggtgcagc tgcaggagag cggccccggc ctggtgaagc ccagcgagac cctgagcctg      60
acctgcaccg tgaccggcta cagcatcagc agcgactacg cctggagctg gatcagacag      120
ccccccggca agggcctgga gtggatcggc ttcatcagct acagcggccc caccagctac      180
aaccacagcc tgaagtccag agtgaccatc agcagagaca ccagcaagaa ccagttcagc      240
ctgaagctga gcagcgtgac cgccgccgac accgccgtgt actactgcgc cagaggcggc      300
gacggcgaca gcttcgacta ctggggccag ggcaccctgg tgaccgtgag cagcgctagc      360
accaagggcc ccagcgtgtt ccccctggcc ccttgacgca gaagcaccag cgagagcaca      420
gccgccctgg gctgcctggg gaaggactac ttccccgagc ccgtgaccgt gtcctggaac      480
agcggcgctc tgaccagcgg cgtgcatacc ttccccgccg tgctccagag cagcggactg      540
tactccctga gcagcgtggg gaccgtgcct tccagcagcc tgggcaccaa gacctacacc      600
tgcaacgtgg accacaagcc cagcaacacc aaggtggaca agagagtggg gagcaagtac      660
ggccctccct gccccccttg ccctgcccc gagttcctgg gcggacctag cgtgttcctg      720
ttcccccca agcccaagga caccctgatg atcagcagaa ccccagagg gacctgcgtg      780
gtggtggacg tgtcccagga ggaccccag gtccagttta attggtacgt ggacggcgtg      840
gaagtgcata acgccaagac caagcccaga gaggagcagt tcaacagcac ctacagagtg      900
gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaggaata caagtgaag      960
gttccaaca agggcctgcc tagcagcatc gagaagacca tcagcaaggc caagggccag     1020
ccacgggagc cccagggtcta caccctgcca cctagccaag aggagatgac caagaaccag     1080
gtgtccctga cctgtctggg gaaaggcttc tatcccagcg atatcgccgt ggagtgggag     1140
agcaacggcc agcccagaaa caactacaag accaccccc ctgtgctgga cagcgacggc     1200
agcttcttcc tgtactccag actgaccgtg gacaagtcca gatggcagga gggcaacgtc     1260
ttcagctgct ccgtgatgca cgaggccctg cacaaccact acaccagaa gtccctgagc     1320
ctgagcctgg gcaagtga

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<210> 56
<211> 657
<212> DNA
<213> Artificial Sequence

```

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<220>
<223> LC

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```

<400> 56
gacgtggtga tgacccagag ccccctgagc ctgcccgtga ccctgggcca gcccgccagc      60
atcagctgca gaagcagcca gagcatcgtg cacagcaacg gcaacaccta cctggactgg      120
tacctgcaga agcccggcaa gagccccaag ctgctgatct acaagggtgag caacagattc      180
agcggcgtgc ccgacagatt cagcggcagc ggacggcga ccgacttcac cctgaagatc      240
agcagagtgg agggcgagga cctgggcgtg tactactgct tccagggcag ccacttcccc      300
accttcggcc agggcaccaa gctggagatc aagcgaactg tggctgcacc atctgtcttc      360
atcttcccg ccatctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg      420
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg      480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc      540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc      600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttag      657

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<210> 57
<211> 657
<212> DNA
<213> Artificial Sequence

```

<220>

<223> LC

<400> 57

gacgtggtga	tgacccagag	ccccctgagc	ctgcccgtga	ccctggggcca	gcccgccagc	60
atcagctgca	gaagcagcca	gagcatcgtg	cacagcaacg	gcaacaccta	cctggactgg	120
tacctgcaga	agcccggcca	gagccccaag	ctgctgatct	acaagggtgag	caacagattc	180
agcggcgtgc	ccgacagatt	cagcggcagc	ggcagcggca	ccagcttcac	cctgaagatc	240
agcagagtgg	aggccgagga	cctgggctgt	tactactgct	tccagggcag	ccacttcccc	300
accttcggcc	agggcaccaa	gctggagatc	aagcgaactg	tggctgcacc	atctgtcttc	360
atcttccccgc	catctgatga	gcagttgaaa	tctggaactg	cctctgttgt	gtgcctgctg	420
aataacttct	atcccagaga	ggccaaagta	cagtgggaagg	tggataacgc	cctccaatcg	480
ggtaactccc	aggagagtgt	cacagagcag	gacagcaagg	acagcaccta	cagcctcagc	540
agcaccctga	cgctgagcaa	agcagactac	gagaaacaca	aagtctacgc	ctgcgaagtc	600
acccatcagg	gcctgagctc	gcccgtcaca	aagagcttca	acaggggaga	gtgttag	657

<210> 58

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> HC

<400> 58

caggtgcagc	tgaggagag	cggccccggc	ctggtgaagc	ccagcgagac	cctgagcctg	60
acctgcaccg	tgagcggcta	cagcatcacc	agcgactacg	cctggagctg	gatcagacag	120
ccccccggca	agggcctgga	gtggatcggc	ttcatcagct	acagcggccc	caccagctac	180
aaccccagcc	tgaagtccag	agtgaccatc	agcagagaca	ccagcaagaa	ccagttcttc	240
ctgcagctga	agtccgtgac	cgccgccgac	accgccgtgt	actactgcgc	cagaggcggc	300
gacggcgaca	gcttcgacta	ctggggccag	ggcaccaccg	tgaccgtgag	cagcgctagc	360
accaaggggcc	ccagcgtgtt	ccccctggcc	ccttgagca	gaagcaccag	cgagagcaca	420
gccgccctgg	gctgcctggg	gaaggactac	ttccccgagc	ccgtgaccgt	gtcctggaac	480
agcggcgctc	tgaccagcgg	cgtgcatacc	ttccccgccg	tgctccagag	cagcggactg	540
tactccctga	gcagcgtggt	gaccgtgcct	tccagcagcc	tgggcaccaa	gacctacacc	600
tgcaacgtgg	accacaagcc	cagcaacacc	aaggtggaca	agagagtgga	gagcaagtac	660
ggccctccct	gcccccttg	ccctgcccc	gagttcctgg	gcggacctag	cgtgttcctg	720
ttccccccca	agcccaagga	caccctgatg	atcagcagaa	cccccgaggt	gacctgcgtg	780
gtggtggacg	tgtcccagga	ggaccccag	gtccagttaa	attggtacgt	ggacggcgtg	840
gaagtgcata	acgccaagac	caagcccaga	gaggagcagt	tcaacagcac	ctacagagtg	900
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gtctccaaca	agggcctgcc	tagcagcatc	gagaagacca	tcagcaaggc	caagggccag	1020
ccacgggagc	cccaggctta	caccctgcca	cctagccaag	aggagatgac	caagaaccag	1080
gtgtccctga	cctgtctggt	gaaaggcttc	tatcccagcg	atatcgccgt	ggagtgggag	1140
agcaacggcc	agcccagaaa	caactacaag	accaccccc	ctgtgctgga	cagcgacggc	1200
agcttcttcc	tgtactccag	actgaccgtg	gacaagtcca	gatggcagga	gggcaacgtc	1260
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ctgagcctgg	gcaagtga					1338

<210> 59
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> LC

<400> 59
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atcagctgca agagcagcca gagcatcgtg cacagcaacg gcaacaccta cctggactgg 120
tacctgcaga agcccggccca gagccccaag ctgctgatct acaagggtgag caacagattc 180
agcggcgtgc ccgacagatt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240
agcagagtgg aggccgagga cgtgggcgtg tactactgct tccagggcag ccacttcccc 300
accttcggcg gcggcaccaa ggtggagatc aagcgaactg tggctgcacc atctgtcttc 360
atcttcccg ccatctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaaagta cagtgggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttag 657

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1

<400> 60
Gly Tyr Ser Ile Thr Ser Asp Tyr Ala
1 5

<210> 61
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2

<400> 61
Ile Ser Tyr Ser Gly Pro Thr
1 5

<210> 62
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> HCDR3

<400> 62

Ala Arg Gly Gly Asp Gly Asp Ser Phe Asp Tyr
1 5 10

<210> 63

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR1

<400> 63

Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 64

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR2

<400> 64

Lys Val Ser
1

<210> 65

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR3

<400> 65

Phe Gln Gly Ser His Phe Pro Thr
1 5

<210> 66

<211> 132

<212> PRT

<213> Homo sapiens

<400> 66

Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser Glu Asp Lys

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

<210> 67
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 67	
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tcagattact acaaccgatc cacctcacct tggaatctcc accgcaatga ggaccctgag	180
agatatccct ctgtgatctg ggaggcaaag tgccgccact tgggctgcat caacgctgat	240
gggaacgtgg actaccacat gaactctgtc cccatccagc aagagatcct ggtcctgcgc	300
agggagcctc cacactgccc caactccttc cggctggaga agatactggt gtccgtgggc	360
tgcacctgtg tcaccccgat tgtccaccat gtggcc	396

<210> 68
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 68	
Arg Lys Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu Ser	
1	5
Cys Pro Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly Ile Ile	
	20
Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu Ser Arg Ser	
	35
Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro Asn Arg Tyr Pro	
	50
Ser Glu Val Val Gln Ala Gln Cys Arg Asn Leu Gly Cys Ile Asn Ala	
65	70
Gln Gly Lys Glu Asp Ile Ser Met Asn Ser Val Pro Ile Gln Gln Glu	
	85
	90
	95

Thr	Leu	Val	Val	Arg	Arg	Lys	His	Gln	Gly	Cys	Ser	Val	Ser	Phe	Gln
			100					105					110		
Leu	Glu	Lys	Val	Leu	Val	Thr	Val	Gly	Cys	Thr	Cys	Val	Thr	Pro	Val
		115					120					125			
Ile	His	His	Val	Gln											
	130														

<210> 69
 <211> 2601
 <212> DNA
 <213> Homo sapiens

<400> 69

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ctgctcctgg	gcgtgctggc	cccgggtggc	gcctccctgc	gactcctgga	ccaccgggcg	120
ctggctctgct	cccagccggg	gctaaactgc	acgggtcaaga	atagtacctg	cctggatgac	180
agctggattc	accctcgaaa	cctgaccccc	tcctcccca	aggacctgca	gatccagctg	240
cactttgccc	acacccaaca	aggagacctg	ttccccgtgg	ctcacatcga	atggacactg	300
cagacagacg	ccagcatcct	gtacctcgag	ggtgcagagt	tatctgtcct	gcagctgaac	360
accaatgaac	gtttgtgctg	caggtttgag	tttctgtcca	aactgaggca	tcaccacagg	420
cgggtggcgtt	ttaccttcag	ccactttgtg	gttgaccctg	accaggaata	tgagggtgacc	480
gttcaccacc	tgcccaagcc	catccctgat	ggggacccaa	accaccagtc	caagaatttc	540
cttgtgcctg	actgtgagca	cgccaggatg	aaggtaacca	cgccatgcat	gagctcaggc	600
agcctgtggg	acccaacat	caccgtggag	accctggagg	cccaccagct	gcgtgtgagc	660
ttcaccctgt	ggaacgaatc	tacccattac	cagatcctgc	tgaccagttt	tccgcacatg	720
gagaaccaca	gttgctttga	gcacatgcac	cacatacctg	cgcccagacc	agaagagttc	780
caccagcgat	ccaacgtcac	actcactcta	cgcaacctta	aagggtgctg	tcgccaccaa	840
gtgcagatcc	agcccttctt	cagcagctgc	ctcaatgact	gcctcagaca	ctccgcgact	900
gtttcctgcc	cagaaaatgcc	agacactcca	gaaccaattc	cggactacat	gcccctgtgg	960
gtgtactggt	tcatcacggg	catctccatc	ctgtgtgtgg	gctccgtcat	cctgctcatc	1020
gtctgcatga	cctggaggct	agctgggcct	ggaagtga	aatacagtga	tgacaccaaa	1080
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