

<223> CH2527-VL7 VL

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<400> 2

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

<210> 3

<211> 5

<212> PRT

<213> Mus musculus

<220>

<223> CH2527-VL7 CDR1H

<400> 3

Thr Tyr Ala Met Asn
1 5

<210> 4

<211> 19

<212> PRT

<213> Mus musculus

<220>

<223> CH2527-VL7 CDR2H

<400> 4

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

<210> 5

<211> 14

<212> PRT

<213> Mus musculus

eolf-othd-000001

<220>

<223> CH2527-VL7 CDR3H

<400> 5

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 6

<211> 14

<212> PRT

<213> Mus musculus

<220>

<223> CH2527-VL7 CDRL1

<400> 6

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 7

<211> 7

<212> PRT

<213> Mus musculus

<220>

<223> CH2527-VL7 CDR2L

<400> 7

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 8

<211> 9

<212> PRT

<213> Mus musculus

<220>

<223> CH2527-VL7 CDR3L

<400> 8

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 9

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

aagcttggat ccatgttgca gatggctggg cagtgtcc

39

<210> 10

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10

gaattcgcg cgcctcatcc ttctactgaa ttggcacac ttgcattac

49

<210> 11

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

acgttagatc tccactcagt cctgcatctt gttccagtta ac

42

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

aacgttgcgg ccgctagttt cacaaacccc agg

33

<210> 13

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

gaattcaagc ttgccaccat gttgcagatg gctgggcagt gctcc

45

<210> 14

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14

gaattctcta gattacctag cagaaattga tttctctatc tccgtagc

48

<210> 15

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<223> pSCHLI333 VH

<400> 15

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

<210> 16

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<223> pSCHLI372 VH

<400> 16

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

<210> 17

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<223> pSCHLI373 VH

<400> 17

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

<210> 18
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 18
 Gly Tyr Met Phe Ser Ser Phe Gly Met Ser
 1 5 10

<210> 19
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 19
 Gly Phe Thr Phe Ser Asn Ser Gly Met Ile
 1 5 10

<210> 20
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 20
 Gly Phe Ser Phe Ser Asn Ser Trp Met Asn
 1 5 10

<210> 21
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 21
 Trp Ile Tyr Pro Val Gly Gln Gly Thr Trp Tyr Ala Gln Lys Phe Gln
 1 5 10 15
 Gly

<210> 22
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 22
 His Ile Arg Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala Pro
 1 5 10 15
 Val Lys Gly

<210> 23
<211> 19
<212> PRT
<213> Homo sapiens

<400> 23
Thr Ile Arg Gln Lys Thr Tyr Gly Gly Thr Thr Asp Tyr Ala Ala Pro
1 5 10 15
Val Lys Gly

<210> 24
<211> 10
<212> PRT
<213> Homo sapiens

<400> 24
Val Ser Tyr Pro Pro Ser His Phe Asp Tyr
1 5 10

<210> 25
<211> 8
<212> PRT
<213> Homo sapiens

<400> 25
Gly Gly Ser Gly Ser Phe Asp Tyr
1 5

<210> 26
<211> 9
<212> PRT
<213> Homo sapiens

<400> 26
Gly Gly Leu Phe Gly Tyr Trp Asp Tyr
1 5

<210> 27
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> pSCHLI333 VH_CH1 x CD3 VH_CH1 Fc knob LALA PG

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<400> 27

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

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370		375		380	
Cys	Leu	Val	Lys	Asp	Tyr
385		390		395	400
Ser	Gly	Ala	Leu	Thr	Ser
		405		410	415
Ser	Ser	Gly	Leu	Tyr	Ser
		420		425	430
Ser	Leu	Gly	Thr	Gln	Thr
		435		440	445
Asn	Thr	Lys	Val	Asp	Lys
		450		455	460
His	Thr	Cys	Pro	Pro	Cys
465				470	475
Val	Phe	Leu	Phe	Pro	Pro
		485		490	495
Thr	Pro	Glu	Val	Thr	Cys
		500		505	510
Glu	Val	Lys	Phe	Asn	Trp
		515		520	525
Lys	Thr	Lys	Pro	Arg	Glu
		530		535	540
Ser	Val	Leu	Thr	Val	Leu
545				550	555
Lys	Cys	Lys	Val	Ser	Asn
		565		570	575
Ile	Ser	Lys	Ala	Lys	Gly
		580		585	590
Pro	Pro	Cys	Arg	Asp	Glu
		595		600	605
Leu	Val	Lys	Gly	Phe	Tyr
		610		615	620
Asn	Gly	Gln	Pro	Glu	Asn
625				630	635
Ser	Asp	Gly	Ser	Phe	Phe
		645		650	655
Arg	Trp	Gln	Gln	Gly	Asn
		660		665	670
Leu	His	Asn	His	Tyr	Thr
		675		680	685

<210> 28

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> pSCHLI333 HC hole LALA PG

<400> 28

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

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

Lys

<210> 29

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3 LC (CLC)

<400> 29

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

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195 200 205
Val Ala Pro Thr Glu Cys Ser
210 215

<210> 30
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> pSCHLI372 VH_CH1 x CD3 VH_CH1 Fc knob LALA PG

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

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275	280	285
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr		
290	295	300
Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser		
305	310	315
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn		
325	330	335
Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr		
340	345	350
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
355	360	365
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
370	375	380
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
385	390	395
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
405	410	415
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
420	425	430
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
435	440	445
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
450	455	460
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser		
465	470	475
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
485	490	495
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
500	505	510
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
515	520	525
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
530	535	540
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
545	550	555
Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr		
565	570	575
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		
580	585	590
Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys		
595	600	605
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
610	615	620
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
625	630	635
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser		
645	650	655
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		

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		660						665					670				
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
		675					680						685				

<210> 31

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> pSCHLI372 HC hole LALA PG

<400> 31

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

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

<210> 32

<211> 689

<212> PRT

<213> Artificial Sequence

<220>

<223> pSCHLI373 VH_CH1 x CD3 VH_CH1 Fc knob LALA PG

<400> 32

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

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			100					105				110			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
			130					135				140			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145						150				155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
			195					200				205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
			210				215					220			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu
225					230					235					240
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
				245					250					255	
Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr	Ala	Met	Asn	Trp	Val	Arg
			260					265					270		
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Arg	Ile	Arg	Ser	Lys
			275				280					285			
Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe
			290			295					300				
Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn
305					310					315					320
Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	Arg	His	Gly
				325					330					335	
Asn	Phe	Gly	Asn	Ser	Tyr	Val	Ser	Trp	Phe	Ala	Tyr	Trp	Gly	Gln	Gly
			340					345					350		
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
			355				360					365			
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu
			370			375					380				
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
385					390				395						400
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
				405					410					415	
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
			420					425					430		
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro
			435				440					445			
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
			450			455					460				
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro
465					470					475					480
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser

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				485				490					495				
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp		
			500					505					510				
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn		
		515					520					525					
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val			
	530					535				540							
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu		
545					550				555						560		
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	Glu	Lys		
			565					570						575			
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr		
			580					585					590				
Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp		
		595				600						605					
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu		
	610					615					620						
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu		
625					630					635					640		
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys		
			645					650					655				
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
			660					665					670				
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly		
		675					680					685					

Lys

<210> 33

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> pSCHLI373 HC hole LALA PG

<400> 33

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

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				85				90					95			
Tyr	Cys	Thr	Thr	Gly	Gly	Leu	Phe	Gly	Tyr	Trp	Asp	Tyr	Trp	Gly	Gln	
			100					105					110			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		115					120					125				
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
	130					135					140					
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
145					150					155					160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
			165					170						175		
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
		180						185					190			
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
	195					200					205					
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	210					215				220						
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	
225				230						235					240	
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
			245					250					255			
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
		260						265					270			
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
	275					280					285					
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
	290					295					300					
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
305				310						315					320	
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	Glu	
			325					330						335		
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	
		340						345					350			
Thr	Leu	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu		
	355					360					365					
Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	
	370					375				380						
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	
385				390						395					400	
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	
			405					410						415		
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	
		420						425					430			
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	
		435					440						445			
Gly	Lys															
	450															

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<210> 34
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<223> 83A10 VH

<400> 34
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Leu Gly Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
Thr Val Ser Ser
 115

<210> 35
<211> 5
<212> PRT
<213> Homo sapiens

<400> 35
Ser Tyr Ala Met Ser
1 5

<210> 36
<211> 17
<212> PRT
<213> Homo sapiens

<400> 36
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 37
<211> 7

eolf-othd-000001

<212> PRT

<213> Homo sapiens

<400> 37

Val Leu Gly Trp Phe Asp Tyr

1 5

<210> 38

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 38

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

<210> 39

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 39

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10