

SEQUENCE LISTING

<110> CHIA TAI TIANQING PHARMACEUTICAL GROUP CO., LTD.

<120> Pharmaceutical Composition Containing Anti-TSLP Antibody

<150> CN202110235660.8

<151> 2021-03-03

<160> 38

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VH-CDR1 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 1

Thr Tyr Trp Met His

1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VH-CDR2 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 2

Val Ile Asp Pro Ser Asp Ser Asp Thr Thr Tyr Asn Gln Lys Phe Lys

1 5 10 15

Gly

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VH-CDR3 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 3

Ser Leu Asp Gly Tyr Tyr Asp Tyr
1 5

<210> 4

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VL-CDR1 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 4

Arg Pro Thr Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 5

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VL-CDR2 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 5

Phe Ala Arg Thr Leu Ala Glu
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VL-CDR3 for mouse, chimeric and humanized 1C5F12E9 antibodies

<400> 6

Gln His His Tyr Gly Thr Pro Trp Thr
1 5

<210> 7

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VH for mouse and chimeric 1C5F12E9 antibodies

<400> 7

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

<210> 8

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> VH for hu1C5F12E9-V1, hu1C5F12E9-V7, and hu1C5F12E9-V13

<400> 8

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

<210> 9

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (67)
<223> Xaa can be Arg or Lys

<220>
<221> UNSURE
<222> (68)
<223> Xaa can be Val or Ala

<220>
<221> UNSURE
<222> (72)
<223> Xaa can be Arg or Val

<220>
<221> UNSURE
<223> VH for hu1C5F12E9-V2 - hu1C5F12E9-V6, hu1C5F12E9-V8 - hu1C5F12E9-V12, and hu1C5F12E9-V14 - hu1C5F12E9-V18

<400> 9
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Asp Pro Ser Asp Ser Asp Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Xaa Xaa Thr Met Thr Xaa 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
Thr Arg Ser Leu Asp Gly Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<223> VL for mouse and chimeric 1C5F12E9 antibodies

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

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

<210> 11
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (43)
 <223> Xaa can Ser or Ala

<220>
 <221> UNSURE
 <222> (48)
 <223> Xaa can be Val or Ile

<220>
 <221> UNSURE
 <223> VL for hu1C5F12E9-V1 - hu1C5F12E9-V18

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

<210> 12
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Human IgG1 heavy chain constant region

<400> 12

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	
Lys	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> 13
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Human IgG4 heavy chain constant region

<400> 13

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

<210> 14
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Human kappa light chain constant region

<400> 14
 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> 15
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Mouse IgG1 heavy chain constant region

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

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

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

<220>
 <221> UNSURE
 <223> Mouse kappa light chain constant region

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

<210> 17
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>

<221> unsure
<223> VH for mouse and chimeric 1C5F12E9 antibodies

<400> 17
caggtccaac tgcagcagcc tgggactgag ctggtgaagc ctggggcttc agtgaagatg 60
tcctgcaagg cttctggcta caccttcacc acctactgga tgcactgggt gaagcagagg 120
cctggacaag gccttgagtg gatcggagtg attgatacct ctgatagtga tactacctac 180
aatcaaaagt tcaagggcaa ggccacattg actgtagaca catcctccag cacagcctac 240
atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtac aaggtccctt 300
gatggttact acgactactg gggccaaggc accactctca cagtctcctc a 351

<210> 18
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> VH for mouse and chimeric 1C5F12E9 antibodies

<400> 18
caggtgcagc tgcagcagcc cggcaccgag ctggtgaagc ctggcgctag cgtgaagatg 60
tcctgtaagg ccagcggcta cacattcact acatactgga tgcactgggt gaagcagaga 120
cctggccagg gcctggagtg gatcggcgctg atcgacccca gcgactccga taccacctac 180
aaccagaagt ttaagggcaa ggccaccctg acagtggata caagctcctc cacagcctac 240
atgcagctgt ccagcctgac ctccgaggat tccgccgtgt actactgcac aaggtccctg 300
gatggctact acgattactg gggccagggc acaaccctga cagtcagcag c 351

<210> 19
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> VH for hu1C5F12E9-V2, hu1C5F12E9-V8, and hu1C5F12E9-V14

<400> 19
caggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ctggcgccctc cgtgaagggtg 60
tcctgcaagg ccagcggcta cacattcacc acatactgga tgcactgggt gagacaggcc 120
cccggccagg gactggagtg gatgggagtg atcgacccca gcgactccga cacaacctac 180
aaccagaagt tcaagggcag ggtgacaatg accagagaca ccagcacaag caccgtgtac 240
atggagctgt cctccctgag gagcgaggac accgccgtgt actactgcac cagatccctg 300
gacggctact acgactactg gggccagggc accctggtga cagtgtccag c 351

<210> 20
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<221> unsure
<223> VL for mouse and chimeric 1C5F12E9 antibodies

<400> 20
gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga aactgtcacc 60
atcacatgtc gaccaactga gaatatttac agttatttag catggtatca gcagaaacag 120
ggaaaatctc ctcacctcct ggtctatfff gcaagaacct tagcagaagg tgtgccatca 180
aggttcagtg gcagtggatc aggcacacag ttttctctga agatcaacag cctgcagcct 240
gaagattttg ggatttatta ctgtcaacac cattatggta ctccgtggac gttcgggtgga 300
ggcaccaagc tggaaatcaa a 321

<210> 21
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> VL for mouse and chimeric 1C5F12E9 antibodies

<400> 21
gacatccaga tgaccagtc ccccgccagc ctgtccgcct ctgtgggaga gaccgtgacc 60
atcacatgca ggcccaccga gaatatctac tcctacctgg cctggtatca acagaagcag 120
ggcaagagcc ctcacctgct ggtgtacttc gccaggacac tggccgaggg cgtgccctct 180
aggttcagcg gcagcgggctc cggcacacag ttttcctga agatcaacag cctgcagcct 240
gaggattttg gcatctacta ctgccagcac cactacggca caccctggac ctttggcggc 300
ggcaccaagc tggagatcaa g 321

<210> 22
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> VL for hu1C5F12E9-V7 - hu1C5F12E9-V12

<400> 22
gatatccaga tgacacagag ccccagcagc ctgagcgcca gcgtgggaga cagggtgaca 60
atcacatgca gaccaccga gaatatctac agctacctgg cctggtatca acagaagcct 120
ggcaaggccc ccaagctgct gatctacttc gccagaacct tggccgaggg cgtgccctct 180
aggttcagcg gctccggcag cggcaccgac ttcacactga ccatctcctc cctgcagccc 240
gaggacttcg ccacatacta ctgccagcac cactacggca caccttggac cttcggcggc 300
ggcacaaagg tggagatcaa g 321

<210> 23
<211> 993
<212> DNA
<213> Artificial Sequence

<220>

<221> unsure
<223> Human IgG1 heavy chain constant region

<400> 23
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggtgtcct acagtctca 180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 300
aaatcttgtg acaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 420
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagga gcagtacaac 540
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccacgagaa aaccatctcc 660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcctccatc ccgggaggag 720
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960
cagaagagcc tctccctgtc tccgggtaaa tga 993

<210> 24
<211> 984
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> Human IgG4 heavy chain constant region

<400> 24
gccagcacia agggcccttc cgtgtttccc ctggccccct gcagcaggag cacctctgag 60
tccaccgccg ccctgggctg tctgggtgaag gactactttc ccgagcccgt gaccgtgagc 120
tggaattccg gcgccctgac atccggcgtg cacaccttcc ccgccgtgct gcagtctctc 180
ggcctgtaca gcctgagctc cgtgggtgaca gtgccttctc cctccctggg caccaagacc 240
tacacatgta atgtggatca caagcccagc aacacaaagg tggataagag agtggagtcc 300
aagtacggcc ctcttgccc tccctgtcct gcccagagt tcctgggagg cccctctgtg 360
ttcctgttcc cccctaagcc caaggacaca ctgatgatct ccaggacccc tgaggtgacc 420
tgcgtgggtg tggacgtgag ccaggaggac cctgaggtgc agttcaattg gtacgtggat 480
ggcgtggagg tgcacaatgc caagacaaag cccagagagg agcagtttaa ttccacatac 540
agggtgggtg ccgtgctgac cgtgctgcac caggattggc tgaacggcaa ggagtacaag 600
tgtaagggtg gcaacaaggg cctgccttcc tccatcgaga agacaatcag caaggccaag 660
ggcagccta gggagcccca ggtgtacaca ctgcctccca gccaggagga gatgaccaag 720
aaccaggtga gcctgacctg cctgggtgaag ggcttctacc ctacgacat cgccgtggag 780
tgggagtcca acggccagcc cgagaataac tacaagacaa cccccccgt gctggattcc 840
gatggcagct tctttctgta ctccaggctg accgtggata agagcaggtg gcaggagggc 900
aatgtgttca gctgctccgt gatgcacgag gccctgcaca atcactacac ccagaagagc 960
ctgtccctga gcctgggcaa gtga 984

<210> 25
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> Human kappa light chain constant region

<400> 25
cgtacggtgg cggcgccatc 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 ggggagagtg ttga 324

<210> 26
<211> 975
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> Mouse IgG1 heavy chain constant region

<400> 26
gccaaaacga caccgccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 60
tccatggtga ccctgggatg cctgggtcaag ggctatttcc ctgagccagt gacagtgacc 120
tggaactctg gatccctgtc cagcgggtgtg cacaccttcc cagctgtcct gcagtctgac 180
ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 240
acctgcaacg ttgcccaccc ggccagcagc accaagggtg acaagaaaat tgtgcccagg 300
gattgtgggt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 360
cccccaaagc ccaaggatgt gctcaccatt actctgactc ctaaggtcac gtgtgtttgtg 420
gtagacatca gcaaggatga tcccagagtc cagttcagct ggttttaga tgatgtggag 480
gtgcacacag ctgagacgca accccgggag gagcagttca acagcacttt ccgctcagtc 540
agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtc 600
aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg 660
aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc 720
agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtg 780
aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct 840
tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc 900
acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctccac 960
tctcctggta aatga 975

<210> 27
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<223> Mouse kappa light chain constant region

<400> 27
 cgggctgatg ctgcaccaac tgtatccatc ttcccaccat ccagtgagca gttaacatct 60
 ggaggtgcct cagtcgtgtg cttcttgaac aacttctacc ccaaagacat caatgtcaag 120
 tggaagattg atggcagtga acgacaaaat ggcgtcctga acagttggac tgatcaggac 180
 agcaaagaca gcacctacag catgagcagc accctcacgt tgactaagga cgagtatgaa 240
 cgacataaca gctatacctg tgaggccact cacaagacat caacttcacc cattgtcaag 300
 agcttcaaca ggggagagtg t 321

<210> 28
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Recombinant human TSLP-his

<400> 28
 Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu
 1 5 10 15
 Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser
 20 25 30
 Thr Glu Phe Asn Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu
 35 40 45
 Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser
 50 55 60
 Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile
 65 70 75 80
 Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met
 85 90 95
 Lys Lys Arg Arg Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln
 100 105 110
 Val Ser Gln Leu Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu
 115 120 125
 Lys Gln Gln His His His His His His His His His His
 130 135 140

<210> 29
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Recombinant cynomolgus monkey TSLP-his

<400> 29
 Met Tyr Asp Phe Thr Asn Cys Asp Phe Gln Lys Ile Glu Ala Asp Tyr
 1 5 10 15
 Leu Arg Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys
 20 25 30

Ser	Thr	Asp	Phe	Asn	Asn	Thr	Val	Ser	Cys	Ser	Asn	Arg	Pro	His	Cys
		35					40					45			
Leu	Thr	Glu	Ile	Gln	Ser	Leu	Thr	Phe	Asn	Pro	Thr	Pro	Arg	Cys	Ala
	50					55					60				
Ser	Leu	Ala	Lys	Glu	Met	Phe	Ala	Arg	Lys	Thr	Lys	Ala	Thr	Leu	Ala
65					70				75					80	
Leu	Trp	Cys	Pro	Gly	Tyr	Ser	Glu	Thr	Gln	Ile	Asn	Ala	Thr	Gln	Ala
				85					90					95	
Met	Lys	Lys	Arg	Arg	Lys	Arg	Lys	Val	Thr	Thr	Asn	Lys	Cys	Leu	Glu
			100				105						110		
Gln	Val	Ser	Gln	Leu	Leu	Gly	Leu	Trp	Arg	Arg	Phe	Ile	Arg	Thr	Leu
		115				120						125			
Leu	Lys	Lys	Gln	Leu	Glu	His	His	His	His	His	His				
	130					135					140				

<210> 30
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> human TSLPR-Fc

<400> 30

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

Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
225					230					235					240
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
				245					250					255	
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
			260					265					270		
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
		275					280					285			
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
	290					295					300				
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
305					310					315					320
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
				325					330					335	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
			340					345					350		
Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
		355					360					365			
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
	370					375					380				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
385					390					395					400
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
			405					410						415	
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
			420				425					430			
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
		435					440					445			

<210> 31
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> human IL7Ra-Fc

<400> 31

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

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

<210> 33

<211> 371

<212> PRT

<213> Homo sapiens

<400> 33

Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe Leu Leu Gly

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

<210> 34
 <211> 459
 <212> PRT
 <213> Homo sapiens

<400> 34

Met	Thr	Ile	Leu	Gly	Thr	Thr	Phe	Gly	Met	Val	Phe	Ser	Leu	Leu	Gln
1				5					10					15	
Val	Val	Ser	Gly	Glu	Ser	Gly	Tyr	Ala	Gln	Asn	Gly	Asp	Leu	Glu	Asp
			20					25					30		
Ala	Glu	Leu	Asp	Asp	Tyr	Ser	Phe	Ser	Cys	Tyr	Ser	Gln	Leu	Glu	Val
		35					40					45			
Asn	Gly	Ser	Gln	His	Ser	Leu	Thr	Cys	Ala	Phe	Glu	Asp	Pro	Asp	Val
	50					55					60				
Asn	Thr	Thr	Asn	Leu	Glu	Phe	Glu	Ile	Cys	Gly	Ala	Leu	Val	Glu	Val
65				70						75				80	
Lys	Cys	Leu	Asn	Phe	Arg	Lys	Leu	Gln	Glu	Ile	Tyr	Phe	Ile	Glu	Thr
			85						90					95	
Lys	Lys	Phe	Leu	Leu	Ile	Gly	Lys	Ser	Asn	Ile	Cys	Val	Lys	Val	Gly
			100					105					110		
Glu	Lys	Ser	Leu	Thr	Cys	Lys	Lys	Ile	Asp	Leu	Thr	Thr	Ile	Val	Lys
		115					120					125			
Pro	Glu	Ala	Pro	Phe	Asp	Leu	Ser	Val	Ile	Tyr	Arg	Glu	Gly	Ala	Asn
	130					135					140				
Asp	Phe	Val	Val	Thr	Phe	Asn	Thr	Ser	His	Leu	Gln	Lys	Lys	Tyr	Val
145					150					155					160
Lys	Val	Leu	Met	His	Asp	Val	Ala	Tyr	Arg	Gln	Glu	Lys	Asp	Glu	Asn
				165					170					175	
Lys	Trp	Thr	His	Val	Asn	Leu	Ser	Ser	Thr	Lys	Leu	Thr	Leu	Leu	Gln
			180					185					190		
Arg	Lys	Leu	Gln	Pro	Ala	Ala	Met	Tyr	Glu	Ile	Lys	Val	Arg	Ser	Ile
		195					200					205			
Pro	Asp	His	Tyr	Phe	Lys	Gly	Phe	Trp	Ser	Glu	Trp	Ser	Pro	Ser	Tyr
	210					215					220				
Tyr	Phe	Arg	Thr	Pro	Glu	Ile	Asn	Asn	Ser	Ser	Gly	Glu	Met	Asp	Pro
225					230					235					240
Ile	Leu	Leu	Thr	Ile	Ser	Ile	Leu	Ser	Phe	Phe	Ser	Val	Ala	Leu	Leu
				245					250					255	
Val	Ile	Leu	Ala	Cys	Val	Leu	Trp	Lys	Lys	Arg	Ile	Lys	Pro	Ile	Val
			260					265					270		
Trp	Pro	Ser	Leu	Pro	Asp	His	Lys	Lys	Thr	Leu	Glu	His	Leu	Cys	Lys
		275					280					285			
Lys	Pro	Arg	Lys	Asn	Leu	Asn	Val	Ser	Phe	Asn	Pro	Glu	Ser	Phe	Leu
	290					295					300				
Asp	Cys	Gln	Ile	His	Arg	Val	Asp	Asp	Ile	Gln	Ala	Arg	Asp	Glu	Val
305					310					315					320
Glu	Gly	Phe	Leu	Gln	Asp	Thr	Phe	Pro	Gln	Gln	Leu	Glu	Glu	Ser	Glu
				325					330					335	
Lys	Gln	Arg	Leu	Gly	Gly	Asp	Val	Gln	Ser	Pro	Asn	Cys	Pro	Ser	Glu
			340					345					350		
Asp	Val	Val	Val	Thr	Pro	Glu	Ser	Phe	Gly	Arg	Asp	Ser	Ser	Leu	Thr
		355					360					365			
Cys	Leu	Ala	Gly	Asn	Val	Ser	Ala	Cys	Asp	Ala	Pro	Ile	Leu	Ser	Ser
	370					375					380				
Ser	Arg	Ser	Leu	Asp	Cys	Arg	Glu	Ser	Gly	Lys	Asn	Gly	Pro	His	Val
385					390					395					400
Tyr	Gln	Asp	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Thr	Asn	Ser	Thr	Leu	Pro
				405					410					415	
Pro	Pro	Phe	Ser	Leu	Gln	Ser	Gly	Ile	Leu	Thr	Leu	Asn	Pro	Val	Ala
			420					425					430		

Gln	Gly	Gln	Pro	Ile	Leu	Thr	Ser	Leu	Gly	Ser	Asn	Gln	Glu	Glu	Ala
		435					440					445			
Tyr	Val	Thr	Met	Ser	Ser	Phe	Tyr	Gln	Asn	Gln					
	450					455									

<210> 35
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <223> Heavy chain of Tezepelumab

<400> 35

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

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

<210> 36

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<223> Light chain of Tezepelumab

<400> 36

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

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205
Ala Pro Thr Glu Cys Ser
210

<210> 37
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<223> Human IgG1 heavy chain constant region

<400> 37
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
Lys 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 Asp Glu
225 230 235 240
Leu 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

