

SEQUENCE LISTING

<110> JUNO THERAPEUTICS, INC.

EDITAS MEDICINE, INC.

SATHER, Blythe D.

BORGES, Christopher

BURLEIGH, Stephen Michael

NYE, Christopher Heath

VONG, Queenie

WELSTEAD, G. Grant

<120> METHODS OF PRODUCING CELLS EXPRESSING A
RECOMBINANT RECEPTOR AND RELATED COMPOSITIONS

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<141> Concurrently Herewith

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

290		295		300
Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro				
305		310		315
Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala				
	325		330	
Thr Gly Met Val Gly Ala Leu Leu Leu Leu Val Val Ala Leu Gly				
	340		345	350
Ile Gly Leu Phe Met				
355				

<210> 13
 <211> 335
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 <213> Artificial Sequence

<220>
 <223> EGFRT

<400> 13

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

Arg	Gly	Pro	Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro
				245					250					255	
His	Cys	Val	Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr
			260					265					270		
Leu	Val	Trp	Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His
		275					280					285			
Pro	Asn	Cys	Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro
	290					295					300				
Thr	Asn	Gly	Pro	Lys	Ile	Pro	Ser	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala
305					310				315						320
Leu	Leu	Leu	Leu	Leu	Val	Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe	Met	
				325					330					335	

<210> 14

<211> 137

<212> PRT

<213> Mus musculus

<220>

<223> Mouse TCR alpha constant

<400> 14

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

<210> 15

<211> 137

<212> PRT

<213> Mus musculus

<220>

<223> Mouse TCR alpha constant

<400> 15

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

<210> 16

<211> 173

<212> PRT

<213> Mus musculus

<220>

<223> Mouse TCR beta constant

<300>

<308> Uniprot P01852

<309> 1986-07-21

<400> 16

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

<400> 18
 gggctctctct ggtagacca gatctgagcc tgggagctct ctggctaact agggaaccca 60
 ctgcttaagc ctcaataaag cttgccttga gtgcttcaag tagtgtgtgc ccgtctgttg 120
 tgtgactctg gtaactagag atccctcaga cccttttagt cagtgtggaa aatctctagc 180
 a 181

<210> 19
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human TCR alpha constant

<300>
 <308> Uniprot P01848
 <309> 2018-07-18

<400> 19
 Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 1 5 10 15
 Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
 20 25 30
 Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 35 40 45
 Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
 50 55 60
 Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 65 70 75 80
 Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
 85 90 95
 Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
 100 105 110
 Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
 115 120 125
 Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135 140

<210> 20
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human TCR beta constant 1

<300>
 <308> Uniprot P01850
 <309> 2018-07-18

<400> 20

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

Phe

<210> 21

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<223> Human TCR beta constant 2

<300>

<308> Uniprot A0A5B9

<309> 2018-07-18

<400> 21

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

65					70					75					80
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln
				85					90					95	
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg
			100					105					110		
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala
		115					120					125			
Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala
	130					135					140				
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val
145					150					155				160	
Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser
				165					170					175	

Arg Gly

<210> 22
 <211> 10
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 <213> Artificial Sequence

<220>
 <223> Linker

<220>
 <221> REPEAT
 <222> (0)...(0)
 <223> SGGGG is repeated 5 or 6 times

<400> 22
 Pro Gly Gly Gly Ser Gly Gly Gly Gly Pro
 1 5 10

<210> 23
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 23
 Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
 1 5 10 15
 Ser

<210> 24
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> human TCR alpha constant

<300>
<308> CAA26636.1
<309> 2016-07-25

<400> 24
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 25
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<223> human TCR beta constant

<300>
<308> A0A0G2JNG9

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

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

<210> 26
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAC gRNA transcription sequence

<400> 26
 agcgctctcg tacagagttg gcattataat acgactcact ataggggaga atcaaaatcg 60
 gtgaatgttt tagagctaga aatagcaagt taaaataaagg ctagtccgtt atcaacttga 120
 aaaagtggca ccgagtcggt gcttttttt 149

<210> 27
 <211> 100
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC gRNA sequence

<400> 27
 gagaaucaaaa aucggugaau guuuuagagc uagaaaauagc aaguuaaaaau aaggcuaguc 60
 cguuaucaac uugaaaaaagu ggcaccgagu cggugcuuuu 100

<210> 28
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-10 gRNA targeting domain

<400> 28
 ucucucagcu gguacacggc 20

<210> 29
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-110 gRNA targeting domain

<400> 29
 uggauuuaga gucucucagc 20

<210> 30
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-116 gRNA targeting domain

<400> 30
 acacggcagg gucagggguuc 20

<210> 31
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-16 gRNA targeting domain

<400> 31
 gagaaucaaa aucggugaau 20

<210> 32
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-4 gRNA targeting domain

<400> 32
 gcugguacac ggcaggguca 20

<210> 33	
<211> 17	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-49 gRNA targeting domain	
<400> 33	
cucagcuggu acacggc	17
<210> 34	
<211> 17	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-2 gRNA targeting domain	
<400> 34	
ugguacacgg caggguc	17
<210> 35	
<211> 17	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-30 gRNA targeting domain	
<400> 35	
gcuagacaug aggucua	17
<210> 36	
<211> 17	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-43 gRNA targeting domain	
<400> 36	
gucagauuug uugcucc	17
<210> 37	
<211> 17	
<212> RNA	
<213> Artificial Sequence	

<220>
 <223> TRAC-23 gRNA targeting domain

<400> 37
 ucagcuggua cacggca 17

<210> 38
 <211> 17
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-34 gRNA targeting domain

<400> 38
 gcagacagac uugucac 17

<210> 39
 <211> 17
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-25 gRNA targeting domain

<400> 39
 gguacacggc aggguca 17

<210> 40
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-128 gRNA targeting domain

<400> 40
 cuucaagagc aacagugcug 20

<210> 41
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TRAC-105 gRNA targeting domain

<400> 41
 agagcaacag ugcuguggcc 20

<210> 42	
<211> 20	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-106 gRNA targeting domain	
<400> 42	
aaagucagau uuguugcucc	20
<210> 43	
<211> 20	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-123 gRNA targeting domain	
<400> 43	
acaaaacugu gcuagacaug	20
<210> 44	
<211> 17	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-64 gRNA targeting domain	
<400> 44	
aaacugugcu agacaug	17
<210> 45	
<211> 20	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-97 gRNA targeting domain	
<400> 45	
ugugcuagac augaggucua	20
<210> 46	
<211> 22	
<212> RNA	
<213> Artificial Sequence	
<220>	

<223> TRAC-148 gRNA targeting domain

<400> 46
ggcugggggaa gaaggugucu uc 22

<210> 47
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC-147 gRNA targeting domain

<400> 47
gcugggggaag aaggugucuu c 21

<210> 48
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC-234 gRNA targeting domain

<400> 48
ggggaagaag gugucuuc 18

<210> 49
<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC-167 gRNA targeting domain

<400> 49
guuuugucug ugauauacac au 22

<210> 50
<211> 24
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC-177 gRNA targeting domain

<400> 50
ggcagacaga cuugucacug gauu 24

<210> 51

<211> 23
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> TRAC-176 gRNA targeting domain

 <400> 51
 gcagacagac uugucacugg auu 23

 <210> 52
 <211> 20
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> TRAC-257 gRNA targeting domain

 <400> 52
 gacagacuug ucacuggauu 20

 <210> 53
 <211> 24
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> TRAC-233 gRNA targeting domain

 <400> 53
 gugaauaggc agacagacuu guca 24

 <210> 54
 <211> 22
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> TRAC-231 gRNA targeting domain

 <400> 54
 gaauaggcag acagacuugu ca 22

 <210> 55
 <211> 22
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> TRAC-163 gRNA targeting domain

<400> 55	
gagucucuca gcugguacac gg	22
<210> 56	
<211> 20	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-241 gRNA targeting domain	
<400> 56	
gucucucagc ugguacacgg	20
<210> 57	
<211> 22	
<212> RNA	
<213> Artificial Sequence	
<220>	
<223> TRAC-179 gRNA targeting domain	
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gguacacggc agggucaggg uu	22
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<223> TRBC-32 gRNA targeting domain

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<210> 97

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<400> 98

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<210> 99

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<223> TRBC-129 gRNA targeting domain

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<210> 100

<211> 17

<212> RNA

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<220>

<223> TRBC-93 gRNA targeting domain

<400> 100

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<210> 101

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 <223> TRBC-415 gRNA targeting domain

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<400> 113
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<210> 114
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<223> HBB splice site acceptor

<400> 119

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25

<210> 120

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<210> 121

<211> 138

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<213> mus musculus

<220>

<223> Mouse TCR alpha constant

<300>

<308> Uniprot P01849

<309> 1986-07-21

<400> 121

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

<210> 122
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<212> PRT
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<220>
<223> Modified mouse TCR alpha constant

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

<210> 123
<211> 173
<212> PRT
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<220>
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<400> 123
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20 25 30
Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys
50 55 60
Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65 70 75 80

Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe
				85					90					95	
His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro
			100					105					110		
Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly
		115					120					125			
Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu
	130					135					140				
Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser
145					150					155					160
Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser			
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<211> 611

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 5' homology arm

<400> 124

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ccaagatgta cagtttgctt tgctgggcct ttttcccatg cctgccttta ctctgccaga 180
gttatattgc tgggggttttg aagaagatcc tattaaataa aagaataagc agtattatta 240
agtagccctg catttcaggt ttccttgagt ggcaggccag gcctggccgt gaacgttcac 300
tgaaatcatg gcctcttggc caagattgat agcttgtgcc tgtccctgag tcccagtcca 360
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cagccccaca gagccccgcc cttgtccatc actggcatct ggactccagc ctgggttggg 480
gcaaagaggg aaatgagatc atgtcctaac cctgatcctc ttgtcccaca gatatccaga 540
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<223> TRAC 3' homology arm

<400> 125

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aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggg gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctgggtca atgatgtcta aaactcctct gattgggtgg 300
ctcggcctta tccattgccca ccaaaaccct ctttttacta agaaacagtg agccttggtc 360

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tttggccctt	actgctcttc	taggcctcat	tctaagcccc	ttctccaagt	tgctctctct	540
tatttctccc	tgtctgccaa	aaaatctttc	ccagctcact	aagtcagtct	cacgcagtca	600
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<210> 126

<211> 347

<212> DNA

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<223> MND promoter

<400> 126

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aagcagttcc	tgccccggct	cagggccaag	aacagatggg	ccccagatgc	ggccccgccc	180
tcagcagttt	ctagagaacc	atcagatggt	tccaggggtgc	cccaaggacc	tgaaatgacc	240
ctgtgcctta	tttgaactaa	ccaatcagtt	cgcttctcgc	ttctgttcgc	gcgcttctgc	300
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<210> 127

<211> 544

<212> DNA

<213> Artificial Sequence

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<223> Ef1alpha promoter with HTLV1 enhancer

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actgggaaag	tgatgtcgtg	tactggctcc	gcctttttcc	cgagggtggg	ggagaaccgt	180
atataagtgc	agtagtcgcc	gtgaacgttc	tttttcgcaa	cgggtttgcc	gccagaacac	240
agctgaagct	tcgaggggct	cgcatctctc	cttcacgcgc	ccgccgccct	acctgaggcc	300
gccatccacg	ccggttgagt	cgcgttctgc	cgcctcccgc	ctgtgggtgcc	tcctgaactg	360
cgtccgccgt	ctaggtaaag	ttaaaagctca	ggtcgagacc	gggcctttgt	ccggcgctcc	420
cttggagcct	acctagactc	agccgggtct	ccacgctttg	cctgaccctg	cttgctcaac	480
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ctac						544

<210> 128

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<213> Artificial Sequence

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<223> P2A nucleotide sequence

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ggacct 66

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<212> PRT
<213> homo sapiens

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

<210> 130
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30
Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80
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85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 131
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<220>
<223> spacer (IgG4hinge)

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<210> 132
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36

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<223> Hinge-CH3 spacer

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

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Leu Ser	Leu Ser Leu Gly Lys		
	115		

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<220>
 <223> Hinge-CH2-CH3 spacer

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

<210> 135
 <211> 282
 <212> PRT
 <213> homo sapiens

<220>

<223> IgD-hinge-Fc

<400> 135

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

<210> 136

<211> 27

<212> PRT

<213> homo sapiens

<220>

<223> CD28

<300>

<308> No. P10747

<309> 1989-07-01

<400> 136

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15
Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 137

<211> 66

<212> PRT

<213> homo sapiens

<220>

<223> CD28

<300>

<308> No. P10747

<309> 1989-07-01

<400> 137

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

<210> 138

<211> 41

<212> PRT

<213> homo sapiens

<220>

<223> CD28

<300>

<308> P10747

<309> 1989-07-01

<400> 138

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

<210> 139
 <211> 41
 <212> PRT
 <213> homo sapiens

<220>
 <223> CD28 (LL to GG)

Arg	Ser	Lys	Arg	Ser	Arg	Gly	Gly	His	Ser	Asp	Tyr	Met	Asn	Met	Thr
1				5					10					15	
Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro
			20					25					30		
Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser							
		35					40								

<210> 140
 <211> 42
 <212> PRT
 <213> homo sapiens

<220>
 <223> 4-1BB

<300>
 <308> Q07011.1
 <309> 1995-02-01

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

<210> 141
 <211> 112
 <212> PRT
 <213> homo sapiens

<220>

<223> CD3 zeta

<400> 141

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

<210> 142

<211> 96

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary gRNA complementary domain

<220>

<221> modified_base

<222> (1)...(20)

<223> a, c, u, g, unknown or other

<220>

<221> misc_feature

<222> (1)...(20)

<223> n is a, c, g, or u

<400> 142

nnnnnnnnnn	nnnnnnnnnn	guuuuagagc	uagaaaauagc	aaguuaaaau	aaggcuaguc	60
cguaaucaac	uugaaaaagu	ggcaccgagu	cggugc			96

<210> 143

<211> 104

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary gRNA complementary domain

<220>
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<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 143
nnnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcugaaa agcauagcaa guaaaaauaa 60
ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg gugc 104

<210> 144
<211> 106
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary gRNA complementary domain

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 144
nnnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuggaa acagcauagc aaguuaaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

<210> 145
<211> 116
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary gRNA complementary domain

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
 <221> misc_feature
 <222> (1)...(20)
 <223> n is a, c, g, or u

<400> 145
 nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuguuu uggaaacaaa acagcrauagc 60
 aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 116

<210> 146
 <211> 96
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> exemplary gRNA

<220>
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 <222> (1)...(20)
 <223> a, c, u, g, unknown or other

<220>
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 <222> (1)...(20)
 <223> n is a, c, g, or u

<400> 146
 nnnnnnnnnn nnnnnnnnnn guuuuagagc uagaaauagc aaguuaauau aaggcuaguc 60
 cguuaucaac uugaaaaagu ggcaccgagu cggugc 96

<210> 147
 <211> 96
 <212> RNA
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1)...(20)
 <223> a, c, u, g, unknown or other

<220>
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 <222> (1)...(20)
 <223> n is a, c, g, or u

<400> 147

nnnnnnnnnn nnnnnnnnnn guuuuagagc uagaaauagc aaguuuuuuu aaggcuaguc 60
cguuaucaac uugaaaaaagu ggcaccgagu cggugc 96

<210> 148
<211> 116
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 148
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuguau uggaaacaau acagcauagc 60
aaguuuuuuu aaggcuaguc cguuaucaac uugaaaaaagu ggcaccgagu cggugc 116

<210> 149
<211> 47
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary proximal and tail domain

<400> 149
aaggcuaguc cguuaucaac uugaaaaaagu ggcaccgagu cggugcu 47

<210> 150
<211> 49
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary proximal and tail domain

<400> 150
aaggcuaguc cguuaucaac uugaaaaaagu ggcaccgagu cgguggugc 49

<210> 151
<211> 51
<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary proximal and tail domain

<400> 151

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcggau c 51

<210> 152

<211> 31

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary proximal and tail domain

<400> 152

aaggcuaguc cguuaucaac uugaaaaagu g 31

<210> 153

<211> 18

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary proximal and tail domain

<400> 153

aaggcuaguc cguuauca 18

<210> 154

<211> 12

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary proximal and tail domain

<400> 154

aaggcuaguc cg 12

<210> 155

<211> 102

<212> RNA

<213> Artificial Sequence

<220>

<223> exemplary chimeric gRNA

<220>

<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 155
nnnnnnnnnn nnnnnnnnnn guuuuagagc uagaaaauagc aaguuaaaaau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uu 102

<210> 156
<211> 102
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary chimeric gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 156
nnnnnnnnnn nnnnnnnnnn guuuuaguac ucuggaaaca gaauacuacua aaacaaggca 60
aaaugccgug uuuaucucgu caacuuguug gcgagauuuu uu 102

<210> 157
<211> 1344
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptococcus mutans Cas9

<400> 157
Lys Lys Pro Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val Gly
1 5 10 15
Trp Ala Val Val Thr Asp Asp Tyr Lys Val Pro Ala Lys Lys Met Lys
20 25 30
Val Leu Gly Asn Thr Asp Lys Ser His Ile Glu Lys Asn Leu Leu Gly
35 40 45

Ala	Leu	Leu	Phe	Asp	Ser	Gly	Asn	Thr	Ala	Glu	Asp	Arg	Arg	Leu	Lys
50						55				60					
Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Arg	Asn	Arg	Ile	Leu	Tyr
65					70				75						80
Leu	Gln	Glu	Ile	Phe	Ser	Glu	Glu	Met	Gly	Lys	Val	Asp	Asp	Ser	Phe
				85					90					95	
Phe	His	Arg	Leu	Glu	Asp	Ser	Phe	Leu	Val	Thr	Glu	Asp	Lys	Arg	Gly
			100					105					110		
Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Leu	Glu	Glu	Glu	Val	Lys	Tyr	His
		115					120					125			
Glu	Asn	Phe	Pro	Thr	Ile	Tyr	His	Leu	Arg	Gln	Tyr	Leu	Ala	Asp	Asn
		130					135				140				
Pro	Glu	Lys	Val	Asp	Leu	Arg	Leu	Val	Tyr	Leu	Ala	Leu	Ala	His	Ile
145					150					155					160
Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile	Glu	Gly	Lys	Phe	Asp	Thr	Arg
				165					170						175
Asn	Asn	Asp	Val	Gln	Arg	Leu	Phe	Gln	Glu	Phe	Leu	Ala	Val	Tyr	Asp
			180					185					190		
Asn	Thr	Phe	Glu	Asn	Ser	Ser	Leu	Gln	Glu	Gln	Asn	Val	Gln	Val	Glu
		195					200						205		
Glu	Ile	Leu	Thr	Asp	Lys	Ile	Ser	Lys	Ser	Ala	Lys	Lys	Asp	Arg	Val
	210					215					220				
Leu	Lys	Leu	Phe	Pro	Asn	Glu	Lys	Ser	Asn	Gly	Arg	Phe	Ala	Glu	Phe
225					230					235					240
Leu	Lys	Leu	Ile	Val	Gly	Asn	Gln	Ala	Asp	Phe	Lys	Lys	His	Phe	Glu
				245					250					255	
Leu	Glu	Glu	Lys	Ala	Pro	Leu	Gln	Phe	Ser	Lys	Asp	Thr	Tyr	Glu	Glu
			260					265					270		
Glu	Leu	Glu	Val	Leu	Leu	Ala	Gln	Ile	Gly	Asp	Asn	Tyr	Ala	Glu	Leu
	275						280					285			
Phe	Leu	Ser	Ala	Lys	Lys	Leu	Tyr	Asp	Ser	Ile	Leu	Leu	Ser	Gly	Ile
	290					295					300				
Leu	Thr	Val	Thr	Asp	Val	Gly	Thr	Lys	Ala	Pro	Leu	Ser	Ala	Ser	Met
305					310					315					320
Ile	Gln	Arg	Tyr	Asn	Glu	His	Gln	Met	Asp	Leu	Ala	Gln	Leu	Lys	Gln
				325					330					335	
Phe	Ile	Arg	Gln	Lys	Leu	Ser	Asp	Lys	Tyr	Asn	Glu	Val	Phe	Ser	Asp
			340					345					350		
Val	Ser	Lys	Asp	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Lys	Thr	Asn	Gln
		355					360					365			
Glu	Ala	Phe	Tyr	Lys	Tyr	Leu	Lys	Gly	Leu	Leu	Asn	Lys	Ile	Glu	Gly
	370					375					380				
Ser	Gly	Tyr	Phe	Leu	Asp	Lys	Ile	Glu	Arg	Glu	Asp	Phe	Leu	Arg	Lys
385					390					395					400
Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	His	Gln	Ile	His	Leu	Gln
				405					410					415	
Glu	Met	Arg	Ala	Ile	Ile	Arg	Arg	Gln	Ala	Glu	Phe	Tyr	Pro	Phe	Leu
			420					425					430		
Ala	Asp	Asn	Gln	Asp	Arg	Ile	Glu	Lys	Leu	Leu	Thr	Phe	Arg	Ile	Pro
		435					440					445			

Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Lys	Ser	Asp	Phe	Ala	Trp	Leu
450						455					460				
Ser	Arg	Lys	Ser	Ala	Asp	Lys	Ile	Thr	Pro	Trp	Asn	Phe	Asp	Glu	Ile
465					470					475					480
Val	Asp	Lys	Glu	Ser	Ser	Ala	Glu	Ala	Phe	Ile	Asn	Arg	Met	Thr	Asn
				485					490					495	
Tyr	Asp	Leu	Tyr	Leu	Pro	Asn	Gln	Lys	Val	Leu	Pro	Lys	His	Ser	Leu
		500						505					510		
Leu	Tyr	Glu	Lys	Phe	Thr	Val	Tyr	Asn	Glu	Leu	Thr	Lys	Val	Lys	Tyr
	515						520					525			
Lys	Thr	Glu	Gln	Gly	Lys	Thr	Ala	Phe	Phe	Asp	Ala	Asn	Met	Lys	Gln
	530					535					540				
Glu	Ile	Phe	Asp	Gly	Val	Phe	Lys	Val	Tyr	Arg	Lys	Val	Thr	Lys	Asp
545					550					555					560
Lys	Leu	Met	Asp	Phe	Leu	Glu	Lys	Glu	Phe	Asp	Glu	Phe	Arg	Ile	Val
				565					570					575	
Asp	Leu	Thr	Gly	Leu	Asp	Lys	Glu	Asn	Lys	Val	Phe	Asn	Ala	Ser	Tyr
			580					585					590		
Gly	Thr	Tyr	His	Asp	Leu	Cys	Lys	Ile	Leu	Asp	Lys	Asp	Phe	Leu	Asp
		595					600					605			
Asn	Ser	Lys	Asn	Glu	Lys	Ile	Leu	Glu	Asp	Ile	Val	Leu	Thr	Leu	Thr
	610					615					620				
Leu	Phe	Glu	Asp	Arg	Glu	Met	Ile	Arg	Lys	Arg	Leu	Glu	Asn	Tyr	Ser
625					630					635					640
Asp	Leu	Leu	Thr	Lys	Glu	Gln	Val	Lys	Lys	Leu	Glu	Arg	Arg	His	Tyr
				645					650					655	
Thr	Gly	Trp	Gly	Arg	Leu	Ser	Ala	Glu	Leu	Ile	His	Gly	Ile	Arg	Asn
			660					665					670		
Lys	Glu	Ser	Arg	Lys	Thr	Ile	Leu	Asp	Tyr	Leu	Ile	Asp	Asp	Gly	Asn
	675					680						685			
Ser	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	Asn	Asp	Asp	Ala	Leu	Ser	Phe
	690					695					700				
Lys	Glu	Glu	Ile	Ala	Lys	Ala	Gln	Val	Ile	Gly	Glu	Thr	Asp	Asn	Leu
705					710					715					720
Asn	Gln	Val	Val	Ser	Asp	Ile	Ala	Gly	Ser	Pro	Ala	Ile	Lys	Lys	Gly
				725					730					735	
Ile	Leu	Gln	Ser	Leu	Lys	Ile	Val	Asp	Glu	Leu	Val	Lys	Ile	Met	Gly
			740					745					750		
His	Gln	Pro	Glu	Asn	Ile	Val	Val	Glu	Met	Ala	Arg	Glu	Asn	Gln	Phe
		755					760					765			
Thr	Asn	Gln	Gly	Arg	Arg	Asn	Ser	Gln	Gln	Arg	Leu	Lys	Gly	Leu	Thr
	770					775					780				
Asp	Ser	Ile	Lys	Glu	Phe	Gly	Ser	Gln	Ile	Leu	Lys	Glu	His	Pro	Val
785					790					795					800
Glu	Asn	Ser	Gln	Leu	Gln	Asn	Asp	Arg	Leu	Phe	Leu	Tyr	Tyr	Leu	Gln
			805					810						815	
Asn	Gly	Arg	Asp	Met	Tyr	Thr	Gly	Glu	Glu	Leu	Asp	Ile	Asp	Tyr	Leu
			820					825					830		
Ser	Gln	Tyr	Asp	Ile	Asp	His	Ile	Ile	Pro	Gln	Ala	Phe	Ile	Lys	Asp
		835					840					845			

Asn	Ser	Ile	Asp	Asn	Arg	Val	Leu	Thr	Ser	Ser	Lys	Glu	Asn	Arg	Gly	850	855	860
Lys	Ser	Asp	Asp	Val	Pro	Ser	Lys	Asp	Val	Val	Arg	Lys	Met	Lys	Ser	865	870	875
Tyr	Trp	Ser	Lys	Leu	Leu	Ser	Ala	Lys	Leu	Ile	Thr	Gln	Arg	Lys	Phe	885	890	895
Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Thr	Asp	Asp	Asp	Lys	900	905	910
Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln	Ile	Thr	Lys	915	920	925
His	Val	Ala	Arg	Ile	Leu	Asp	Glu	Arg	Phe	Asn	Thr	Glu	Thr	Asp	Glu	930	935	940
Asn	Asn	Lys	Lys	Ile	Arg	Gln	Val	Lys	Ile	Val	Thr	Leu	Lys	Ser	Asn	945	950	955
Leu	Val	Ser	Asn	Phe	Arg	Lys	Glu	Phe	Glu	Leu	Tyr	Lys	Val	Arg	Glu	965	970	975
Ile	Asn	Asp	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ala	Val	Ile	980	985	990
Gly	Lys	Ala	Leu	Leu	Gly	Val	Tyr	Pro	Gln	Leu	Glu	Pro	Glu	Phe	Val	995	1000	1005
Tyr	Gly	Asp	Tyr	Pro	His	Phe	His	Gly	His	Lys	Glu	Asn	Lys	Ala	Thr	1010	1015	1020
Ala	Lys	Lys	Phe	Phe	Tyr	Ser	Asn	Ile	Met	Asn	Phe	Phe	Lys	Lys	Asp	1025	1030	1035
Asp	Val	Arg	Thr	Asp	Lys	Asn	Gly	Glu	Ile	Ile	Trp	Lys	Lys	Asp	Glu	1045	1050	1055
His	Ile	Ser	Asn	Ile	Lys	Lys	Val	Leu	Ser	Tyr	Pro	Gln	Val	Asn	Ile	1060	1065	1070
Val	Lys	Lys	Val	Glu	Glu	Gln	Thr	Gly	Gly	Phe	Ser	Lys	Glu	Ser	Ile	1075	1080	1085
Leu	Pro	Lys	Gly	Asn	Ser	Asp	Lys	Leu	Ile	Pro	Arg	Lys	Thr	Lys	Lys	1090	1095	1100
Phe	Tyr	Trp	Asp	Thr	Lys	Lys	Tyr	Gly	Gly	Phe	Asp	Ser	Pro	Ile	Val	1105	1110	1115
Ala	Tyr	Ser	Ile	Leu	Val	Ile	Ala	Asp	Ile	Glu	Lys	Gly	Lys	Ser	Lys	1125	1130	1135
Lys	Leu	Lys	Thr	Val	Lys	Ala	Leu	Val	Gly	Val	Thr	Ile	Met	Glu	Lys	1140	1145	1150
Met	Thr	Phe	Glu	Arg	Asp	Pro	Val	Ala	Phe	Leu	Glu	Arg	Lys	Gly	Tyr	1155	1160	1165
Arg	Asn	Val	Gln	Glu	Glu	Asn	Ile	Ile	Lys	Leu	Pro	Lys	Tyr	Ser	Leu	1170	1175	1180
Phe	Lys	Leu	Glu	Asn	Gly	Arg	Lys	Arg	Leu	Leu	Ala	Ser	Ala	Arg	Glu	1185	1190	1195
Leu	Gln	Lys	Gly	Asn	Glu	Ile	Val	Leu	Pro	Asn	His	Leu	Gly	Thr	Leu	1205	1210	1215
Leu	Tyr	His	Ala	Lys	Asn	Ile	His	Lys	Val	Asp	Glu	Pro	Lys	His	Leu	1220	1225	1230
Asp	Tyr	Val	Asp	Lys	His	Lys	Asp	Glu	Phe	Lys	Glu	Leu	Leu	Asp	Val	1235	1240	1245

Val	Ser	Asn	Phe	Ser	Lys	Lys	Tyr	Thr	Leu	Ala	Glu	Gly	Asn	Leu	Glu
1250						1255					1260				
Lys	Ile	Lys	Glu	Leu	Tyr	Ala	Gln	Asn	Asn	Gly	Glu	Asp	Leu	Lys	Glu
1265					1270					1275				1280	
Leu	Ala	Ser	Ser	Phe	Ile	Asn	Leu	Leu	Thr	Phe	Thr	Ala	Ile	Gly	Ala
				1285					1290					1295	
Pro	Ala	Thr	Phe	Lys	Phe	Phe	Asp	Lys	Asn	Ile	Asp	Arg	Lys	Arg	Tyr
			1300					1305					1310		
Thr	Ser	Thr	Thr	Glu	Ile	Leu	Asn	Ala	Thr	Leu	Ile	His	Gln	Ser	Ile
		1315				1320					1325				
Thr	Gly	Leu	Tyr	Glu	Thr	Arg	Ile	Asp	Leu	Asn	Lys	Leu	Gly	Gly	Asp
	1330					1335					1340				

<210> 158

<211> 1367

<212> PRT

<213> Artificial Sequence

<220>

<223> Streptococcus pyogenes Cas9

<400> 158

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

210		215		220
Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu				
225		230		240
Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe Asp				
	245		250	255
Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp Asp				
	260		265	270
Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp Leu				
	275		280	285
Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp Ile				
	290		295	300
Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser Met				
305		310		320
Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys Ala				
	325		330	335
Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp				
	340		345	350
Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser Gln				
	355		360	365
Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp Gly				
	370		375	380
Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg Lys				
385		390		400
Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu Gly				
	405		410	415
Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe Leu				
	420		425	430
Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile Pro				
	435		440	445
Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp Met				
	450		455	460
Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu Val				
465		470		480
Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr Asn				
	485		490	495
Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser Leu				
	500		505	510
Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys Tyr				
	515		520	525
Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln Lys				
	530		535	540
Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr Val				
545		550		560
Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp Ser				
	565		570	575
Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly Thr				
	580		585	590
Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp Asn				
	595		600	605
Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu				

610		615		620											
Phe	Glu	Asp	Arg	Glu	Met	Ile	Glu	Glu	Arg	Leu	Lys	Thr	Tyr	Ala	His
625					630					635					640
Leu	Phe	Asp	Asp	Lys	Val	Met	Lys	Gln	Leu	Lys	Arg	Arg	Arg	Tyr	Thr
				645						650					655
Gly	Trp	Gly	Arg	Leu	Ser	Arg	Lys	Leu	Ile	Asn	Gly	Ile	Arg	Asp	Lys
			660					665					670		
Gln	Ser	Gly	Lys	Thr	Ile	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Gly	Phe	Ala
		675					680					685			
Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ser	Leu	Thr	Phe	Lys
		690				695					700				
Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val	Ser	Gly	Gln	Gly	Asp	Ser	Leu	His
705					710					715					720
Glu	His	Ile	Ala	Asn	Leu	Ala	Gly	Ser	Pro	Ala	Ile	Lys	Lys	Gly	Ile
				725					730						735
Leu	Gln	Thr	Val	Lys	Val	Val	Asp	Glu	Leu	Val	Lys	Val	Met	Gly	Arg
			740					745					750		
His	Lys	Pro	Glu	Asn	Ile	Val	Ile	Glu	Met	Ala	Arg	Glu	Asn	Gln	Thr
		755					760					765			
Thr	Gln	Lys	Gly	Gln	Lys	Asn	Ser	Arg	Glu	Arg	Met	Lys	Arg	Ile	Glu
		770				775					780				
Glu	Gly	Ile	Lys	Glu	Leu	Gly	Ser	Gln	Ile	Leu	Lys	Glu	His	Pro	Val
785					790					795					800
Glu	Asn	Thr	Gln	Leu	Gln	Asn	Glu	Lys	Leu	Tyr	Leu	Tyr	Tyr	Leu	Gln
				805					810						815
Asn	Gly	Arg	Asp	Met	Tyr	Val	Asp	Gln	Glu	Leu	Asp	Ile	Asn	Arg	Leu
			820				825						830		
Ser	Asp	Tyr	Asp	Val	Asp	His	Ile	Val	Pro	Gln	Ser	Phe	Leu	Lys	Asp
		835					840					845			
Asp	Ser	Ile	Asp	Asn	Lys	Val	Leu	Thr	Arg	Ser	Asp	Lys	Asn	Arg	Gly
		850				855					860				
Lys	Ser	Asp	Asn	Val	Pro	Ser	Glu	Glu	Val	Val	Lys	Lys	Met	Lys	Asn
865					870					875					880
Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	Leu	Ile	Thr	Gln	Arg	Lys	Phe
				885					890						895
Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Ser	Glu	Leu	Asp	Lys
		900						905					910		
Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln	Ile	Thr	Lys
		915					920					925			
His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	Met	Asn	Thr	Lys	Tyr	Asp	Glu
		930				935					940				
Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	Val	Ile	Thr	Leu	Lys	Ser	Lys
945					950					955					960
Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	Gln	Phe	Tyr	Lys	Val	Arg	Glu
				965					970						975
Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ala	Val	Val
		980						985					990		
Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	Lys	Leu	Glu	Ser	Glu	Phe	Val
		995					1000						1005		
Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	Arg	Lys	Met	Ile	Ala	Lys	Ser

1010	1015	1020
Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr Ser Asn		
1025	1030	1035
Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn Gly Glu Ile		1040
	1045	1050
Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu Thr Gly Glu Ile Val		1055
	1060	1065
Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val Leu Ser Met		1070
	1075	1080
Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly Phe		1085
	1090	1095
Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu Ile Ala		1100
	1105	1110
Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe Asp Ser Pro		1115
	1120	1125
Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val Glu Lys Gly Lys		1130
	1135	1140
Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met		1145
	1150	1155
Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys		1160
	1165	1170
Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr		1175
	1180	1185
Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala		1190
	1195	1200
Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val		1205
	1210	1215
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser Pro		1220
	1225	1230
Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys His Tyr		1235
	1240	1245
Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys Arg Val Ile		1250
	1255	1260
Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys His		1265
	1270	1275
Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile Ile His Leu Phe		1280
	1285	1290
Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr Phe Asp Thr		1295
	1300	1305
Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val Leu Asp Ala		1310
	1315	1320
Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr Arg Ile Asp		1325
	1330	1335
Leu Ser Gln Leu Gly Gly Asp		1340
	1345	1350
	1355	1360
	1365	

<210> 159

<211> 1387

<212> PRT

<213> Artificial Sequence

<220>

<223> Streptococcus thermophilus Cas9

<400> 159

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

Asp	Thr	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Lys	Thr	Asn	Gln
		355					360					365			
Glu	Asp	Phe	Tyr	Val	Tyr	Leu	Lys	Lys	Leu	Leu	Ala	Glu	Phe	Glu	Gly
	370					375					380				
Ala	Asp	Tyr	Phe	Leu	Glu	Lys	Ile	Asp	Arg	Glu	Asp	Phe	Leu	Arg	Lys
385					390					395					400
Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	Tyr	Gln	Ile	His	Leu	Gln
			405					410						415	
Glu	Met	Arg	Ala	Ile	Leu	Asp	Lys	Gln	Ala	Lys	Phe	Tyr	Pro	Phe	Leu
			420				425						430		
Ala	Lys	Asn	Lys	Glu	Arg	Ile	Glu	Lys	Ile	Leu	Thr	Phe	Arg	Ile	Pro
	435						440					445			
Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Asn	Ser	Asp	Phe	Ala	Trp	Ser
	450					455					460				
Ile	Arg	Lys	Arg	Asn	Glu	Lys	Ile	Thr	Pro	Trp	Asn	Phe	Glu	Asp	Val
465					470					475					480
Ile	Asp	Lys	Glu	Ser	Ser	Ala	Glu	Ala	Phe	Ile	Asn	Arg	Met	Thr	Ser
				485					490					495	
Phe	Asp	Leu	Tyr	Leu	Pro	Glu	Glu	Lys	Val	Leu	Pro	Lys	His	Ser	Leu
			500					505					510		
Leu	Tyr	Glu	Thr	Phe	Asn	Val	Tyr	Asn	Glu	Leu	Thr	Lys	Val	Arg	Phe
	515						520					525			
Ile	Ala	Glu	Ser	Met	Arg	Asp	Tyr	Gln	Phe	Leu	Asp	Ser	Lys	Gln	Lys
	530					535					540				
Lys	Asp	Ile	Val	Arg	Leu	Tyr	Phe	Lys	Asp	Lys	Arg	Lys	Val	Thr	Asp
545					550				555						560
Lys	Asp	Ile	Ile	Glu	Tyr	Leu	His	Ala	Ile	Tyr	Gly	Tyr	Asp	Gly	Ile
				565				570						575	
Glu	Leu	Lys	Gly	Ile	Glu	Lys	Gln	Phe	Asn	Ser	Ser	Leu	Ser	Thr	Tyr
			580					585					590		
His	Asp	Leu	Leu	Asn	Ile	Ile	Asn	Asp	Lys	Glu	Phe	Leu	Asp	Asp	Ser
	595						600					605			
Ser	Asn	Glu	Ala	Ile	Ile	Glu	Glu	Ile	Ile	His	Thr	Leu	Thr	Ile	Phe
	610					615					620				
Glu	Asp	Arg	Glu	Met	Ile	Lys	Gln	Arg	Leu	Ser	Lys	Phe	Glu	Asn	Ile
625					630					635					640
Phe	Asp	Lys	Ser	Val	Leu	Lys	Lys	Leu	Ser	Arg	Arg	His	Tyr	Thr	Gly
			645					650						655	
Trp	Gly	Lys	Leu	Ser	Ala	Lys	Leu	Ile	Asn	Gly	Ile	Arg	Asp	Glu	Lys
			660					665					670		
Ser	Gly	Asn	Thr	Ile	Leu	Asp	Tyr	Leu	Ile	Asp	Asp	Gly	Ile	Ser	Asn
	675					680						685			
Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ala	Leu	Ser	Phe	Lys	Lys
	690					695				700					
Lys	Ile	Gln	Lys	Ala	Gln	Ile	Ile	Gly	Asp	Glu	Asp	Lys	Gly	Asn	Ile
705					710				715						720
Lys	Glu	Val	Val	Lys	Ser	Leu	Pro	Gly	Ser	Pro	Ala	Ile	Lys	Lys	Gly
				725				730						735	
Ile	Leu	Gln	Ser	Ile	Lys	Ile	Val	Asp	Glu	Leu	Val	Lys	Val	Met	Gly
			740					745					750		

Gly	Arg	Lys	Pro	Glu	Ser	Ile	Val	Val	Glu	Met	Ala	Arg	Glu	Asn	Gln
		755					760					765			
Tyr	Thr	Asn	Gln	Gly	Lys	Ser	Asn	Ser	Gln	Gln	Arg	Leu	Lys	Arg	Leu
		770				775					780				
Glu	Lys	Ser	Leu	Lys	Glu	Leu	Gly	Ser	Lys	Ile	Leu	Lys	Glu	Asn	Ile
785					790					795					800
Pro	Ala	Lys	Leu	Ser	Lys	Ile	Asp	Asn	Asn	Ala	Leu	Gln	Asn	Asp	Arg
				805					810					815	
Leu	Tyr	Leu	Tyr	Tyr	Leu	Gln	Asn	Gly	Lys	Asp	Met	Tyr	Thr	Gly	Asp
			820					825					830		
Asp	Leu	Asp	Ile	Asp	Arg	Leu	Ser	Asn	Tyr	Asp	Ile	Asp	His	Ile	Ile
		835					840				845				
Pro	Gln	Ala	Phe	Leu	Lys	Asp	Asn	Ser	Ile	Asp	Asn	Lys	Val	Leu	Val
	850					855					860				
Ser	Ser	Ala	Ser	Asn	Arg	Gly	Lys	Ser	Asp	Asp	Val	Pro	Ser	Leu	Glu
865					870					875					880
Val	Val	Lys	Lys	Arg	Lys	Thr	Phe	Trp	Tyr	Gln	Leu	Leu	Lys	Ser	Lys
				885					890					895	
Leu	Ile	Ser	Gln	Arg	Lys	Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly
			900					905					910		
Gly	Leu	Ser	Pro	Glu	Asp	Lys	Ala	Gly	Phe	Ile	Gln	Arg	Gln	Leu	Val
		915					920					925			
Glu	Thr	Arg	Gln	Ile	Thr	Lys	His	Val	Ala	Arg	Leu	Leu	Asp	Glu	Lys
		930				935					940				
Phe	Asn	Asn	Lys	Lys	Asp	Glu	Asn	Asn	Arg	Ala	Val	Arg	Thr	Val	Lys
945					950					955					960
Ile	Ile	Thr	Leu	Lys	Ser	Thr	Leu	Val	Ser	Gln	Phe	Arg	Lys	Asp	Phe
				965					970					975	
Glu	Leu	Tyr	Lys	Val	Arg	Glu	Ile	Asn	Asp	Phe	His	His	Ala	His	Asp
			980					985					990		
Ala	Tyr	Leu	Asn	Ala	Val	Val	Ala	Ser	Ala	Leu	Leu	Lys	Lys	Tyr	Pro
		995					1000					1005			
Lys	Leu	Glu	Pro	Glu	Phe	Val	Tyr	Gly	Asp	Tyr	Pro	Lys	Tyr	Asn	Ser
		1010				1015					1020				
Phe	Arg	Glu	Arg	Lys	Ser	Ala	Thr	Glu	Lys	Val	Tyr	Phe	Tyr	Ser	Asn
1025					1030					1035					1040
Ile	Met	Asn	Ile	Phe	Lys	Lys	Ser	Ile	Ser	Leu	Ala	Asp	Gly	Arg	Val
				1045					1050					1055	
Ile	Glu	Arg	Pro	Leu	Ile	Glu	Val	Asn	Glu	Glu	Thr	Gly	Glu	Ser	Val
			1060					1065					1070		
Trp	Asn	Lys	Glu	Ser	Asp	Leu	Ala	Thr	Val	Arg	Arg	Val	Leu	Ser	Tyr
		1075					1080					1085			
Pro	Gln	Val	Asn	Val	Val	Lys	Lys	Val	Glu	Glu	Gln	Asn	His	Gly	Leu
	1090					1095					1100				
Asp	Arg	Gly	Lys	Pro	Lys	Gly	Leu	Phe	Asn	Ala	Asn	Leu	Ser	Ser	Lys
1105					1110					1115					1120
Pro	Lys	Pro	Asn	Ser	Asn	Glu	Asn	Leu	Val	Gly	Ala	Lys	Glu	Tyr	Leu
				1125					1130					1135	
Asp	Pro	Lys	Lys	Tyr	Gly	Gly	Tyr	Ala	Gly	Ile	Ser	Asn	Ser	Phe	Thr
			1140					1145					1150		

Val	Leu	Val	Lys	Gly	Thr	Ile	Glu	Lys	Gly	Ala	Lys	Lys	Lys	Ile	Thr
	1155						1160					1165			
Asn	Val	Leu	Glu	Phe	Gln	Gly	Ile	Ser	Ile	Leu	Asp	Arg	Ile	Asn	Tyr
	1170					1175					1180				
Arg	Lys	Asp	Lys	Leu	Asn	Phe	Leu	Leu	Glu	Lys	Gly	Tyr	Lys	Asp	Ile
1185					1190					1195				1200	
Glu	Leu	Ile	Ile	Glu	Leu	Pro	Lys	Tyr	Ser	Leu	Phe	Glu	Leu	Ser	Asp
			1205						1210					1215	
Gly	Ser	Arg	Arg	Met	Leu	Ala	Ser	Ile	Leu	Ser	Thr	Asn	Asn	Lys	Arg
		1220						1225						1230	
Gly	Glu	Ile	His	Lys	Gly	Asn	Gln	Ile	Phe	Leu	Ser	Gln	Lys	Phe	Val
		1235					1240						1245		
Lys	Leu	Leu	Tyr	His	Ala	Lys	Arg	Ile	Ser	Asn	Thr	Ile	Asn	Glu	Asn
	1250					1255					1260				
His	Arg	Lys	Tyr	Val	Glu	Asn	His	Lys	Lys	Glu	Phe	Glu	Glu	Leu	Phe
1265					1270					1275				1280	
Tyr	Tyr	Ile	Leu	Glu	Phe	Asn	Glu	Asn	Tyr	Val	Gly	Ala	Lys	Lys	Asn
			1285						1290					1295	
Gly	Lys	Leu	Leu	Asn	Ser	Ala	Phe	Gln	Ser	Trp	Gln	Asn	His	Ser	Ile
		1300						1305					1310		
Asp	Glu	Leu	Cys	Ser	Ser	Phe	Ile	Gly	Pro	Thr	Gly	Ser	Glu	Arg	Lys
	1315						1320					1325			
Gly	Leu	Phe	Glu	Leu	Thr	Ser	Arg	Gly	Ser	Ala	Ala	Asp	Phe	Glu	Phe
	1330					1335				1340					
Leu	Gly	Val	Lys	Ile	Pro	Arg	Tyr	Arg	Asp	Tyr	Thr	Pro	Ser	Ser	Leu
1345					1350				1355					1360	
Leu	Lys	Asp	Ala	Thr	Leu	Ile	His	Gln	Ser	Val	Thr	Gly	Leu	Tyr	Glu
			1365					1370						1375	
Thr	Arg	Ile	Asp	Leu	Ala	Lys	Leu	Gly	Glu	Gly					
		1380						1385							

<210> 160

<211> 1333

<212> PRT

<213> Artificial Sequence

<220>

<223> *Listeria innocua* Cas9

<400> 160

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

65					70					75					80
Leu	Gln	Gly	Ile	Phe	Ala	Glu	Glu	Met	Ser	Lys	Thr	Asp	Ala	Asn	Phe
				85					90					95	
Phe	Cys	Arg	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Asp	Asn	Glu	Lys	Arg	Asn
			100					105					110		
Ser	Arg	His	Pro	Phe	Phe	Ala	Thr	Ile	Glu	Glu	Glu	Val	Glu	Tyr	His
		115					120					125			
Lys	Asn	Tyr	Pro	Thr	Ile	Tyr	His	Leu	Arg	Glu	Glu	Leu	Val	Asn	Ser
	130					135				140					
Ser	Glu	Lys	Ala	Asp	Leu	Arg	Leu	Val	Tyr	Leu	Ala	Leu	Ala	His	Ile
145					150				155					160	
Ile	Lys	Tyr	Arg	Gly	Asn	Phe	Leu	Ile	Glu	Gly	Ala	Leu	Asp	Thr	Gln
				165					170					175	
Asn	Thr	Ser	Val	Asp	Gly	Ile	Tyr	Lys	Gln	Phe	Ile	Gln	Thr	Tyr	Asn
		180						185					190		
Gln	Val	Phe	Ala	Ser	Gly	Ile	Glu	Asp	Gly	Ser	Leu	Lys	Lys	Leu	Glu
	195						200					205			
Asp	Asn	Lys	Asp	Val	Ala	Lys	Ile	Leu	Val	Glu	Lys	Val	Thr	Arg	Lys
	210					215					220				
Glu	Lys	Leu	Glu	Arg	Ile	Leu	Lys	Leu	Tyr	Pro	Gly	Glu	Lys	Ser	Ala
225					230					235					240
Gly	Met	Phe	Ala	Gln	Phe	Ile	Ser	Leu	Ile	Val	Gly	Ser	Lys	Gly	Asn
				245					250					255	
Phe	Gln	Lys	Pro	Phe	Asp	Leu	Ile	Glu	Lys	Ser	Asp	Ile	Glu	Cys	Ala
			260					265					270		
Lys	Asp	Ser	Tyr	Glu	Glu	Asp	Leu	Glu	Ser	Leu	Leu	Ala	Leu	Ile	Gly
		275				280						285			
Asp	Glu	Tyr	Ala	Glu	Leu	Phe	Val	Ala	Ala	Lys	Asn	Ala	Tyr	Ser	Ala
	290					295					300				
Val	Val	Leu	Ser	Ser	Ile	Ile	Thr	Val	Ala	Glu	Thr	Glu	Thr	Asn	Ala
305					310					315					320
Lys	Leu	Ser	Ala	Ser	Met	Ile	Glu	Arg	Phe	Asp	Thr	His	Glu	Glu	Asp
				325					330					335	
Leu	Gly	Glu	Leu	Lys	Ala	Phe	Ile	Lys	Leu	His	Leu	Pro	Lys	His	Tyr
			340					345					350		
Glu	Glu	Ile	Phe	Ser	Asn	Thr	Glu	Lys	His	Gly	Tyr	Ala	Gly	Tyr	Ile
		355					360					365			
Asp	Gly	Lys	Thr	Lys	Gln	Ala	Asp	Phe	Tyr	Lys	Tyr	Met	Lys	Met	Thr
	370					375					380				
Leu	Glu	Asn	Ile	Glu	Gly	Ala	Asp	Tyr	Phe	Ile	Ala	Lys	Ile	Glu	Lys
385					390					395					400
Glu	Asn	Phe	Leu	Arg	Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ala	Ile	Pro
				405					410					415	
His	Gln	Leu	His	Leu	Glu	Glu	Leu	Glu	Ala	Ile	Leu	His	Gln	Gln	Ala
			420					425					430		
Lys	Tyr	Tyr	Pro	Phe	Leu	Lys	Glu	Asn	Tyr	Asp	Lys	Ile	Lys	Ser	Leu
		435					440					445			
Val	Thr	Phe	Arg	Ile	Pro	Tyr	Phe	Val	Gly	Pro	Leu	Ala	Asn	Gly	Gln
	450					455					460				
Ser	Glu	Phe	Ala	Trp	Leu	Thr	Arg	Lys	Ala	Asp	Gly	Glu	Ile	Arg	Pro

465					470					475					480
Trp	Asn	Ile	Glu	Glu	Lys	Val	Asp	Phe	Gly	Lys	Ser	Ala	Val	Asp	Phe
				485					490					495	
Ile	Glu	Lys	Met	Thr	Asn	Lys	Asp	Thr	Tyr	Leu	Pro	Lys	Glu	Asn	Val
				500					505					510	
Leu	Pro	Lys	His	Ser	Leu	Cys	Tyr	Gln	Lys	Tyr	Leu	Val	Tyr	Asn	Glu
				515					520					525	
Leu	Thr	Lys	Val	Arg	Tyr	Ile	Asn	Asp	Gln	Gly	Lys	Thr	Ser	Tyr	Phe
				530					535					540	
Ser	Gly	Gln	Glu	Lys	Glu	Gln	Ile	Phe	Asn	Asp	Leu	Phe	Lys	Gln	Lys
				545					550					555	
Arg	Lys	Val	Lys	Lys	Lys	Asp	Leu	Glu	Leu	Phe	Leu	Arg	Asn	Met	Ser
				565					570					575	
His	Val	Glu	Ser	Pro	Thr	Ile	Glu	Gly	Leu	Glu	Asp	Ser	Phe	Asn	Ser
				580					585					590	
Ser	Tyr	Ser	Thr	Tyr	His	Asp	Leu	Leu	Lys	Val	Gly	Ile	Lys	Gln	Glu
				595					600					605	
Ile	Leu	Asp	Asn	Pro	Val	Asn	Thr	Glu	Met	Leu	Glu	Asn	Ile	Val	Lys
				610					615					620	
Ile	Leu	Thr	Val	Phe	Glu	Asp	Lys	Arg	Met	Ile	Lys	Glu	Gln	Leu	Gln
				625					630					635	
Gln	Phe	Ser	Asp	Val	Leu	Asp	Gly	Val	Val	Leu	Lys	Lys	Leu	Glu	Arg
				645					650					655	
Arg	His	Tyr	Thr	Gly	Trp	Gly	Arg	Leu	Ser	Ala	Lys	Leu	Leu	Met	Gly
				660					665					670	
Ile	Arg	Asp	Lys	Gln	Ser	His	Leu	Thr	Ile	Leu	Asp	Tyr	Leu	Met	Asn
				675					680					685	
Asp	Asp	Gly	Leu	Asn	Arg	Asn	Leu	Met	Gln	Leu	Ile	Asn	Asp	Ser	Asn
				690					695					700	
Leu	Ser	Phe	Lys	Ser	Ile	Ile	Glu	Lys	Glu	Gln	Val	Thr	Thr	Ala	Asp
				705					710					715	
Lys	Asp	Ile	Gln	Ser	Ile	Val	Ala	Asp	Leu	Ala	Gly	Ser	Pro	Ala	Ile
				725					730					735	
Lys	Lys	Gly	Ile	Leu	Gln	Ser	Leu	Lys	Ile	Val	Asp	Glu	Leu	Val	Ser
				740					745					750	
Val	Met	Gly	Tyr	Pro	Pro	Gln	Thr	Ile	Val	Val	Glu	Met	Ala	Arg	Glu
				755					760					765	
Asn	Gln	Thr	Thr	Gly	Lys	Gly	Lys	Asn	Asn	Ser	Arg	Pro	Arg	Tyr	Lys
				770					775					780	
Ser	Leu	Glu	Lys	Ala	Ile	Lys	Glu	Phe	Gly	Ser	Gln	Ile	Leu	Lys	Glu
				785					790					795	
His	Pro	Thr	Asp	Asn	Gln	Glu	Leu	Arg	Asn	Asn	Arg	Leu	Tyr	Leu	Tyr
				805					810					815	
Tyr	Leu	Gln	Asn	Gly	Lys	Asp	Met	Tyr	Thr	Gly	Gln	Asp	Leu	Asp	Ile
				820					825					830	
His	Asn	Leu	Ser	Asn	Tyr	Asp	Ile	Asp	His	Ile	Val	Pro	Gln	Ser	Phe
				835					840					845	
Ile	Thr	Asp	Asn	Ser	Ile	Asp	Asn	Leu	Val	Leu	Thr	Ser	Ser	Ala	Gly
				850					855					860	
Asn	Arg	Glu	Lys	Gly	Asp	Asp	Val	Pro	Pro	Leu	Glu	Ile	Val	Arg	Lys

865					870					875				880
Arg	Lys	Val	Phe	Trp	Glu	Lys	Leu	Tyr	Gln	Gly	Asn	Leu	Met	Ser
				885					890					895
Arg	Lys	Phe	Asp	Tyr	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Thr
			900					905					910	
Ala	Asp	Lys	Ala	Arg	Phe	Ile	His	Arg	Gln	Leu	Val	Glu	Thr	Arg
		915					920					925		
Ile	Thr	Lys	Asn	Val	Ala	Asn	Ile	Leu	His	Gln	Arg	Phe	Asn	Tyr
	930					935					940			
Lys	Asp	Asp	His	Gly	Asn	Thr	Met	Lys	Gln	Val	Arg	Ile	Val	Thr
945					950					955				960
Lys	Ser	Ala	Leu	Val	Ser	Gln	Phe	Arg	Lys	Gln	Phe	Gln	Leu	Tyr
			965						970					975
Val	Arg	Asp	Val	Asn	Asp	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu
		980						985					990	
Gly	Val	Val	Ala	Asn	Thr	Leu	Leu	Lys	Val	Tyr	Pro	Gln	Leu	Glu
		995					1000					1005		
Glu	Phe	Val	Tyr	Gly	Asp	Tyr	His	Gln	Phe	Asp	Trp	Phe	Lys	Ala
	1010					1015					1020			
Lys	Ala	Thr	Ala	Lys	Lys	Gln	Phe	Tyr	Thr	Asn	Ile	Met	Leu	Phe
1025					1030					1035				1040
Ala	Gln	Lys	Asp	Arg	Ile	Ile	Asp	Glu	Asn	Gly	Glu	Ile	Leu	Trp
			1045						1050					1055
Lys	Lys	Tyr	Leu	Asp	Thr	Val	Lys	Lys	Val	Met	Ser	Tyr	Arg	Gln
		1060						1065					1070	
Asn	Ile	Val	Lys	Lys	Thr	Glu	Ile	Gln	Lys	Gly	Glu	Phe	Ser	Lys
	1075					1080						1085		
Thr	Ile	Lys	Pro	Lys	Gly	Asn	Ser	Ser	Lys	Leu	Ile	Pro	Arg	Lys
	1090					1095						1100		
Asn	Trp	Asp	Pro	Met	Lys	Tyr	Gly	Gly	Leu	Asp	Ser	Pro	Asn	Met
1105				1110						1115				1120
Tyr	Ala	Val	Val	Ile	Glu	Tyr	Ala	Lys	Gly	Lys	Asn	Lys	Leu	Val
			1125						1130					1135
Glu	Lys	Lys	Ile	Ile	Arg	Val	Thr	Ile	Met	Glu	Arg	Lys	Ala	Phe
		1140						1145					1150	
Lys	Asp	Glu	Lys	Ala	Phe	Leu	Glu	Gln	Gly	Tyr	Arg	Gln	Pro	Lys
	1155						1160				1165			
Val	Leu	Ala	Lys	Leu	Pro	Lys	Tyr	Thr	Leu	Tyr	Glu	Cys	Glu	Gly
	1170					1175					1180			
Arg	Arg	Arg	Met	Leu	Ala	Ser	Ala	Asn	Glu	Ala	Gln	Lys	Gly	Asn
1185				1190						1195				1200
Gln	Val	Leu	Pro	Asn	His	Leu	Val	Thr	Leu	Leu	His	His	Ala	Ala
			1205						1210					1215
Cys	Glu	Val	Ser	Asp	Gly	Lys	Ser	Leu	Asp	Tyr	Ile	Glu	Ser	Asn
		1220						1225				1230		
Glu	Met	Phe	Ala	Glu	Leu	Leu	Ala	His	Val	Ser	Glu	Phe	Ala	Lys
	1235						1240					1245		
Tyr	Thr	Leu	Ala	Glu	Ala	Asn	Leu	Asn	Lys	Ile	Asn	Gln	Leu	Phe
	1250					1255					1260			
Gln	Asn	Lys	Glu	Gly	Asp	Ile	Lys	Ala	Ile	Ala	Gln	Ser	Phe	Val

1265		1270		1275		1280
Leu Met Ala Phe Asn Ala Met Gly Ala Pro Ala Ser Phe Lys Phe Phe						
		1285		1290		1295
Glu Thr Thr Ile Glu Arg Lys Arg Tyr Asn Asn Leu Lys Glu Leu Leu						
		1300		1305		1310
Asn Ser Thr Ile Ile Tyr Gln Ser Ile Thr Gly Leu Tyr Glu Ser Arg						
		1315		1320		1325
Lys Arg Leu Asp Asp						
1330						

<210> 161
 <211> 1082
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Neisseria meningitidis Cas9

<400> 161

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

Thr	Gln	Arg	Pro	Ala	Leu	Ser	Gly	Asp	Ala	Val	Gln	Lys	Met	Leu	Gly
				245					250					255	
His	Cys	Thr	Phe	Glu	Pro	Ala	Glu	Pro	Lys	Ala	Ala	Lys	Asn	Thr	Tyr
			260					265					270		
Thr	Ala	Glu	Arg	Phe	Ile	Trp	Leu	Thr	Lys	Leu	Asn	Asn	Leu	Arg	Ile
		275					280					285			
Leu	Glu	Gln	Gly	Ser	Glu	Arg	Pro	Leu	Thr	Asp	Thr	Glu	Arg	Ala	Thr
	290					295				300					
Leu	Met	Asp	Glu	Pro	Tyr	Arg	Lys	Ser	Lys	Leu	Thr	Tyr	Ala	Gln	Ala
305					310					315					320
Arg	Lys	Leu	Leu	Gly	Leu	Glu	Asp	Thr	Ala	Phe	Phe	Lys	Gly	Leu	Arg
				325					330					335	
Tyr	Gly	Lys	Asp	Asn	Ala	Glu	Ala	Ser	Thr	Leu	Met	Glu	Met	Lys	Ala
			340					345					350		
Tyr	His	Ala	Ile	Ser	Arg	Ala	Leu	Glu	Lys	Glu	Gly	Leu	Lys	Asp	Lys
	355						360					365			
Lys	Ser	Pro	Leu	Asn	Leu	Ser	Pro	Glu	Leu	Gln	Asp	Glu	Ile	Gly	Thr
	370					375					380				
Ala	Phe	Ser	Leu	Phe	Lys	Thr	Asp	Glu	Asp	Ile	Thr	Gly	Arg	Leu	Lys
385					390					395					400
Asp	Arg	Ile	Gln	Pro	Glu	Ile	Leu	Glu	Ala	Leu	Leu	Lys	His	Ile	Ser
			405						410					415	
Phe	Asp	Lys	Phe	Val	Gln	Ile	Ser	Leu	Lys	Ala	Leu	Arg	Arg	Ile	Val
		420						425					430		
Pro	Leu	Met	Glu	Gln	Gly	Lys	Arg	Tyr	Asp	Glu	Ala	Cys	Ala	Glu	Ile
	435						440					445			
Tyr	Gly	Asp	His	Tyr	Gly	Lys	Lys	Asn	Thr	Glu	Glu	Lys	Ile	Tyr	Leu
	450					455					460				
Pro	Pro	Ile	Pro	Ala	Asp	Glu	Ile	Arg	Asn	Pro	Val	Val	Leu	Arg	Ala
465					470					475					480
Leu	Ser	Gln	Ala	Arg	Lys	Val	Ile	Asn	Gly	Val	Val	Arg	Arg	Tyr	Gly
			485						490					495	
Ser	Pro	Ala	Arg	Ile	His	Ile	Glu	Thr	Ala	Arg	Glu	Val	Gly	Lys	Ser
		500						505					510		
Phe	Lys	Asp	Arg	Lys	Glu	Ile	Glu	Lys	Arg	Gln	Glu	Glu	Asn	Arg	Lys
	515						520					525			
Asp	Arg	Glu	Lys	Ala	Ala	Ala	Lys	Phe	Arg	Glu	Tyr	Phe	Pro	Asn	Phe
	530					535					540				
Val	Gly	Glu	Pro	Lys	Ser	Lys	Asp	Ile	Leu	Lys	Leu	Arg	Leu	Tyr	Glu
545					550					555					560
Gln	Gln	His	Gly	Lys	Cys	Leu	Tyr	Ser	Gly	Lys	Glu	Ile	Asn	Leu	Gly
			565						570					575	
Arg	Leu	Asn	Glu	Lys	Gly	Tyr	Val	Glu	Ile	Asp	His	Ala	Leu	Pro	Phe
		580						585					590		
Ser	Arg	Thr	Trp	Asp	Asp	Ser	Phe	Asn	Asn	Lys	Val	Leu	Val	Leu	Gly
	595						600					605			
Ser	Glu	Asn	Gln	Asn	Lys	Gly	Asn	Gln	Thr	Pro	Tyr	Glu	Tyr	Phe	Asn
	610					615					620				
Gly	Lys	Asp	Asn	Ser	Arg	Glu	Trp	Gln	Glu	Phe	Lys	Ala	Arg	Val	Glu
625					630					635					640

Thr	Ser	Arg	Phe	Pro	Arg	Ser	Lys	Lys	Gln	Arg	Ile	Leu	Leu	Gln	Lys
				645					650					655	
Phe	Asp	Glu	Asp	Gly	Phe	Lys	Glu	Arg	Asn	Leu	Asn	Asp	Thr	Arg	Tyr
			660					665					670		
Val	Asn	Arg	Phe	Leu	Cys	Gln	Phe	Val	Ala	Asp	Arg	Met	Arg	Leu	Thr
		675					680					685			
Gly	Lys	Gly	Lys	Lys	Arg	Val	Phe	Ala	Ser	Asn	Gly	Gln	Ile	Thr	Asn
	690					695					700				
Leu	Leu	Arg	Gly	Phe	Trp	Gly	Leu	Arg	Lys	Val	Arg	Ala	Glu	Asn	Asp
705					710					715					720
Arg	His	His	Ala	Leu	Asp	Ala	Val	Val	Val	Ala	Cys	Ser	Thr	Val	Ala
			725						730					735	
Met	Gln	Gln	Lys	Ile	Thr	Arg	Phe	Val	Arg	Tyr	Lys	Glu	Met	Asn	Ala
			740					745					750		
Phe	Asp	Gly	Lys	Thr	Ile	Asp	Lys	Glu	Thr	Gly	Glu	Val	Leu	His	Gln
		755					760					765			
Lys	Thr	His	Phe	Pro	Gln	Pro	Trp	Glu	Phe	Phe	Ala	Gln	Glu	Val	Met
	770					775					780				
Ile	Arg	Val	Phe	Gly	Lys	Pro	Asp	Gly	Lys	Pro	Glu	Phe	Glu	Glu	Ala
785					790					795					800
Asp	Thr	Leu	Glu	Lys	Leu	Arg	Thr	Leu	Leu	Ala	Glu	Lys	Leu	Ser	Ser
			805						810					815	
Arg	Pro	Glu	Ala	Val	His	Glu	Tyr	Val	Thr	Pro	Leu	Phe	Val	Ser	Arg
			820					825					830		
Ala	Pro	Asn	Arg	Lys	Met	Ser	Gly	Gln	Gly	His	Met	Glu	Thr	Val	Lys
		835					840					845			
Ser	Ala	Lys	Arg	Leu	Asp	Glu	Gly	Val	Ser	Val	Leu	Arg	Val	Pro	Leu
	850					855					860				
Thr	Gln	Leu	Lys	Leu	Lys	Asp	Leu	Glu	Lys	Met	Val	Asn	Arg	Glu	Arg
865					870					875					880
Glu	Pro	Lys	Leu	Tyr	Glu	Ala	Leu	Lys	Ala	Arg	Leu	Glu	Ala	His	Lys
			885						890					895	
Asp	Asp	Pro	Ala	Lys	Ala	Phe	Ala	Glu	Pro	Phe	Tyr	Lys	Tyr	Asp	Lys
			900					905					910		
Ala	Gly	Asn	Arg	Thr	Gln	Gln	Val	Lys	Ala	Val	Arg	Val	Glu	Gln	Val
		915					920					925			
Gln	Lys	Thr	Gly	Val	Trp	Val	Arg	Asn	His	Asn	Gly	Ile	Ala	Asp	Asn
	930					935					940				
Ala	Thr	Met	Val	Arg	Val	Asp	Val	Phe	Glu	Lys	Gly	Asp	Lys	Tyr	Tyr
945					950					955					960
Leu	Val	Pro	Ile	Tyr	Ser	Trp	Gln	Val	Ala	Lys	Gly	Ile	Leu	Pro	Asp
			965						970					975	
Arg	Ala	Val	Val	Gln	Gly	Lys	Asp	Glu	Glu	Asp	Trp	Gln	Leu	Ile	Asp
			980					985					990		
Asp	Ser	Phe	As												

Ile	Gly	Lys	Asn	Gly	Ile	Leu	Glu	Gly	Ile	Gly	Val	Lys	Thr	Ala	Leu
			1045						1050					1055	
Ser	Phe	Gln	Lys	Tyr	Gln	Ile	Asp	Glu	Leu	Gly	Lys	Glu	Ile	Arg	Pro
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Cys	Arg	Leu	Lys	Lys	Arg	Pro	Pro	Val	Arg						
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<212> PRT

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<223> Streptococcus pyogenes Cas9

<400> 162

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

			260					265				270			
Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile	Gly	Asp	Gln	Tyr	Ala	Asp
		275					280					285			
Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp	Ala	Ile	Leu	Leu	Ser	Asp
	290					295					300				
Ile	Leu	Arg	Val	Asn	Thr	Glu	Ile	Thr	Lys	Ala	Pro	Leu	Ser	Ala	Ser
305					310					315					320
Met	Ile	Lys	Arg	Tyr	Asp	Glu	His	His	Gln	Asp	Leu	Thr	Leu	Leu	Lys
				325					330					335	
Ala	Leu	Val	Arg	Gln	Gln	Leu	Pro	Glu	Lys	Tyr	Lys	Glu	Ile	Phe	Phe
			340					345					350		
Asp	Gln	Ser	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Gly	Ala	Ser
		355					360					365			
Gln	Glu	Glu	Phe	Tyr	Lys	Phe	Ile	Lys	Pro	Ile	Leu	Glu	Lys	Met	Asp
	370					375					380				
Gly	Thr	Glu	Glu	Leu	Leu	Val	Lys	Leu	Asn	Arg	Glu	Asp	Leu	Leu	Arg
385					390					395					400
Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	His	Gln	Ile	His	Leu
				405					410					415	
Gly	Glu	Leu	His	Ala	Ile	Leu	Arg	Arg	Gln	Glu	Asp	Phe	Tyr	Pro	Phe
			420					425					430		
Leu	Lys	Asp	Asn	Arg	Glu	Lys	Ile	Glu	Lys	Ile	Leu	Thr	Phe	Arg	Ile
		435					440					445			
Pro	Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Asn	Ser	Arg	Phe	Ala	Trp
	450					455					460				
Met	Thr	Arg	Lys	Ser	Glu	Glu	Thr	Ile	Thr	Pro	Trp	Asn	Phe	Glu	Glu
465					470					475					480
Val	Val	Asp	Lys	Gly	Ala	Ser	Ala	Gln	Ser	Phe	Ile	Glu	Arg	Met	Thr
				485					490					495	
Asn	Phe	Asp	Lys	Asn	Leu	Pro	Asn	Glu	Lys	Val	Leu	Pro	Lys	His	Ser
			500					505					510		
Leu	Leu	Tyr	Glu	Tyr	Phe	Thr	Val	Tyr	Asn	Glu	Leu	Thr	Lys	Val	Lys
		515					520					525			
Tyr	Val	Thr	Glu	Gly	Met	Arg	Lys	Pro	Ala	Phe	Leu	Ser	Gly	Glu	Gln
	530					535						540			
Lys	Lys	Ala	Ile	Val	Asp	Leu	Leu	Phe	Lys	Thr	Asn	Arg	Lys	Val	Thr
545					550					555					560
Val	Lys	Gln	Leu	Lys	Glu	Asp	Tyr	Phe	Lys	Lys	Ile	Glu	Cys	Phe	Asp
				565					570					575	
Ser	Val	Glu	Ile	Ser	Gly	Val	Glu	Asp	Arg	Phe	Asn	Ala	Ser	Leu	Gly
			580					585					590		
Thr	Tyr	His	Asp	Leu	Leu	Lys	Ile	Ile	Lys	Asp	Lys	Asp	Phe	Leu	Asp
		595					600					605			
Asn	Glu	Glu	Asn	Glu	Asp	Ile	Leu	Glu	Asp	Ile	Val	Leu	Thr	Leu	Thr
	610					615					620				
Leu	Phe	Glu	Asp	Arg	Glu	Met	Ile	Glu	Glu	Arg	Leu	Lys	Thr	Tyr	Ala
625					630					635					640
His	Leu	Phe	Asp	Asp	Lys	Val	Met	Lys	Gln	Leu	Lys	Arg	Arg	Arg	Tyr
				645					650					655	
Thr	Gly	Trp	Gly	Arg	Leu	Ser	Arg	Lys	Leu	Ile	Asn	Gly	Ile	Arg	Asp

			660				665				670				
Lys	Gln	Ser	Gly	Lys	Thr	Ile	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Gly	Phe
		675					680					685			
Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ser	Leu	Thr	Phe
	690					695					700				
Lys	Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val	Ser	Gly	Gln	Gly	Asp	Ser	Leu
705					710					715					720
His	Glu	His	Ile	Ala	Asn	Leu	Ala	Gly	Ser	Pro	Ala	Ile	Lys	Lys	Gly
			725						730					735	
Ile	Leu	Gln	Thr	Val	Lys	Val	Val	Asp	Glu	Leu	Val	Lys	Val	Met	Gly
			740					745					750		
Arg	His	Lys	Pro	Glu	Asn	Ile	Val	Ile	Glu	Met	Ala	Arg	Glu	Asn	Gln
		755					760					765			
Thr	Thr	Gln	Lys	Gly	Gln	Lys	Asn	Ser	Arg	Glu	Arg	Met	Lys	Arg	Ile
	770					775					780				
Glu	Glu	Gly	Ile	Lys	Glu	Leu	Gly	Ser	Gln	Ile	Leu	Lys	Glu	His	Pro
785					790					795					800
Val	Glu	Asn	Thr	Gln	Leu	Gln	Asn	Glu	Lys	Leu	Tyr	Leu	Tyr	Tyr	Leu
			805					810						815	
Gln	Asn	Gly	Arg	Asp	Met	Tyr	Val	Asp	Gln	Glu	Leu	Asp	Ile	Asn	Arg
		820						825					830		
Leu	Ser	Asp	Tyr	Asp	Val	Asp	His	Ile	Val	Pro	Gln	Ser	Phe	Leu	Lys
	835						840					845			
Asp	Asp	Ser	Ile	Asp	Asn	Lys	Val	Leu	Thr	Arg	Ser	Asp	Lys	Asn	Arg
	850					855					860				
Gly	Lys	Ser	Asp	Asn	Val	Pro	Ser	Glu	Glu	Val	Val	Lys	Lys	Met	Lys
865					870					875					880
Asn	Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	Leu	Ile	Thr	Gln	Arg	Lys
			885					890						895	
Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Ser	Glu	Leu	Asp
		900						905					910		
Lys	Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln	Ile	Thr
	915						920					925			
Lys	His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	Met	Asn	Thr	Lys	Tyr	Asp
	930					935					940				
Glu	Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	Val	Ile	Thr	Leu	Lys	Ser
945					950					955					960
Lys	Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	Gln	Phe	Tyr	Lys	Val	Arg
			965					970						975	
Glu	Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ala	Val
		980						985					990		
Val	Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	Lys	Leu	Glu	Ser	Glu	Phe
	995						1000					1005			
Val	Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	Arg	Lys	Met	Ile	Ala	Lys
	1010					1015					1020				
Ser	Glu	Gln	Glu	Ile	Gly	Lys	Ala	Thr	Ala	Lys	Tyr	Phe	Phe	Tyr	Ser
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Asn	Ile	Met	Asn	Phe	Phe	Lys	Thr	Glu	Ile	Thr	Leu	Ala	Asn	Gly	Glu
			1045						1050					1055	
Ile	Arg	Lys	Arg	Pro	Leu	Ile	Glu	Thr	Asn	Gly	Glu	Thr	Gly	Glu	Ile

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Val	Trp	Asp	Lys	Gly	Arg	Asp	Phe	Ala	Thr	Val	Arg	Lys	Val	Leu	Ser
	1075						1080						1085		
Met	Pro	Gln	Val	Asn	Ile	Val	Lys	Lys	Thr	Glu	Val	Gln	Thr	Gly	Gly
	1090						1095						1100		
Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	Arg	Asn	Ser	Asp	Lys	Leu	Ile
1105					1110					1115					1120
Ala	Arg	Lys	Lys	Asp	Trp	Asp	Pro	Lys	Lys	Tyr	Gly	Gly	Phe	Asp	Ser
			1125						1130					1135	
Pro	Thr	Val	Ala	Tyr	Ser	Val	Leu	Val	Val	Ala	Lys	Val	Glu	Lys	Gly
			1140				1145						1150		
Lys	Ser	Lys	Lys	Leu	Lys	Ser	Val	Lys	Glu	Leu	Leu	Gly	Ile	Thr	Ile
		1155					1160						1165		
Met	Glu	Arg	Ser	Ser	Phe	Glu	Lys	Asn	Pro	Ile	Asp	Phe	Leu	Glu	Ala
	1170						1175					1180			
Lys	Gly	Tyr	Lys	Glu	Val	Lys	Lys	Asp	Leu	Ile	Ile	Lys	Leu	Pro	Lys
1185					1190					1195					1200
Tyr	Ser	Leu	Phe	Glu	Leu	Glu	Asn	Gly	Arg	Lys	Arg	Met	Leu	Ala	Ser
			1205						1210					1215	
Ala	Gly	Glu	Leu	Gln	Lys	Gly	Asn	Glu	Leu	Ala	Leu	Pro	Ser	Lys	Tyr
			1220					1225					1230		
Val	Asn	Phe	Leu	Tyr	Leu	Ala	Ser	His	Tyr	Glu	Lys	Leu	Lys	Gly	Ser
	1235						1240					1245			
Pro	Glu	Asp	Asn	Glu	Gln	Lys	Gln	Leu	Phe	Val	Glu	Gln	His	Lys	His
	1250						1255					1260			
Tyr	Leu	Asp	Glu	Ile	Ile	Glu	Gln	Ile	Ser	Glu	Phe	Ser	Lys	Arg	Val
1265					1270					1275					1280
Ile	Leu	Ala	Asp	Ala	Asn	Leu	Asp	Lys	Val	Leu	Ser	Ala	Tyr	Asn	Lys
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His	Arg	Asp	Lys	Pro	Ile	Arg	Glu	Gln	Ala	Glu	Asn	Ile	Ile	His	Leu
		1300					1305					1310			
Phe	Thr	Leu	Thr	Asn	Leu	Gly	Ala	Pro	Ala	Ala	Phe	Lys	Tyr	Phe	Asp
		1315					1320					1325			
Thr	Thr	Ile	Asp	Arg	Lys	Arg	Tyr	Thr	Ser	Thr	Lys	Glu	Val	Leu	Asp
	1330						1335					1340			
Ala	Thr	Leu	Ile	His	Gln	Ser	Ile	Thr	Gly	Leu	Tyr	Glu	Thr	Arg	Ile
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<223> TRAC target sequence 2

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<210> 164

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<212> DNA

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<223> TRBC target sequence 2

<400> 164

ggcctcggcg ctgacgatct 20

<210> 165

<211> 23

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<223> TRAC target sequence with PAM 3

<400> 165

gagaatcaaaa atcgggtgaat agg 23

<210> 166

<211> 23

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<223> TRAC target sequence with PAM 4

<400> 166

ttcaaaacct gtcagtgaatt ggg 23

<210> 167

<211> 23

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<210> 168

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 <210> 184
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 <210> 186
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23

<210> 187

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<210> 189

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23

<210> 191

<211> 23
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 <210> 192
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 <400> 192
 ccactttcag gaggaggatt cgg 23

 <210> 193
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 <400> 193
 ctgacaggtt ttgaaagttt agg 23

 <210> 194
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 <400> 200
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 <210> 201
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 <400> 201
 acacggcagg gtcagggttc tgg 23

 <210> 202
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 <400> 202
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 <210> 203
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 <213> Artificial Sequence

 <220>
 <223> TRAC target sequence with PAM 41

 <400> 203
 ctggggaaga aggtgtcttc tgg 23

 <210> 204
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC target sequence with PAM 42

<400> 204	
tcctcctcct gaaagtggcc ggg	23
<210> 205	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> TRAC target sequence with PAM 43	
<400> 205	
ttaatctgct catgacgctg cgg	23
<210> 206	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> TRAC target sequence with PAM 44	
<400> 206	
acccggccac tttcaggagg agg	23
<210> 207	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> TRAC target sequence with PAM 45	
<400> 207	
ttcttcccca gcccaggtaa ggg	23
<210> 208	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> TRAC target sequence with PAM 46	
<400> 208	
cttacctggg ctggggaaga agg	23
<210> 209	
<211> 23	
<212> DNA	

<213> Artificial Sequence

<220>

<223> TRAC target sequence with PAM 47

<400> 209

gacaccttct tccccagccc agg 23

<210> 210

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC target sequence with PAM 48

<400> 210

gctgtggtcc agctgaggtg agg 23

<210> 211

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC target sequence with PAM 49

<400> 211

ccgaatcctc ctctgaaag tgg 23

<210> 212

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> TRBC target sequence with PAM 3

<400> 212

gctgtcaagt ccagttctac ggg 23

<210> 213

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC ZFN target sequence 1

<400> 213

ctatggactt caagagcaac agtgctgt 28

<210> 214

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC ZFN target sequence 2

<400> 214

ctcatgtcta gcacagtttt gtctgtga 28

<210> 215

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC ZFN target sequence 3

<400> 215

gtgctgtggc ctggagcaac aaatctga 28

<210> 216

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC ZFN target sequence 4

<400> 216

ttgctcttga agtccataga cctcatgt 28

<210> 217

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC ZFN target sequence 5

<400> 217

ctgtggcctg gagcaacaaa tctgact 27

<210> 218

<211> 28

<212> DNA

<213> Artificial Sequence

<220>
 <223> TRAC ZFN target sequence 6

 <400> 218
 ctgttgctct tgaagtccat agacctca 28

 <210> 219
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 7

 <400> 219
 ctgtggcctg gagcaacaaa tctgactt 28

 <210> 220
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 8

 <400> 220
 ctgactttgc atgtgcaaac gccttcaa 28

 <210> 221
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 9

 <400> 221
 ttgttgctcc aggccacagc actgttgc 28

 <210> 222
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 10

 <400> 222
 tgaaagtggc cgggtttaat ctgctcat 28

<210> 223
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 11

 <400> 223
 aggaggattc ggaacccaat cactgaca 28

 <210> 224
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAC ZFN target sequence 12

 <400> 224
 gaggaggatt cggaacccaa tcactgac 28

 <210> 225
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRBC ZFN target sequence 1

 <400> 225
 ccgtagaact ggacttgaca gcggaagt 28

 <210> 226
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRBC ZFN target sequence 2

 <400> 226
 tctcggagaa tgacgagtgg acccagga 28

 <210> 227
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> TRAC 50 bp 5' Homology Arm

<400> 227

agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 50

<210> 228

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 100 bp 5' Homology Arm

<400> 228

ctgatcctct tgtccacag atatccagaa ccctgaccct gccgtgtacc agctgagaga 60
ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 100

<210> 229

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 200 bp 5' Homology Arm

<400> 229

gtgacttgcc agccccacag agccccgccc ttgtccatca ctggcatctg gactccagcc 60
tggtttgggg caaagaggga aatgagatca tgtcctaacc ctgatcctct tgtccacag 120
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 180
ctgtctgcct attcaccgat 200

<210> 230

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 300 bp 5' Homology Arm

<400> 230

cctcttgccc aagattgata gcttgtgcct gtccctgagt cccagtccat cagagcagc 60
tggtttctaa gatgctatct cccgtataaa gcatgagacc gtgacttgcc agccccacag 120
agccccgccc ttgtccatca ctggcatctg gactccagcc tggtttgggg caaagaggga 180
aatgagatca tgtcctaacc ctgatcctct tgtccacag atatccagaa ccctgaccct 240
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 300

<210> 231

<211> 400

<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 400 bp 5' Homology Arm

<400> 231
attaaataaa agaataagca gtattattaa gtagccctgc atttcagggtt tccttgagtg 60
gcaggccagg cctggccgtg aacgttcact gaaatcatgg cctcttggcc aagattgata 120
gcttgtgcct gtccctgagt cccagtccat cacgagcagc tggtttctaa gatgctat 180
cccgtataaa gcatgagacc gtgacttgcc agccccacag agccccgccc ttgtccatca 240
ctggcatctg gactccagcc tgggttgggg caaagaggga aatgagatca tgtcctaacc 300
ctgatcctct tgtcccacag atatccagaa ccctgaccct gccgtgtacc agctgagaga 360
ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 400

<210> 232
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 500 bp 5' Homology Arm

<400> 232
ctccagattc caagatgtac agtttgcttt gctgggcctt tttcccatgc ctgcctttac 60
tctgccagag ttatattgct ggggttttga agaagatcct attaaataaa agaataagca 120
gtattattaa gtagccctgc atttcagggtt tccttgagtg gcaggccagg cctggccgtg 180
aacgttcact gaaatcatgg cctcttggcc aagattgata gcttgtgcct gtccctgagt 240
cccagtccat cacgagcagc tggtttctaa gatgctat 300
gtgacttgcc agccccacag agccccgccc ttgtccatca ctggcatctg gactccagcc 360
tgggttgggg caaagaggga aatgagatca tgtcctaacc ctgatcctct tgtcccacag 420
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 480
ctgtctgcct attcaccgat 500

<210> 233
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 600 bp 5' Homology Arm

<400> 233
agagagcaat ctcttggtta tgtgatagat ttcccaactt aatgccaaca taccataaac 60
ctcccattct gctaattgcc agcctaagtt ggggagacca ctccagattc caagatgtac 120
agtttgcttt gctgggcctt tttcccatgc ctgcctttac tctgccagag ttatattgct 180
gggggttttga agaagatcct attaaataaa agaataagca gtattattaa gtagccctgc 240
atttcagggtt tccttgagtg gcaggccagg cctggccgtg aacgttcact gaaatcatgg 300
cctcttggcc aagattgata gcttgtgcct gtccctgagt cccagtccat cacgagcagc 360
tggtttctaa gatgctat 420

agccccgccc ttgtccatca ctggcatctg gactccagcc tgggttgggg caaagagggga 480
aatgagatca tgtcctaacc ctgatcctct tgtcccacag atatccagaa ccctgaccct 540
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 600

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 50 bp 3' Homology Arm

<400> 234

tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat 50

<210> 235

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 100 bp 3' Homology Arm

<400> 235

tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca 100

<210> 236

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 200 bp 3' Homology Arm

<400> 236

tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg 200

<210> 237

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 300 bp 3' Homology Arm

<400> 237

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tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggg gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctgggtca atgatgtcta aaactcctct gattggtggt 300
```

<210> 238

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 400 bp 3' Homology Arm

<400> 238

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tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggg gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctgggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttggtc 360
tggcagtcca gagaatgaca cgggaaaaaaa gcagatgaag 400
```

<210> 239

<211> 500

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 500 bp 3' Homology Arm

<400> 239

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tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggg gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctgggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttggtc 360
tggcagtcca gagaatgaca cgggaaaaaaa gcagatgaag agaaggtggc aggagagggc 420
acgtggccca gcctcagtct ctccaactga gttcctgcct gcctgccttt gctcagactg 480
tttggcccctt actgctcttc 500
```

<210> 240

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAC 600 bp 3' Homology Arm

<400> 240

```
tttgattctc aaacaaatgt gtcacaaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgagggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcc acaaaaccct ctttttacta agaaacagtg agccttggtc 360
tggcagtcca gagaatgaca cgggaaaaaaa gcagatgaag agaagggtggc aggagagggc 420
acgtggccca gcctcagtct ctccaactga gttcctgcct gcctgccttt gctcagactg 480
tttggccctt actgctcttc taggcctcat tctaagcccc ttctccaagt tgcctctcct 540
tatttctccc tgtctgccaa aaaatctttc ccagctcact aagtcagtct cacgcagtca 600
```

<210> 241

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 241

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

<210> 242

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 242

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

<210> 243

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 243

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

<210> 244
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 244
Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 245
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 245
Pro Asn Ile Gln Lys Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
1 5 10 15
Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
20 25 30
Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
35 40 45
Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
50 55 60
Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
65 70 75 80

Ser	Ile	Ile	Pro	Ala	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
				85					90					95	
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn
			100					105					110		
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val
		115					120					125			
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
	130					135					140				

<210> 246
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCR alpha constant

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

<210> 247
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCR alpha constant

His	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
1				5					10					15	

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

<210> 248

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 248

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

<210> 249

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 249

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

<210> 250

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 250

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

	115		120		125
Gly	Phe Asn Leu Leu Met Thr	Leu Arg Leu Trp Ser	Ser		
	130		135		140

<210> 251
 <211> 177
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCR beta constant

<400> 251
 Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1 5 10 15
 Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30
 Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45
 Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
 50 55 60
 Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
 65 70 75 80
 Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
 85 90 95
 Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
 100 105 110
 Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
 115 120 125
 Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
 130 135 140
 Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
 145 150 155 160
 Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
 165 170 175
 Phe

<210> 252
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCR beta constant

<400> 252
 Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu

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

<210> 253

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR beta constant

<400> 253

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

Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu
130						135					140				
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
145					150					155					160
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys
				165					170						175
Asp	Ser	Arg	Gly												
			180												

<210> 254

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR beta constant

<400> 254

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

<210> 255

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR beta constant

<400> 255

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

<210> 256

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCR beta constant

<400> 256

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

			85				90				95				
Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln
			100				105				110				
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly
			115				120				125				
Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			130				135				140				
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
			145				150				155				
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys
			165				170				175				
Asp	Ser	Arg	Gly												
			180												