

SEQUENCE LISTING

<110> JUNO THERAPEUTICS, INC.
 GOLDFLESS, Stephen Jacob
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 BRANDT, Cameron
 CROFT, Alexandra
 HUSS, David Jeffrey

<120> T CELL RECEPTORS AND ENGINEERED
 CELLS EXPRESSING SAME

<130> 735042015140

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> 62/653,516

<151> 2018-04-05

<150> 62/739,145

<151> 2018-09-28

<160> 424

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 870

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Native with Codon Optimized Human
 Constant

<400> 1

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gttttccttc tttatgtttc catgaagatg ggaggcacta caggacaaaa cattgaccag 120
cccactgaga tgacagctac ggaagggtgcc attgtccaga tcaactgcac gtaccagaca 180
tctgggttca acgggctgtt ctggtaccag caacatgctg gcgaagcacc cacatttctg 240
tcttacaatg ttctggatgg tttggaggag aaaggctcgtt tttcttcatt ccttagtcgg 300
tctaaagggg acagttacct ccttttgaag gagctccaga tgaaagactc tgcctcttac 360
ctctgtgctg tgagagattg gggatatggt ggtgctacaa acaagctcat ctttggaact 420
ggcactctgc ttgtgtcca gccaaatatc cagaatccgg accccgcggg atatcaactg 480
cgcgactcaa aatcatccga taagagtgtc tgtttgttta ctgacttcga cagtcaaact 540
aatgtctctc agagcaaaga ttccgatgtc tacatcactg acaagtgcgt tctggatatg 600
cggagcatgg attttaagtc caactccgcc gtagcctggg ccaacaagtc agactttgcc 660
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tgtgcaaatg	ctttcaacaa	ctcaattatc	cctgaggaca	ctttctttcc	ttcaccggag	720
tcctcatgcg	atgttaaact	ggtcgaaaaa	tcttttgaga	cggatacgaa	cctcaacttc	780
caaaatttga	gcgttattgg	ctttaggatt	ctgcttctca	aggttgcggg	gttcaatctc	840
ctgatgacgt	tgcggctttg	gagcagctaa				870

<210> 2

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Native with Codon Optimized Mouse
Constant

<400> 2

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gttttccttc	tttatgtttc	catgaagatg	ggaggcacta	caggacaaaa	cattgaccag	120
cccactgaga	tgacagctac	ggaagggtgcc	attgtccaga	tcaactgcac	gtaccagaca	180
tctgggttca	acgggctgtt	ctggtaccag	caacatgctg	gcgaagcacc	cacatttctg	240
tcttacaatg	ttctggatgg	tttggaggag	aaaggctcgtt	tttcttcatt	ccttagtcgg	300
tctaaagggg	acagttacct	ccttttgaag	gagctccaga	tgaaagactc	tgctctttac	360
ctctgtgctg	tgagagattg	gggatatggg	ggtgctacaa	acaagctcat	ctttggaact	420
ggcactctgc	ttgctgtcca	gccaaatatc	cagaatccgg	agcctgccgt	gtaccagctg	480
aaggacccac	ggagccagga	tagcaccctg	tgctgttca	ccgactttga	ttctcagatc	540
aacgtgcccc	agaccatgga	gagcggcacc	ttcatcacag	acaagtgcgt	gctggatatg	600
aaggccatgg	acagcaagtc	caacggcgcc	atcgctggg	ccaatcagac	atctttcacc	660
tgccaggata	tctttaagga	gacaaatgcc	acctatcctt	cctctgacgt	gccatgtgat	720
gccaccctga	cagagaagag	cttcgagacc	gacatgaacc	tgaattttca	gaatctgctc	780
gtgattgtcc	tgagaatcct	gctgctgaag	gtggccggct	ttaacctgct	gatgaccctg	840
aggctgtgga	gctcctga					858

<210> 3

<211> 907

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Codon-Optimized with Codon Optimized
Human Constant

<400> 3

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gtgttcctgc	tgtacgtgtc	catgaagatg	ggcggcacca	ccggccagaa	catcgatcag	120
cctacagaga	tgaccgccac	cgagggcgcc	atcgtgcaga	tcaattgcac	ctaccagacc	180
agcggcttca	acggcctgtt	ctggtatcag	cagcatgccg	gcgaggcccc	taccttcctg	240
agctacaatg	tgctggacgg	cctggaagag	aagggcagat	tcagcagctt	cctgtccaga	300
agcaagggct	acagctacct	gctgctgaaa	gaactgcaga	tgaaggacag	cgcttcctac	360
ctgtgcgccg	ttagagattg	gggatacggc	ggagccacca	acaagctgat	ctttggcaca	420
ggcacactgc	tggccgtgca	gcctaatatc	cagaatccgg	agcctgccgt	gtaccagctg	480
aaatatccag	aatccggacc	ccgcggtata	tcaactgcgc	gactcaaaa	catccgataa	540

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gagtgtctgt ttgtttactg acttcgacag tcaaactaat gtctctcaga gcaaagattc 600
cgatgtctac atcactgaca agtgcgttct ggatatgcgg agcatggatt ttaagtccaa 660
ctccgccgta gcctgggtcca acaagtcaga ctttgcctgt gcaaatgctt tcaacaactc 720
aattatccct gaggacactt tctttccttc accggagtcc tcatgcatg ttaaactggg 780
cgaaaaatct tttagacgga atacgaacct caacttccaa aatttgagcg ttattggctt 840
taggattctg cttctcaagg ttgcgggggt caatctcctg atgacgttgc ggctttggag 900
cagctaa
907

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<210> 4

<211> 895

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Codon-Optimized with Codon Optimized
Mouse Constant

<400> 4

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atggctcaag agctgggcat gcagtgtcag gccagaggaa tcctgcagca gatgtgggga 60
gtgttcctgc tgtacgtgtc catgaagatg ggcggcacca ccggccagaa catcgatcag 120
cctacagaga tgaccgccac cgagggcgcc atcgtgcaga tcaattgcac ctaccagacc 180
agcggcttca acggcctgtt ctggtatcag cagcatgccg gcgaggcccc taccttcctg 240
agctacaatg tgctggacgg cctggaagag aagggcagat tcagcagctt cctgtccaga 300
agcaagggtc acagctacct gctgctgaaa gaactgcaga tgaaggacag cgcttcctac 360
ctgtgcgccg ttagagattg gggatacggc ggagccacca acaagctgat ctttggcaca 420
ggcacactgc tggccgtgca gcctaatac cagaatccgg agcctgccgt gtaccagctg 480
aaatatccag aatccggagc ctgccgtgta ccagctgaag gacccacgga gccaggatag 540
caccctgtgc ctgttcaccg actttgattc tcagatcaac gtgccaaga ccatggagag 600
cggcaccttc atcacagaca agtgcgtgct ggatatgaag gccatggaca gcaagtccaa 660
cggcgccatc gcctgggtcca atcagacatc tttcacctgc caggatatct ttaaggagac 720
aaatgccacc tatccttcct ctgacgtgcc atgtgatgcc accctgacag agaagagctt 780
cgagaccgac atgaacctga attttcagaa tctgctcgtg attgtcctga gaatcctgct 840
gctgaagggtg gccggcttta acctgctgat gaccctgagg ctgtggagct cctga 895

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<210> 5

<211> 255

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha with Codon Optimized Human Constant

<400> 5

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

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

<210> 6

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha with Codon Optimized Mouse Constant

<400> 6

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

Gln	Pro	Asn	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp
		115					120					125			
Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser
	130					135					140				
Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp
145					150					155					160
Lys	Cys	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala
			165						170					175	
Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys
		180						185					190		
Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr
		195					200					205			
Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn
	210					215					220				
Leu	Leu	Val	Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe
225					230					235					240
Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser					
				245					250						

<210> 7

<211> 289

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 7

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

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

Ser

<210> 8

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 8

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

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

<210> 9

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha variable region

<400> 9

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

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha CDR1

<400> 10

Thr Ser Gly Phe Asn Gly
1 5

<210> 11

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha CDR2

<400> 11

Asn Val Leu Asp Gly Leu
1 5

<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha CDR3

<400> 12

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

<210> 13

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Signal peptide

<400> 13

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

<210> 14
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha Human constant region

<400> 14
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> 15
<211> 137
<212> PRT
<213> Mus musculus

<220>
<223> Alpha Mouse constant region

<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 Cys
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	Leu				
			100					105					110						
Val	Ile	Val	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> 957
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 56 Beta Native with Codon Optimized Human Constant

<400> 16
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 gcaggctctt caaatgccgg cgatcatgcag aaccaagac acctgggtcag gaggagggga 120
 caggaggcaa gactgagatg cagcccaatg aaaggacaca gtcatgttta ctggtatcgg 180
 cagctccag aggaagggtct gaaattcatg gtttatctcc agaaagaaaa tatcatagat 240
 gagtcaggaa tgccaaagga acgattttct gctgaatttc ccaaagaggg cccagcatc 300
 ctgaggatcc agcaggtagt gcgaggagat tcggcagctt atttctgtgc cagctcacca 360
 gacgaaagca gggatagcaa tcagcccccag catitttggtg atgggactcg actctccatc 420
 ctagaggacc tgaataaggt gttccccctt gaggtggccg tgtttgagcc aagcgaggcc 480
 gagatctccc acaccagaa ggccaccctg gtgtgcctgg caaccggctt ctttccgat 540
 cacgtggagc tgtcctgggt ggtgaacggc aaggaggtgc actctggcgt gtgcacagac 600
 ccacagcccc tgaaggagca gcctgccctg aatgattccc gctattgtct gtcctctcgg 660
 ctgagagtgt ctgccacctt ttggcagaac ccacggaatc acttcagatg ccagggtgcag 720
 ttttacggcc tgtctgagaa cgacgagtg acccaggatc gggccaagcc tgtgacacag 780
 atcgtgagcg cggaagcatg gggcagagcc gactgtggct tcaccagcgt gtcctatcag 840
 cagggcggtgc tgtccgccac catcctgtac gagatcctgc tgggcaaggc cacactgtat 900
 gccgtgctgg tgtctgccct ggtgctgatg gccatggtga agagaaaaga cttctaa 957

<210> 17
 <211> 945
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 56 Beta Native with Codon Optimized Mouse Constant

<400> 17
 atggccaact ctgctatgga caccagagta ctctgctgtg cggatcatctg tcttctgggg 60
 gcaggctctt caaatgccgg cgatcatgcag aaccaagac acctgggtcag gaggagggga 120
 caggaggcaa gactgagatg cagcccaatg aaaggacaca gtcatgttta ctggtatcgg 180
 cagctccag aggaagggtct gaaattcatg gtttatctcc agaaagaaaa tatcatagat 240

gagtcaggaa	tgccaaagga	acgattttct	gctgaatttc	ccaaagaggg	ccccagcatc	300
ctgaggatcc	agcaggtagt	gcgaggagat	tcggcagctt	atttctgtgc	cagctcacca	360
gacgaaaagca	gggatagcaa	tcagccccag	catttttggtg	atgggactcg	actctccatc	420
ctagaggacc	tgcgcaatgt	gacccccct	aaggtgtccc	tgtttgagcc	ctctaaggcc	480
gagatcgcca	acaagcagaa	ggccaccctg	gtgtgcctgg	ccagaggctt	cttccctgat	540
cacgtggagc	tgagctgggtg	ggtgaatggc	aaggagggtgc	actccggcgt	gtgcaccgac	600
ccacaggcct	acaaggagtc	caactactct	tattgtctgt	cctctaggct	gcgcgtgagc	660
gccacattct	ggcacaaccc	tcggaatcac	ttcagatgcc	aggtgcagtt	tcacggcctg	720
agcgaggagg	ataagtggcc	agagggtccc	ccaaagcccg	tgaccagaa	tatctctgcc	780
gaggcatggg	gcagggccga	ctgtggaatc	acctccgcct	cttatcagca	gggcgtgctg	840
tccgccacaa	tcctgtacga	gatcctgctg	ggcaaggcca	ccctgtatgc	cgctgctggg	900
tccacactgg	tggtcatggc	catggtgaag	cgcaagaaca	gctaa		945

<210> 18

<211> 966

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Beta Codon-Optimized with Codon Optimized
Human Constant

<400> 18

atgggaccca	tggccaatag	cgccatggat	accagagtgc	tgtgctgcgc	cgatgatctgt	60
ctgcttggag	ccggactgtc	taatgccggc	gtgatgcaga	accccagaca	cctcgttcgg	120
agaagaggcc	aagaggccag	actgagatgc	agccctatga	agggccacag	ccacgtgtac	180
tggtacagac	agctgcctga	agagggcctg	aagttcatgg	tgtacctgca	gaaagagaac	240
atcatcgacg	agagcggcat	gccccaaagag	cggttctctg	ccgagtttcc	caaagagggc	300
cccagcatcc	tgagaatcca	gcaggttgtg	cggggagata	gcgccgccta	cttttgtgcc	360
agctctcccc	atgagagccg	ggactctaata	cagcctcagc	actttggcga	cggcaccagg	420
ctgtctattc	tcgaggacct	gaataagggtg	ttccccctg	aggtggccgt	gtttgagcca	480
agcgaggccg	agatctccca	caccagaag	gccaccctgg	tgtgcctggc	aaccggcttc	540
tttcccgatc	acgtggagct	gtcctgggtg	gtgaacggca	aggagggtgca	ctctggcgtg	600
tgcacagacc	cacagcccct	gaaggagcag	cctgccctga	atgattcccg	ctattgtctg	660
tcctctcggc	tgagagtgtc	tgccaccttt	tggcagaacc	cacggaatca	cttcagatgc	720
caggtgcagt	tttacggcct	gtctgagaac	gacgagtgga	cccaggatcg	ggccaagcct	780
gtgacacaga	tcgtgagcgc	ggaagcatgg	ggcagagccg	actgtggctt	caccagcgtg	840
tcctatcagc	agggcgtgct	gtccgccacc	atcctgtacg	agatcctgct	gggcaaggcc	900
acactgtatg	ccgtgctggg	gtctgccctg	gtgctgatgg	ccatgggtgaa	gagaaaaagac	960
ttctaa						966

<210> 19

<211> 954

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Beta Codon-Optimized with Codon Optimized
Mouse Constant

<400> 19

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atgggaccca tggccaatag cgccatggat accagagtgc tgtgctgcgc cgtgatctgt 60
ctgcttggag ccggactgtc taatgccggc gtgatgcaga accccagaca cctcgttcgg 120
agaagaggcc aagaggccag actgagatgc agccctatga agggccacag ccacgtgtac 180
tggtagacag agctgcctga agagggcctg aagttcatgg tgtacctgca gaaagagaac 240
atcatcgacg agagcggcat gccc aaagag cggttctctg ccgagtttcc caaagagggc 300
cccagcatcc tgagaatcca gcaggttgtg cggggagata gcgccgccta cttttgtgcc 360
agctctcccc atgagagccg ggactctaata cagcctcagc actttggcga cggcaccagg 420
ctgtctattc tcgaggacct gcgcaatgtg acccccccta aggtgtccct gtttgagccc 480
tctaaggccg agatcgccaa caagcagaag gccaccctgg tgtgcctggc cagaggcttc 540
ttccctgata acgtggagct gagctggtgg gtgaatggca aggaggtgca ctccggcggtg 600
tgcaccgacc cacaggccta caaggagtcc aactactctt attgtctgtc ctctaggctg 660
cgcgtgagcg ccacattctg gcacaaccct cggaatcact tcagatgcca ggtgcagttt 720
cacggcctga gcgaggagga taagtggcca gagggctccc caaagccgtg gaccagaat 780
atctctgccg aggcattggg cagggccgac tgtggaatca cctccgcctc ttatcagcag 840
ggcgtgctgt ccgccacaat cctgtacgag atcctgctgg gcaaggccac cctgtatgcc 900
gtgctggtgt ccacactggt ggtcatggcc atggtgaagc gcaagaacag ctaa 954
```

<210> 20

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta with Codon Optimized Human Constant

<400> 20

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

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

<210> 21

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta with Codon Optimized Mouse Constant

<400> 21

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

Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg
	195						200					205			
Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu
	210					215					220				
Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly
225					230					235					240
Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			245						250					255	
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
		260					265						270		
Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys
	275					280						285			
Asn	Ser														
	290														

<210> 22

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta with Codon Optimized Human Constant
and signal peptide

<400> 22

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

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

<210> 23
 <211> 314
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 56 Beta with Codon Optimized Mouse Constant
 and signal peptide

<400> 23

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

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

<210> 24

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta variable region

<400> 24

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

<210> 25

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta CDR1

<400> 25

Lys Gly His Ser His
1 5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta CDR2

<400> 26

Leu Gln Lys Glu Asn Ile
1 5

<210> 27

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta CDR3

<400> 27

Ala Ser Ser Pro Asp Glu Ser Arg Asp Ser Asn Gln Pro Gln His
1 5 10 15

<210> 28

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Beta signal peptide

<400> 28

Met Ala Asn Ser Ala Met Asp Thr Arg Val Leu Cys Cys Ala Val Ile
1 5 10 15
Cys Leu Leu Gly Ala Gly Leu Ser
20

<210> 29
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<223> Beta human constant region

<400> 29
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> 30
<211> 173
<212> PRT
<213> Mus musculus

<220>
<223> Beta mouse constant region

<400> 30
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	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			
			165						170						

<210> 31
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P2A

<400> 31
 ggctccggag caaccaattt cagcctgctg aagcaggccg gcgatgtgga ggagaatcct 60
 ggccca 66

<210> 32
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P2A

<400> 32
 Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
 1 5 10 15
 Glu Glu Asn Pro Gly Pro
 20

<210> 33
 <211> 1026
 <212> DNA
 <213> Artificial Sequence

<220>

<223> TCR 56 Native full sequence with human constant

<400> 33

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gaggacctga ataaggtgtt cccccctgag gtggccgtgt ttgagccaag cgaggccgag 60
atctcccaca cccagaaggc caccctggtg tgcctggcaa ccggcttctt tcccgatcac 120
gtggagctgt cctggtgggt gaacggcaag gaggtgact ctggcgtgtg cacagacca 180
cagcccctga aggagcagcc tgccctgaat gattcccgtt attgtctgtc ctctcggtg 240
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tacggcctgt ctgagaacga cgagtggacc caggatcggg ccaagcctgt gacacagatc 360
gtgagcgcgg aagcatgggg cagagccgac tgtggcttca ccagcgtgtc ctatcagcag 420
ggcgtgctgt ccgccaccat cctgtacgag atcctgctgg gcaaggccac actgtatgcc 480
gtgctggtgt ctgccctggt gctgatggcc atggtgaaga gaaaagactt ctaaggctcc 540
ggagcaacca atttcagcct gctgaagcag gccggcgtat tggaggagaa tcctggccca 600
aatatccaga atccggaccc cgcggtatat caactgcgcg actcaaaatc atccgataag 660
agtgtctgtt tgtttactga cttcgacagt caaactaatg tctctcagag caaagattcc 720
gatgtctaca tcactgacaa gtgcgttctg gatatgcgga gcatggattt taagtccaac 780
tccgccgtag cctggtccaa caagtcagac tttgcctgtg caaatgcttt caacaactca 840
attatccctg aggacacttt ctttccttca ccggagtcct catgcgatgt taaactggtc 900
gaaaaatctt ttgagacgga tacgaacctc aacttccaaa atttgagcgt tattggcttt 960
aggattctgc ttctcaaggt tgcgggggtc aatctcctga tgacgttgcg gctttggagc 1020
agctaa 1026
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<210> 34

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Nativefull sequence with mouse constant

<400> 34

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gcaggctctt caaatgccgg cgtcatgcag aaccaagac acctggtcag gaggagggga 120
caggaggcaa gactgagatg cagcccaatg aaaggacaca gtcatgttta ctggtatcgg 180
cagctcccag aggaaggtct gaaattcatg gtttatctcc agaaagaaaa tatcatagat 240
gagtcaggaa tgccaaagga acgattttct gctgaatttc ccaaagaggg cccagcatc 300
ctgaggatcc agcaggtagt gcgaggagat tcggcagctt atttctgtgc cagctcacca 360
gacgaaaagca gggatagcaa tcagccccag ctttttggtg atgggactcg actctccatc 420
ctagaggacc tgcgcaatgt gacccccctt aaggtgtccc tgtttgagcc ctctaaggcc 480
gagatcgcca acaagcagaa ggccaccctg gtgtgcctgg ccagaggctt cttccctgat 540
cacgtggagc tgagctggtg ggtgaatggc aaggaggtgc actccggcgt gtgcaccgac 600
ccacaggcct acaaggagtc caactactct tattgtctgt cctctaggct gcgcgtgagc 660
gccacattct ggcacaaccc tcggaatcac ttcagatgcc aggtgcagtt tcacggcctg 720
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gaggcatggg gcaggggcga ctgtggaatc acctccgcct cttatcagca gggcgtgctg 840
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tccacactgg tggatcatggc catggtgaag cgcaagaaca gctaaggctc cggagcaacc 960
aatttcagcc tgctgaagca ggccggcgtat gtggaggaga atcctggccc aatggctcag 1020
```

gaactgggaa	tgcagtgcc	ggctcgtggt	atcctgcagc	agatgtgggg	agttttcctt	1080
ctttatgttt	ccatgaagat	gggaggcact	acaggacaaa	acattgacca	gcccactgag	1140
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gttctggatg	gtttggagga	gaaaggctgt	ttttcttcat	tccttagtcg	gtctaaaggg	1320
tacagttacc	tccttttgaa	ggagctccag	atgaaagact	ctgcctctta	cctctgtgct	1380
gtgagagatt	ggggatatgg	tgggtgctaca	aacaagctca	tccttggaac	tggcactctg	1440
cttgctgtcc	agccaaatat	ccagaatccg	gagcctgccg	tgtaccagct	gaaggaccca	1500
cggagccagg	atagcaccct	gtgcctgttc	accgactttg	attctcagat	caacgtgccc	1560
aagaccatgg	agagcggcac	cttcatcaca	gacaagtgcg	tgctggatat	gaaggccatg	1620
gacagcaagt	ccaacggcgc	catcgctgg	tccaatcaga	catctttcac	ctgccaggat	1680
atctttaagg	agacaaatgc	cacctatcct	tcctctgacg	tgccatgtga	tgccaccctg	1740
acagagaaga	gcttcgagac	cgacatgaac	ctgaattttc	agaatctgct	cgtgattgtc	1800
ctgagaatcc	tgctgctgaa	ggtggccggc	tttaacctgc	tgatgaccct	gaggctgtgg	1860
agctcctga						1869

<210> 35

<211> 1939

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with human constant

<400> 35

atgggaccca	tggccaatag	cgccatggat	accagagtgc	tgtgctgcgc	cgtgatctgt	60
ctgcttggag	ccggactgtc	taatgccggc	gtgatgcaga	accccagaca	cctcgttcgg	120
agaagaggcc	aagaggccag	actgagatgc	agccctatga	agggccacag	ccacgtgtac	180
tggtagagac	agctgcctga	agagggcctg	aagtctcatgg	tgtacctgca	gaaagagaac	240
atcatcgacg	agagcggcat	gccc aaaagag	cggttctctg	ccgagtttcc	caaagagggc	300
cccagcatcc	tgagaatcca	gcaggttgtg	cggggagata	gcgccgccta	cttttgtgcc	360
agctctcccc	atgagagccg	ggactctaata	cagcctcagc	actttggcga	cggcaccagg	420
ctgtctattc	tcgaggacct	gaataagggtg	ttccccctg	aggtagccgt	gtttgagcca	480
agcaggcccg	agatctcca	caccagaag	gccaccctgg	tgtgcctggc	aaccggcttc	540
tttcccgatc	acgtggagct	gtcctgggtg	gtgaacggca	aggaggtgca	ctctggcgtg	600
tgcacagacc	cacagcccct	gaaggagcag	cctgccctga	atgattccc	ctattgtctg	660
tcctctcggc	tgagagtgtc	tgccaccttt	tggcagaacc	cacggaatca	cttcagatgc	720
cagggtgcagt	tttacggcct	gtctgagaac	gacgagtggg	cccaggatcg	ggccaagcct	780
gtgacacaga	tcgtgagcgc	ggaagcatgg	ggcagagccg	actgtggctt	caccagcgtg	840
tcctatcagc	agggcggtgct	gtccgccacc	atcctgtacg	agatcctgct	gggcaaggcc	900
acactgtatg	ccgtgctggt	gtctgccctg	gtgctgatgg	ccatggtgaa	gagaaaagac	960
ttctaaggct	ccggagcaac	caatttcagc	ctgctgaagc	aggccggcga	tgtggaggag	1020
aatcctggcc	caatggctca	agagctgggc	atgcagtgtc	aggccagagg	aatcctgcag	1080
cagatgtggg	gagtgttcct	gctgtacgtg	tccatgaaga	tgggcggcac	caccggccag	1140
aacatcgatc	agcctacaga	gatgaccgcc	accgaggcg	ccatcgtgca	gatcaattgc	1200
acctaccaga	ccagcggcct	caacggcctg	ttctggtatc	agcagcatgc	cggcgaggcc	1260
cctaccttcc	tgagctacaa	tgtgctggac	ggcctggaag	agaagggcag	attcagcagc	1320
ttcctgtcca	gaagcaaggg	ctacagctac	ctgctgctga	aagaactgca	gatgaaggac	1380
agcgcctcct	acctgtgcgc	cgtagagat	tggggatagc	gcggagccac	caacaagctg	1440

atctttggca	caggcacact	gctggccgtg	cagcctaata	tccagaatcc	ggagcctgcc	1500
gtgtaccagc	tgaatatcc	agaatccgga	ccccgcggtg	tatcaactgc	gcgactcaaa	1560
atcatccgat	aagagtgtct	gtttgtttac	tgacttcgac	agtcaaaacta	atgtctctca	1620
gagcaaaagat	tccgatgtct	acatcactga	caagtgcgtt	ctggatatgc	ggagcatgga	1680
ttttaagtcc	aactccgccg	tagcctgggtc	caacaagtca	gactttgcct	gtgcaaatgc	1740
tttcaacaac	tcaattatcc	ctgaggacac	tttctttcct	tcaccggagt	cctcatgcga	1800
tgtaaactg	gtcgaaaaat	cttttgagac	ggatacgaac	ctcaacttcc	aaaatttgag	1860
cgttattggc	tttaggattc	tgcttctcaa	ggttgcgggg	ttcaatctcc	tgatgacgtt	1920
gcggctttgg	agcagctaa					1939

<210> 36

<211> 1915

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with mouse constant

<400> 36

atgggaccca	tggccaatag	cgccatggat	accagagtgc	tgtgctgcgc	cgtgatctgt	60
ctgcttggag	ccggactgtc	taatgccggc	gtgatgcaga	accccagaca	cctcgttcgg	120
agaagaggcc	aagaggccag	actgagatgc	agccctatga	agggccacag	ccacgtgtac	180
tggtacagac	agctgcctga	agagggcctg	aagtcatggt	tgtacctgca	gaaagagaac	240
atcatcgacg	agagcggcat	gccccaaagag	cggttctctg	ccgagtttcc	caaagagggc	300
cccagcatcc	tgagaatcca	gcaggttgtg	cggggagata	gcgccgccta	cttttgtgcc	360
agctctcccc	atgagagccg	ggactctaata	cagcctcagc	actttggcga	cggcaccagg	420
ctgtctattc	tcgaggacct	gcgcaatgtg	accccccta	agggtgtccct	gtttgagccc	480
tctaaggccg	agatcgccaa	caagcagaag	gccaccctgg	tgtgcctggc	cagaggcttc	540
ttccctgatc	acgtggagct	gagctggtgg	gtgaatggca	aggaggtgca	ctccggcgtg	600
tgcaccgacc	cacaggccta	caaggagtcc	aactactctt	attgtctgtc	ctctaggctg	660
cgcgtgagcg	ccacattctg	gcacaaccct	cggaatcact	tcagatgcca	ggtgcagttt	720
cacggcctga	gcgaggagga	taagtggcca	gagggtctcc	caaagcccgt	gaccagaat	780
atctctgccg	aggcatgggg	cagggccgac	tgtggaatca	cctccgcctc	ttatcagcag	840
ggcgtgctgt	ccgccacaat	cctgtacgag	atcctgctgg	gcaaggccac	cctgtatgcc	900
gtgctggtgt	ccacactggt	ggtcatggcc	atggtgaagc	gcaagaacag	ctaaggctcc	960
ggagcaacca	atttcagcct	gctgaagcag	gccggcgtatg	tggaggagaa	tcctggccca	1020
atggctcaag	agctgggcat	gcagtgtcag	gccagaggaa	tcctgcagca	gatgtgggga	1080
gtgttcctgc	tgtacgtgtc	catgaagatg	ggcggcacca	ccggccagaa	catcgatcag	1140
cctacagaga	tgaccgccac	cgagggcgcc	atcgtgcaga	tcaattgcac	ctaccagacc	1200
agcggcttca	acggcctgtt	ctggtatcag	cagcatgccg	gcgaggcccc	taccttcctg	1260
agctacaatg	tgctggacgg	cctggaagag	aagggcagat	tcagcagctt	cctgtccaga	1320
agcaagggtc	acagctacct	gctgctgaaa	gaactgcaga	tgaaggacag	cgcttcctac	1380
ctgtgcgccg	ttagagattg	gggatacggc	ggagccacca	acaagctgat	ctttggcaca	1440
ggcacactgc	tggccgtgca	gcctaataatc	cagaatccgg	agcctgccgt	gtaccagctg	1500
aaatatccag	aatccggagc	ctgccgtgta	ccagctgaag	gacccacgga	gccaggatag	1560
caccctgtgc	ctgttcaccg	actttgattc	tcagatcaac	gtgcccaaga	ccatggagag	1620
cggcaccttc	atcacagaca	agtgcgtgct	ggatatgaag	gccatggaca	gcaagtccaa	1680
cggcgccatc	gcctgggtcca	atcagacatc	tttcacctgc	caggatatct	ttaaggagac	1740
aaatgccacc	tatccttcct	ctgacgtgcc	atgtgatgcc	accctgacag	agaagagctt	1800

cgagaccgac atgaacctga attttcagaa tctgctcgtg attgtcctga gaatcctgct 1860
gctgaagggtg gccggcttta acctgctgat gaccctgagg ctgtggagct cctga 1915

<210> 37

<211> 629

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Full sequence with human constant

<400> 37

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

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

<210> 38

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 Full sequence with mouse constant

<400> 38

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

370		375		380	
Gly Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn					
385		390		395	400
Gly Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu					
	405		410		415
Ser Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser					
	420		425		430
Phe Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu					
	435		440		445
Gln Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Val Arg Asp Trp Gly					
	450		455		460
Tyr Gly Gly Ala Thr Asn Lys Leu Ile Phe Gly Thr Gly Thr Leu Leu					
465		470		475	480
Ala Val Gln Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu					
	485		490		495
Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe					
	500		505		510
Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile					
	515		520		525
Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn					
	530		535		540
Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile					
545		550		555	560
Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp					
	565		570		575
Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe					
	580		585		590
Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala					
	595		600		605
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser					
610		615		620	

<210> 39

<211> 810

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha Native with Codon Optimized Human
Constant

<400> 39

```

atggtcctga aattctccgt gtccattctt tggattcagt tggcatgggt gagcaccag 60
ctgctggagc agagccctca gtttctaagc atccaagagg gagaaaatct cactgtgtac 120
tgcaactcct caagtgtttt ttccagctta caatgggtaca gacaggagcc tggggaaggt 180
cctgtcctcc tggtgacagt agttacgggt ggagaagtga agaagctgaa gagactaacc 240
tttcagtttg gtgatgcaag aaaggacagt tctctccaca tcactgcagc ccagcctggt 300
gatacaggcc tctacctctg tgcaggagct cgcaacttca acaaatttta ctttggatct 360
gggaccaaac tcaatgtaaa accaaatatt cagaatccgg accccgcggg atatcaactg 420

```

cgcgactcaa	aatcatccga	taagagtgtc	tgtttgttta	ctgacttcga	cagtcaaact	480
aatgtctctc	agagcaaaga	ttccgatgtc	tacatcactg	acaagtgcgt	tctggatatg	540
cggagcatgg	attttaagtc	caactccgcc	gtagcctggg	ccaacaagtc	agactttgcc	600
tgtgcaaatg	ctttcaacaa	ctcaattatc	cctgaggaca	ctttctttcc	ttcaccggag	660
tcctcatgcg	atgttaaact	ggtcgaaaaa	tcttttgaga	cggatacgaa	cctcaacttc	720
caaaatttga	gcgttattgg	ctttaggatt	ctgcttctca	aggttgcggg	gttcaatctc	780
ctgatgacgt	tgcggctttg	gagcagctaa				810

<210> 40

<211> 798

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha Native with Codon Optimized Mouse
Constant

<400> 40

atggctctga	aattctccgt	gtccattctt	tggattcagt	tggcatgggt	gagcaccag	60
ctgctggagc	agagccctca	gtttctaagc	atccaagagg	gagaaaatct	cactgtgtac	120
tgcaactcct	caagtgtttt	ttccagctta	caatggtaca	gacaggagcc	tggggaagg	180
cctgtcctcc	tgggtgacagt	agttacgggt	ggagaagtga	agaagctgaa	gagactaacc	240
tttcagtttg	gtgatgcaag	aaaggacagt	tctctccaca	tactgcagc	ccagcctgg	300
gatacaggcc	tctacctctg	tgcaggagct	cgcaacttca	acaaaattta	ctttggatct	360
gggaccaaac	tcaatgtaaa	acaaaatatc	cagaatccgg	agcctgccc	gtaccagctg	420
aaggacccac	ggagccagga	tagcaccctg	tgcctgttca	ccgactttga	ttctcagatc	480
aacgtgcccc	agaccatgga	gagcggcacc	ttcatcacag	acaagtgcgt	gctggatatg	540
aaggccatgg	acagcaagtc	caacggcgcc	atcgctggg	ccaatcagac	atctttcacc	600
tgccaggata	tctttaagga	gacaaatgcc	acctatcctt	cctctgacgt	gccatgtgat	660
gccaccctga	cagagaagag	cttcgagacc	gacatgaacc	tgaattttca	gaatctgctc	720
gtgattgtcc	tgagaatcct	gctgctgaag	gtggccggct	ttaacctgct	gatgaccctg	780
aggctgtgga	gctcctga					798

<210> 41

<211> 810

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha Codon-Optimized with Codon Optimized
Human Constant

<400> 41

atggtgctga	agttttctgt	gagcatcctg	tggattcagc	tggcctgggt	gtccaccag	60
ctcctggagc	agagccccc	gttcctgtcc	atccaggagg	gcgagaacct	gaccgtgtac	120
tgcaacagct	cttctgtctt	ttcatcactg	cagtgggtata	gacaagaacc	gggtgaagg	180
ccagtctgc	tgggtgaccg	cgtcaccggc	ggcgagggtga	agaagctaaa	gcgctgacg	240
ttccagttcg	gagacgcgcg	gaaggactcg	tcgctgcaca	tcaccgccgc	ccagcccggc	300
gacaccggcc	tgtacctgtg	cgctggcgcg	cgcaacttca	acaagttcta	cttcggcagc	360
ggcaccaagc	tgaacgtgaa	accgaatatc	cagaatccgg	accccgcggt	atatcaactg	420

```

cgcgactcaa aatcatccga taagagtgtc tgtttgttta ctgacttcga cagtcaaact 480
aatgtctctc agagcaaaga ttccgatgtc tacatcactg acaagtgcgt tctggatatg 540
cggagcatgg attttaagtc caactccgcc gtagcctggg ccaacaagtc agactttgcc 600
tgtgcaaatg ctttcaacaa ctcaattatc cctgaggaca ctttctttcc ttcaccggag 660
tcctcatgcg atgttaaact ggtcgaaaaa tcttttgaga cggatacgaa cctcaacttc 720
caaaatttga gcgttattgg ctttaggatt ctgcttctca aggttgcggg gttcaatctc 780
ctgatgacgt tgcggctttg gagcagctaa 810

```

<210> 42

<211> 798

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha Codon-Optimized with Codon Optimized
Mouse Constant

<400> 42

```

atgggtgctga agttttctgt gagcatcctg tggattcagc tggcctgggt gtccacccag 60
ctcctggagc agagcccca gttcctgtcc atccaggagg gcgagaacct gaccgtgtac 120
tgcaacagct cttctgtctt ttcatcactg cagtgggtata gacaagaacc ggggtgaagg 180
ccagtctgc tgggtgaccgt cgtcaccggc ggcgagggtga agaagctaaa gcgcctgacg 240
ttccagttcg gagacgcgcg gaaggactcg tcgctgcaca tcaccgccgc ccagcccggc 300
gacaccggcc tgtacctgtg cgctggcgcg cgcaacttca acaagttcta cttcggcagc 360
ggcaccaagc tgaacgtgaa accgaatatc cagaatccgg agcctgccgt gtaccagctg 420
aaggacccac ggagccagga tagcaccctg tgcctgttca ccgactttga ttctcagatc 480
aacgtgcca agaccatgga gagcggcacc ttcatcacag acaagtgcgt gctggatatg 540
aaggccatgg acagcaagtc caacggcgcc atcgctggg ccaatcagac atctttcacc 600
tgccaggata tctttaagga gacaaatgcc acctatcctt cctctgacgt gccatgtgat 660
gccaccctga cagagaagag cttcgagacc gacatgaacc tgaattttca gaatctgctc 720
gtgattgtcc tgagaatcct gctgctgaag gtggccggct ttaacctgct gatgaccctg 780
aggctgtgga gctcctga 798

```

<210> 43

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha with Codon Optimized Human Constant

<400> 43

```

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

```

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

<210> 44

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha with Codon Optimized Mouse Constant

<400> 44

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

				165					170					175			
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala		
			180					185					190				
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser		
		195					200					205					
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp		
	210					215					220						
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe		
225				230						235					240		
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala		
			245					250						255			
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser					
		260						265									

<210> 46

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 46

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

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

<220>
<223> TCR 57 Alpha CDR2

<400> 49
Val Val Thr Gly Gly Glu Val
1 5

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Alpha CDR3

<400> 50
Ala Gly Ala Arg Asn Phe Asn Lys Phe Tyr
1 5 10

<210> 51
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Alpha Signal peptide

<400> 51
Met Val Leu Lys Phe Ser Val Ser Ile Leu Trp Ile Gln Leu Ala Trp
1 5 10 15
Val Ser

<210> 52
<211> 924
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 57 Beta Native with Codon Optimized Human
Constant

<400> 52

```

atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag 240
tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct 300
gaagacagca gcttctacat ctgcagtgct agatcttggc gggggggcct tgagcagttc 360
ttcgggccag ggacacggct caccgtgcta gaggacctga ataagggtgt ccccccctgag 420
gtggccgtgt ttgagccaag cgaggccgag atctcccaca cccagaaggc caccctggtg 480
tgcttgcaaa ccggcttctt tcccgatcac gtggagctgt cctggtgggt gaacggcaag 540
gaggtgcact ctggcgctgt cacagaccca cagcccctga aggagcagcc tgccctgaat 600
gattcccgtc attgtctgtc ctctcggtg agagtgtctg ccaccttttg gcagaacca 660
cggaatcact tcagatgcca ggtgcagttt tacggcctgt ctgagaacga cgagtggacc 720
caggatcggg ccaagcctgt gacacagatc gtgagcgagg aagcatgggg cagagccgac 780
tgtggcttca ccagcgctgt ctatcagcag ggcgtgctgt ccgccaccat cctgtacgag 840
atcctgctgg gcaaggccac actgtatgcc gtgctggtgt ctgccctggt gctgatggcc 900
atggtgaaga gaaaagactt ctaa 924

```

<210> 53

<211> 912

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Beta Native with Codon Optimized Mouse
Constant

<400> 53

```

atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag 240
tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct 300
gaagacagca gcttctacat ctgcagtgct agatcttggc gggggggcct tgagcagttc 360
ttcgggccag ggacacggct caccgtgcta gaggacctgc gcaatgtgac cccccctaag 420
gtgtccctgt ttgagccctc taaggccgag atcgccaaca agcagaaggc caccctggtg 480
tgcttgcaaa gaggccttct ccctgatcac gtggagctga gctggtgggt gaatggcaag 540
gaggtgcact ccggcgctgt caccgaccca caggcctaca aggagtccaa ctactcttat 600
tgtctgtcct ctaggctgag cgtgagcgcc acattctggc acaaccctcg gaatcacttc 660
agatgccagg tgcagtttca cggcctgagc gaggaggata agtggccaga gggctcccca 720
aagcccgtga cccagaatat ctctgccgag gcatggggca gggccgactg tggaatcacc 780
tccgcctctt atcagcaggg cgtgctgtcc gccacaatcc tgtacgagat cctgctgggc 840
aaggccaccc tgtatgccgt gctggtgtcc acactggtgg tcatggccat ggtgaagcgc 900
aagaacagct aa 912

```

<210> 54

<211> 924

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Beta Codon-Optimized with Codon Optimized
Human Constant

<400> 54

```
atgctcctgc tgcttctgct cctcgggccc ggcagcggtc tcggcgccgt cgtgtcgcag 60
caccgcgtcg ggggtgatttg caagagcgga acgagcgtga agatcgagtg ccgctcgctc 120
gacttccagg ccacaaccat gttctggtac cgccagtttc ccaagcagag cctcatgctg 180
atggccacaa gcaatgaagg cagcaaggcc acttatgaac agggcgtgga gaaggacaag 240
tttctgatca accacgcctc cctgaccctg tccaccctca ctgtgaccag cgcccaccct 300
gaggacagca gcttctacat ctgcagcgcc cgcagctgga ggggcggcct ggagcagttc 360
ttcggccctg gcacccggct gacagtgtgt gaggacctga ataagggtgt cccccctgag 420
gtggccgtgt ttgagccaag cgaggccgag atctcccaca cccagaaggc caccctggtg 480
tgcctggcaa ccggcttctt tccgatcac gtggagctgt cctggtgggt gaacggcaag 540
gaggtgcact ctggcgtgtg cacagaccca cagcccctga aggagcagcc tgccctgaat 600
gattcccgtc attgtctgtc ctctcggtgt agagtgtctg ccaccttttg gcagaacca 660
cggaatcact tcagatgccg ggtgcagttt tacggcctgt ctgagaacga cgagtggacc 720
caggatcggg ccaagcctgt gacacagatc gtgagcgagg aagcatgggg cagagccgac 780
tgtggcttca ccagcgtgtc ctatcagcag ggcgtgtgtt ccgccaccat cctgtacgag 840
atcctgtctg gcaaggccac actgtatgcc gtgtgtgtgt ctgccctggt gctgatggcc 900
atggtgaaga gaaaagactt ctaa 924
```

<210> 55

<211> 912

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Beta Codon-Optimized with Codon Optimized
Mouse Constant

<400> 55

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atgctcctgc tgcttctgct cctcgggccc ggcagcggtc tcggcgccgt cgtgtcgcag 60
caccgcgtcg ggggtgatttg caagagcgga acgagcgtga agatcgagtg ccgctcgctc 120
gacttccagg ccacaaccat gttctggtac cgccagtttc ccaagcagag cctcatgctg 180
atggccacaa gcaatgaagg cagcaaggcc acttatgaac agggcgtgga gaaggacaag 240
tttctgatca accacgcctc cctgaccctg tccaccctca ctgtgaccag cgcccaccct 300
gaggacagca gcttctacat ctgcagcgcc cgcagctgga ggggcggcct ggagcagttc 360
ttcggccctg gcacccggct gacagtgtgt gaggacctgc gcaatgtgac cccccctaag 420
gtgtccctgt ttgagccctc taaggccgag atcgccaaca agcagaaggc caccctggtg 480
tgcctggcca gaggcttctt ccctgatcac gtggagctga gctggtgggt gaatggcaag 540
gaggtgcact ccggcgtgtg caccgaccca caggcctaca aggagtcaa ctactcttat 600
tgtctgtcct ctaggctgctg cgtgagcgcc acattctggc acaaccctcg gaatcacttc 660
agatgccagg tgcagtttca cggcctgagc gaggaggata agtggccaga gggctcccca 720
aagcccgtga cccagaatat ctctgccgag gcatggggca gggccgactg tggaatcacc 780
tccgcctctt atcagcaggg cgtgtgttcc gccacaatcc tgtacgagat cctgtctggc 840
aaggccaccc tgtatgccgt gctggtgtcc acactgggtg tcatggccat ggtgaagcgc 900
aagaacagct aa 912
```

<210> 56

<211> 293

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Beta with Codon Optimized Human Constant

<400> 56

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

<210> 57

<211> 289

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Beta with Codon Optimized Mouse Constant

<400> 57

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

Ser

<210> 58

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Beta with Codon Optimized Human Constant
and signal peptide

<400> 58

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

<210> 59

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 59

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

<210> 60

<211> 116

<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Beta variable region

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

<210> 61
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Beta CDR1

<400> 61
Asp Phe Gln Ala Thr Thr
1 5

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Beta CDR2

<400> 62
Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 63
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Beta CDR3

<400> 63
Ser Ala Arg Ser Trp Arg Gly Gly Leu Glu Gln Phe
1 5 10

<210> 64
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Beta signal peptide

<400> 64
Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu
1 5 10

<210> 65
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 57 Native full sequence with human constant

<400> 65
atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
gactttcagg ccacaactat gtttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgctga gaaggacaag 240
tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct 300
gaagacagca gcttctacat ctgcagtgt agatcttggc gggggggcct tgagcagttc 360
ttcgggccag ggacacggct caccgtgcta gaggacctga ataagggtgt cccccctgag 420
gtggccgtgt ttgagccaag cgaggccgag atctcccaca cccagaaggc caccctggtg 480
tgcttggaac ccggcttctt tcccgatcac gtggagctgt cctggtgggt gaacggcaag 540
gaggtgcact ctggcggtg cacagaccca cagcccctga aggagcagcc tgccctgaat 600
gattcccgtg attgtctgtc ctctcggtg agagtgtctg ccaccttttg gcagaaccca 660
cggaatcact tcagatgcca ggtgcagttt tacggcctgt ctgagaacga cgagtggacc 720
caggatcggg ccaagcctgt gacacagatc gtgagcgctg aagcatgggg cagagccgac 780
tgtggcttca ccagcgtgtc ctatcagcag ggcgtgctgt ccgccaccat cctgtacgag 840

atcctgctgg	gcaaggccac	actgtatgcc	gtgctggtgt	ctgccctggt	gctgatggcc	900
atggtgaaga	gaaaagactt	ctaaggctcc	ggagcaacca	atttcagcct	gctgaagcag	960
gccggcgatg	tggaggagaa	tcctggccca	atggtcctga	aattctccgt	gtccattctt	1020
tggattcagt	tggcatgggt	gagcaccag	ctgctggagc	agagccctca	gtttctaagc	1080
atccaagagg	gagaaaatct	cactgtgtac	tgcaactcct	caagtgtttt	ttccagctta	1140
caatggtaca	gacaggagcc	tggggaaggt	cctgtcctcc	tggtgacagt	agttacgggt	1200
ggagaagtga	agaagctgaa	gagactaacc	tttcagtttg	gtgatgcaag	aaaggacagt	1260
tctctccaca	tcactgcagc	ccagcctggt	gatacaggcc	tctacctctg	tgaggagct	1320
cgcaacttca	acaaaatttta	ctttggatct	gggaccaaac	tcaatgtaaa	accaaataatc	1380
cagaatccgg	accccgcggt	atatcaactg	cgcgactcaa	aatcatccga	taagagtgtc	1440
tgtttgttta	ctgacttcga	cagtcaaaact	aatgtctctc	agagcaaaga	ttccgatgtc	1500
tacatcactg	acaagtgcgt	tctggatatg	cggagcatgg	attttaagtc	caactccgcc	1560
gtagcctggt	ccaacaagtc	agactttgcc	tgtgcaaatg	ctttcaacaa	ctcaattatc	1620
cctgaggaca	ctttctttcc	ttcaccggag	tcctcatgcg	atgttaaact	ggtcgaaaaa	1680
tcttttgaga	cggatacga	cctcaacttc	caaaaattga	gcgttattgg	ctttaggatt	1740
ctgcttctca	aggttgcggg	gttcaatctc	ctgatgacgt	tgcggttttg	gagcagctaa	1800

<210> 66

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Nativefull sequence with mouse constant

<400> 66

atgctgctgc	ttctgctgct	tctggggcca	ggctccgggc	ttggtgctgt	cgtctctcaa	60
catccgagct	gggttatctg	taagagtgga	acctctgtga	agatcgagtg	ccgttccctg	120
gactttcagg	ccacaactat	gttttggat	cgtcagttcc	cgaaacagag	tctcatgctg	180
atggcaactt	ccaatgaggg	ctccaaggcc	acatacgagc	aaggcgctga	gaaggacaag	240
tttctcatca	accatgcaag	cctgaccttg	tccactctga	cagtgaccag	tgcccatcct	300
gaagacagca	gcttctacat	ctgcagtgtc	agatcttggc	ggggggggcct	tgagcagttc	360
ttcgggccag	ggacacggct	caccgtgcta	gaggacctgc	gcaatgtgac	ccccctaag	420
gtgtccctgt	ttgagccctc	taaggccgag	atcgccaaca	agcagaaggc	caccctgggtg	480
tgcttgccca	gaggcttctt	ccctgatcac	gtggagctga	gctggtgggt	gaatggcaag	540
gaggtgcact	ccggcgctgtg	caccgaccca	caggcctaca	aggagtccaa	ctactcttat	600
tgtctgtcct	ctaggctgcg	cgtgagcgcc	acattctggc	acaaccctcg	gaatcacttc	660
agatgccagg	tgcagtttca	cggcctgagc	gaggaggata	agtggccaga	gggctcccca	720
aagcccgtga	cccagaatat	ctctgccgag	gcatggggca	gggccgactg	tggaatcacc	780
tccgcctctt	atcagcaggg	cgtgctgtcc	gccacaatcc	tgtacgagat	cctgctgggc	840
aaggccaccc	tgtatgccgt	gctggtgtcc	acactgggtg	tcatggccat	ggtgaagcgc	900
aagaacagct	aaggctccgg	agcaaccaat	ttcagcctgc	tgaagcaggc	cggcgatgtg	960
gaggagaatc	ctggcccaat	ggtcctgaaa	ttctccgtgt	ccattctttg	gattcagttg	1020
gcatgggtga	gcacccagct	gctggagcag	agccctcagt	ttctaagcat	ccaagaggga	1080
gaaaaatctca	ctgtgtactg	caactcctca	agtgtttttt	ccagcttaca	atggtacaga	1140
caggagcctg	gggaagggtcc	tgtcctcctg	gtgacagtag	ttacgggtgg	agaagtgaag	1200
aagctgaaga	gactaacctt	tcagtttggg	gatgcaagaa	aggacagttc	tctccacatc	1260
actgcagccc	agcctgggtga	tacaggcctc	tacctctgtg	caggagctcg	caacttcaac	1320
aaattttact	ttggatctgg	gaccaaactc	aatgtaaaac	caaatatcca	gaatccggag	1380

cctgccgtgt	accagctgaa	ggacccacgg	agccaggata	gcaccctgtg	cctgttcacc	1440
gactttgatt	ctcagatcaa	cgtgcccagg	accatggaga	gcggcacctt	catcacagac	1500
aagtgcgtgc	tggatatgaa	ggccatggac	agcaagtcca	acggcgccat	cgcttggtcc	1560
aatcagacat	ctttcacctg	ccaggatata	tttaaggaga	caaatgccac	ctatccttcc	1620
tctgacgtgc	catgtgatgc	caccctgaca	gagaagagct	tcgagaccga	catgaacctg	1680
aattttcaga	atctgctcgt	gattgtcctg	agaatcctgc	tgctgaaggt	ggccggcttt	1740
aacctgctga	tgaccctgag	gctgtggagc	tcctga			1776

<210> 67

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Codon-optimized full sequence with human constant

<400> 67

atgctcctgc	tgcttctgct	cctcgggccc	ggcagcggtc	tcggcgccgt	cgtgtcgcag	60
cacccgtcgt	gggtgatttg	caagagcgga	acgagcgtga	agatcgagtg	ccgctcgtc	120
gacttccagg	ccacaaccat	gttctggtag	cgccagtttc	ccaagcagag	cctcatgctg	180
atggccacaa	gcaatgaagg	cagcaaggcc	acttatgaac	agggcgtgga	gaaggacaag	240
tttctgatca	accacgcctc	cctgaccctg	tccaccctca	ctgtgaccag	cgcccaccct	300
gaggacagca	gcttctacat	ctgcagcgcc	cgcagctgga	ggggcggcct	ggagcagttc	360
ttcggccctg	gcacccggct	gacagtgtg	gaggacctga	ataaggtgtt	ccccctgag	420
gtggccgtgt	ttgagccaag	cgaggccgag	atctcccaca	cccagaaggc	caccctgggtg	480
tgcttgga	ccggcttctt	tccgatcac	gtggagctgt	cctggtgggt	gaacggcaag	540
gaggtgcact	ctggcgtgtg	cacagaccca	cagcccctga	aggagcagcc	tgccctgaat	600
gattcccgt	attgtctgtc	ctctcggtg	agagtgtctg	ccaccttttg	gcagaacca	660
cggaatcact	tcagatgcc	ggtgcagttt	tacggcctgt	ctgagaacga	cgagtggacc	720
caggatcggg	ccaagcctgt	gacacagatc	gtgagcgcg	aagcatgggg	cagagccgac	780
tgtggcttca	ccagcgtgtc	ctatcagcag	ggcgtgctgt	ccgccaccat	cctgtacgag	840
atcctgctgg	gcaaggccac	actgtatgcc	gtgctgggtg	ctgccctggt	gctgatggcc	900
atggtgaaga	gaaaagactt	ctaaggctcc	ggagcaacca	atttcagcct	gctgaagcag	960
gccggcgatg	tggaggagaa	tcctggccca	atggtgctga	agttttctgt	gagcatcctg	1020
tggattcagc	tggcctgggt	gtccaccag	ctcctggagc	agagcccca	gttcctgtcc	1080
atccaggagg	gcgagaacct	gaccgtgtac	tgcaacagct	cttctgtctt	ttcatcactg	1140
cagtgggtata	gacaagaacc	gggtgaagg	ccagttctgc	tggtgaccgt	cgtcaccggc	1200
ggcgagggtga	agaagctaaa	gcgcctgacg	ttccagttcg	gagacgcgcg	gaaggactcg	1260
tcgctgcaca	tcaccgccgc	ccagcccggc	gacaccggcc	tgtacctgtg	cgctggcgcg	1320
cgcaacttca	acaagtctta	cttcggcagc	ggcaccaagc	tgaacgtgaa	accgaatatc	1380
cagaatccgg	accccgcggt	atatcaactg	cgcgactcaa	aatcatccga	taagagtgtc	1440
tgtttgttta	ctgacttca	cagtcaaaact	aatgtctctc	agagcaaaga	ttccgatgtc	1500
tacatcactg	acaagtgcgt	tctggatatg	cggagcatgg	attttaagtc	caactccgcc	1560
gtagcctggt	ccaacaagtc	agactttgcc	tgtgcaaatg	ctttcaacaa	ctcaattatc	1620
cctgaggaca	ctttctttcc	ttcaccggag	tcctcatgcg	atgttaaaact	ggtcgaaaaa	1680
tcttttgaga	cggatacgaa	cctcaacttc	caaaaatttga	gcgttattgg	ctttaggatt	1740
ctgcttctca	aggttgcggg	gttcaatctc	ctgatgacgt	tgccggctttg	gagcagctaa	1800

<210> 68
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 57 Codon-optimized full sequence with mouse
constant

<400> 68
atgctcctgc tgcttctgct cctcgggccc ggcagcggtc tcggcgccgt cgtgtcgcag 60
caccgcgtcgt ggggtgatttg caagagcggga acgagcgtga agatcgagtgc ccgctcgcctc 120
gacttccagg ccacaacccat gttctgggtac cgccagtttc ccaagcagag cctcatgctg 180
atggccacaa gcaatgaagg cagcaaggcc acttatgaac agggcgtgga gaaggacaag 240
tttctgatca accacgcctc cctgaccctg tccaccctca ctgtgaccag cgccccacct 300
gaggacagca gcttctacat ctgcagcgcc cgcagctgga ggggcggcct ggagcagttc 360
ttcggccctg gcacccggct gacagtgtgaggaggacctgc gcaatgtgac cccccctaag 420
gtgtccctgt ttgagccctc taaggccgag atcgccaaca agcagaaggc caccctgggtg 480
tgcctggcca gaggcttctt ccctgatcac gtggagctga gctgggtgggt gaatggcaag 540
gaggtgcact ccggcgtgtg caccgaccca caggcctaca aggagtccaa ctactcttat 600
tgtctgtcct ctaggctgcg cgtgagcgcc acattctggc acaaccctcg gaatcacttc 660
agatgccagg tgcagtttca cggcctgagc gaggaggata agtggccaga gggctcccca 720
aagcccgtga cccagaatat ctctgccgag gcatggggca gggccgactg tggaatcacc 780
tccgcctctt atcagcaggg cgtgctgtcc gccacaatcc tgtacgagat cctgctgggc 840
aaggccaccc tgtatgccgt gctggtgtcc aacttggtgg tcatggccat ggtgaagcgc 900
aagaacagct aaggctccgg agcaaccaat ttcagcctgc tgaagcaggc cggcgtatgtg 960
gaggagaatc ctggccaat ggtgctgaag ttttctgtga gcatcctgtg gattcagctg 1020
gcctgggtgt ccaccagct cctggagcag agccccagc tcctgtccat ccaggagggc 1080
gagaacctga ccgtgtactg caacagctct tctgtctttt catcactgca gtggtataga 1140
caagaaccgg gtgaaggctc agttctgtg gtgaccgtcg tcaccggcgg cgaggtgaag 1200
aagctaaagc gcctgacgtt ccagttcgga gacgcgcgga aggactcgtc gctgcacatc 1260
accgccgccc agcccggcga caccggcctg tacctgtgag ctggcgcgcg caacttcaac 1320
aagttctact tcggcagcgg caccaagctg aacgtgaaac cgaatatcca gaatccggag 1380
cctgccgtgt accagctgaa ggacccacgg agccaggata gcaccctgtg cctgttcacc 1440
gactttgatt ctcagatcaa cgtgcccagg accatggaga gcggcacctt catcacagac 1500
aagtgcgtgc tggatatgaa ggccatggac agcaagtcca acggcgccat cgcctgggtc 1560
aatcagacat ctttcacctg ccaggatatc tttaaggaga caaatgccac ctatccttcc 1620
tctgacgtgc catgtgatgc caccctgaca gagaagagct tcgagaccga catgaacctg 1680
aattttcaga atctgtctgt gattgtcctg agaatcctgc tgctgaagggt ggccggcttt 1740
aacctgctga tgaccctgag gctgtggagc tcctga 1776

<210> 69
<211> 598
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 57 Full sequence with human constant

<400> 69

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

Glu Val Lys Lys Leu Lys Arg Leu Thr Phe Gln Phe Gly Asp Ala Arg
 405 410 415
 Lys Asp Ser Ser Leu His Ile Thr Ala Ala Gln Pro Gly Asp Thr Gly
 420 425 430
 Leu Tyr Leu Cys Ala Gly Ala Arg Asn Phe Asn Lys Phe Tyr Phe Gly
 435 440 445
 Ser Gly Thr Lys Leu Asn Val Lys Pro Asn Ile Gln Asn Pro Asp Pro
 450 455 460
 Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys
 465 470 475 480
 Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp
 485 490 495
 Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met
 500 505 510
 Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe
 515 520 525
 Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe
 530 535 540
 Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser
 545 550 555 560
 Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly
 565 570 575
 Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr
 580 585 590
 Leu Arg Leu Trp Ser Ser
 595

<210> 70

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 57 Full sequence with mouse constant

<400> 70

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

			100					105				110			
Trp	Arg	Gly	Gly	Leu	Glu	Gln	Phe	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr
		115					120					125			
Val	Leu	Glu	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val	Ser	Leu	Phe
	130					135					140				
Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr	Leu	Val
145					150					155					160
Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp
			165					170						175	
Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Ala
		180						185					190		
Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val
	195						200					205			
Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val
	210					215					220				
Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro
225					230					235					240
Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp
				245					250					255	
Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr
		260						265					270		
Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu
	275						280					285			
Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser	Gly
	290					295					300				
Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu
305					310					315					320
Glu	Asn	Pro	Gly	Pro	Met	Val	Leu	Lys	Phe	Ser	Val	Ser	Ile	Leu	Trp
				325					330					335	
Ile	Gln	Leu	Ala	Trp	Val	Ser	Thr	Gln	Leu	Leu	Glu	Gln	Ser	Pro	Gln
		340						345					350		
Phe	Leu	Ser	Ile	Gln	Glu	Gly	Glu	Asn	Leu	Thr	Val	Tyr	Cys	Asn	Ser
	355						360					365			
Ser	Ser	Val	Phe	Ser	Ser	Leu	Gln	Trp	Tyr	Arg	Gln	Glu	Pro	Gly	Glu
	370					375					380				
Gly	Pro	Val	Leu	Leu	Val	Thr	Val	Val	Thr	Gly	Gly	Glu	Val	Lys	Lys
385					390					395					400
Leu	Lys	Arg	Leu	Thr	Phe	Gln	Phe	Gly	Asp	Ala	Arg	Lys	Asp	Ser	Ser
			405						410					415	
Leu	His	Ile	Thr	Ala	Ala	Gln	Pro	Gly	Asp	Thr	Gly	Leu	Tyr	Leu	Cys
		420						425					430		
Ala	Gly	Ala	Arg	Asn	Phe	Asn	Lys	Phe	Tyr	Phe	Gly	Ser	Gly	Thr	Lys
	435						440					445			
Leu	Asn	Val	Lys	Pro	Asn	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln
	450					455					460				
Leu	Lys	Asp	Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp
465					470					475					480
Phe	Asp	Ser	Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe
			485						490					495	
Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser

			500					505					510				
Asn	Gly	Ala	Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp		
		515					520					525					
Ile	Phe	Lys	Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys		
		530				535					540						
Asp	Ala	Thr	Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn		
545					550				555					560			
Phe	Gln	Asn	Leu	Leu	Val	Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val		
			565					570						575			
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
			580					585					590				

<210> 71
 <211> 825
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 58 Alpha Native with Codon Optimized Human
 Constant

<400> 71
 atgatgatat ccttgagagt tttactgggtg atcctgtggc ttcagttaag ctgggtttgg 60
 agccaacgga aggagggtgga gcaggatcct ggacccttca atgttccaga gggagccact 120
 gtcgctttca actgtactta cagcaacagt gcttctcagt ctttcttctg gtacagacag 180
 gattgcagga aagaacctaa gttgctgatg tccgtatact ccagtggtaa tgaagatgga 240
 aggtttacag cacagctcaa tagagccagc cagtataatt ccctgctcat cagagactcc 300
 aagctcagtg attcagccac ctacctctgt gtggtgaaca gggataacta tggtcagaat 360
 tttgtctttg gtcccggaac cagattgtcc gtgctgcca atatccagaa tccggacccc 420
 gcggtatatc aactgcgcga ctcaaaaatca tccgataaga gtgtctgttt gtttactgac 480
 ttcgacagtc aaactaatgt ctctcagagc aaagattccg atgtctacat cactgacaag 540
 tgcgttctgg atatgcggag catggatttt aagtccaact ccgccgtagc ctggtccaac 600
 aagtcagact ttgcctgtgc aaatgctttc aacaactcaa ttatccctga ggacactttc 660
 tttccttcac cggagtcctc atgcgatgtt aaactggctg aaaaatcttt tgagacggat 720
 acgaacctca acttccaaaa tttgagcgtt attggcttta ggattctgct tctcaagggt 780
 gcgggggttca atctcctgat gacgttgcggt ctttggagca gctaa 825

<210> 72
 <211> 812
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Alpha Native with Codon Optimized Mouse
 Constant

<400> 72
 Ala Thr Gly Ala Thr Gly Ala Thr Ala Thr Cys Cys Thr Thr Gly Ala
 1 5 10 15

Gly	Ala	Gly	Thr	Thr	Thr	Thr	Ala	Cys	Thr	Gly	Gly	Thr	Gly	Ala	Thr	20	25	30
Cys	Cys	Thr	Gly	Thr	Gly	Gly	Cys	Thr	Thr	Cys	Ala	Gly	Thr	Thr	Ala	35	40	45
Ala	Gly	Cys	Thr	Gly	Gly	Gly	Thr	Thr	Thr	Gly	Gly	Ala	Gly	Cys	Cys	50	55	60
Ala	Ala	Cys	Gly	Gly	Ala	Ala	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Gly	Ala	65	70	75
Gly	Cys	Ala	Gly	Gly	Ala	Thr	Cys	Cys	Thr	Gly	Gly	Ala	Cys	Cys	Cys	85	90	95
Thr	Thr	Cys	Ala	Ala	Thr	Gly	Thr	Thr	Cys	Cys	Ala	Gly	Ala	Gly	Gly	100	105	110
Gly	Ala	Gly	Cys	Cys	Ala	Cys	Thr	Gly	Thr	Cys	Gly	Cys	Thr	Thr	Thr	115	120	125
Cys	Ala	Ala	Cys	Thr	Gly	Thr	Ala	Cys	Thr	Thr	Ala	Cys	Ala	Gly	Cys	130	135	140
Ala	Ala	Cys	Ala	Gly	Thr	Gly	Cys	Thr	Thr	Cys	Thr	Cys	Ala	Gly	Thr	145	150	155
Cys	Thr	Thr	Thr	Cys	Thr	Thr	Cys	Thr	Gly	Gly	Thr	Ala	Cys	Ala	Gly	165	170	175
Ala	Cys	Ala	Gly	Gly	Ala	Thr	Thr	Gly	Cys	Ala	Gly	Gly	Ala	Ala	Ala	180	185	190
Gly	Ala	Ala	Cys	Cys	Thr	Ala	Ala	Gly	Thr	Thr	Gly	Cys	Thr	Gly	Ala	195	200	205
Thr	Gly	Thr	Cys	Gly	Thr	Ala	Thr	Ala	Cys	Thr	Cys	Cys	Ala	Gly	Thr	210	215	220
Gly	Gly	Thr	Ala	Ala	Thr	Gly	Ala	Ala	Gly	Ala	Thr	Gly	Gly	Ala	Ala	225	230	235
Gly	Gly	Thr	Thr	Thr	Ala	Cys	Ala	Gly	Cys	Ala	Cys	Ala	Gly	Cys	Thr	245	250	255
Cys	Ala	Ala	Thr	Ala	Gly	Ala	Gly	Cys	Cys	Ala	Gly	Cys	Cys	Ala	Gly	260	265	270
Thr	Ala	Thr	Ala	Thr	Thr	Thr	Cys	Cys	Cys	Thr	Gly	Cys	Thr	Cys	Ala	275	280	285
Thr	Cys	Ala	Gly	Ala	Gly	Ala	Cys	Thr	Cys	Cys	Ala	Ala	Gly	Cys	Thr	290	295	300
Cys	Ala	Gly	Thr	Gly	Ala	Thr	Thr	Cys	Ala	Gly	Cys	Cys	Ala	Cys	Cys	305	310	315
Thr	Ala	Cys	Cys	Thr	Cys	Thr	Gly	Thr	Gly	Thr	Gly	Gly	Thr	Gly	Ala	325	330	335
Ala	Cys	Ala	Gly	Gly	Gly	Ala	Thr	Ala	Ala	Cys	Thr	Ala	Thr	Gly	Gly	340	345	350
Thr	Cys	Ala	Gly	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Cys	Thr	Thr	Thr	355	360	365
Gly	Gly	Thr	Cys	Cys	Cys	Gly	Gly	Ala	Ala	Cys	Cys	Ala	Gly	Ala	Thr	370	375	380
Thr	Gly	Thr	Cys	Cys	Gly	Thr	Gly	Cys	Thr	Gly	Cys	Cys	Cys	Ala	Ala	385	390	395
Thr	Ala	Thr	Cys	Cys	Ala	Gly	Ala	Ala	Thr	Cys	Cys	Gly	Gly	Ala	Gly	405	410	415

Cys	Cys	Thr	Gly	Cys	Cys	Gly	Thr	Gly	Thr	Ala	Cys	Cys	Ala	Gly	Cys	420	425	430
Thr	Gly	Ala	Ala	Gly	Gly	Ala	Cys	Cys	Cys	Ala	Cys	Gly	Gly	Ala	Gly	435	440	445
Cys	Cys	Ala	Gly	Gly	Ala	Thr	Ala	Gly	Cys	Ala	Cys	Cys	Cys	Thr	Gly	450	455	460
Thr	Gly	Cys	Cys	Thr	Gly	Thr	Thr	Cys	Ala	Cys	Cys	Gly	Ala	Cys	Thr	465	470	475
Thr	Thr	Gly	Ala	Thr	Thr	Cys	Thr	Cys	Ala	Gly	Ala	Thr	Cys	Ala	Ala	485	490	495
Cys	Gly	Thr	Gly	Cys	Cys	Cys	Ala	Ala	Gly	Ala	Cys	Cys	Ala	Thr	Gly	500	505	510
Gly	Ala	Gly	Ala	Gly	Cys	Gly	Gly	Cys	Ala	Cys	Cys	Thr	Thr	Cys	Ala	515	520	525
Thr	Cys	Ala	Cys	Ala	Gly	Ala	Cys	Ala	Ala	Gly	Thr	Gly	Cys	Gly	Thr	530	535	540
Gly	Cys	Thr	Gly	Gly	Ala	Thr	Ala	Thr	Gly	Ala	Ala	Gly	Gly	Cys	Cys	545	550	555
Ala	Thr	Gly	Gly	Ala	Cys	Ala	Gly	Cys	Ala	Ala	Gly	Thr	Cys	Cys	Ala	565	570	575
Ala	Cys	Gly	Gly	Cys	Gly	Cys	Cys	Ala	Thr	Cys	Gly	Cys	Cys	Thr	Gly	580	585	590
Gly	Thr	Cys	Cys	Ala	Ala	Thr	Cys	Ala	Gly	Ala	Cys	Ala	Thr	Cys	Thr	595	600	605
Thr	Thr	Cys	Ala	Cys	Cys	Thr	Gly	Cys	Cys	Ala	Gly	Gly	Ala	Thr	Ala	610	615	620
Thr	Cys	Thr	Thr	Thr	Ala	Ala	Gly	Gly	Ala	Gly	Ala	Cys	Ala	Ala	Ala	625	630	635
Thr	Gly	Cys	Cys	Ala	Cys	Cys	Thr	Ala	Thr	Cys	Cys	Thr	Thr	Cys	Cys	645	650	655
Thr	Cys	Thr	Gly	Ala	Cys	Gly	Thr	Gly	Cys	Cys	Ala	Thr	Gly	Thr	Gly	660	665	670
Ala	Thr	Gly	Cys	Cys	Ala	Cys	Cys	Cys	Thr	Gly	Ala	Cys	Ala	Gly	Ala	675	680	685
Gly	Ala	Ala	Gly	Ala	Gly	Cys	Thr	Thr	Cys	Gly	Ala	Gly	Ala	Cys	Cys	690	695	700
Gly	Ala	Cys	Ala	Thr	Gly	Ala	Ala	Cys	Cys	Thr	Gly	Ala	Ala	Thr	Thr	705	710	715
Thr	Thr	Cys	Ala	Gly	Ala	Ala	Thr	Cys	Thr	Gly	Cys	Thr	Cys	Gly	Thr	725	730	735
Gly	Ala	Thr	Thr	Gly	Thr	Cys	Cys	Thr	Gly	Ala	Gly	Ala	Ala	Thr	Cys	740	745	750
Cys	Thr	Gly	Cys	Thr	Gly	Cys	Thr	Gly	Ala	Ala	Gly	Gly	Thr	Gly	Gly	755	760	765
Cys	Cys	Gly	Gly	Cys	Thr	Thr	Thr	Ala	Ala	Cys	Cys	Thr	Gly	Cys	Thr	770	775	780
Gly	Ala	Thr	Gly	Ala	Cys	Cys	Cys	Thr	Gly	Ala	Gly	Gly	Cys	Thr	Gly	785	790	795
Thr	Gly	Gly	Ala	Gly	Cys	Thr	Cys	Cys	Thr	Gly	Ala					805	810	

<210> 73
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 58 Alpha with Codon Optimized Human Constant

<400> 73
Arg Lys Glu Val Glu Gln Asp Pro Gly Pro Phe Asn Val Pro Glu Gly
1 5 10 15
Ala Thr Val Ala Phe Asn Cys Thr Tyr Ser Asn Ser Ala Ser Gln Ser
20 25 30
Phe Phe Trp Tyr Arg Gln Asp Cys Arg Lys Glu Pro Lys Leu Leu Met
35 40 45
Ser Val Tyr Ser Ser Gly Asn Glu Asp Gly Arg Phe Thr Ala Gln Leu
50 55 60
Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser Lys Leu
65 70 75 80
Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Arg Asp Asn Tyr Gly
85 90 95
Gln Asn Phe Val Phe Gly Pro Gly Thr Arg Leu Ser Val Leu Pro Asn
100 105 110
Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
115 120 125
Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
130 135 140
Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
145 150 155 160
Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
165 170 175
Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
180 185 190
Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
195 200 205
Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
210 215 220
Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
225 230 235 240
Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
245 250

<210> 74
<211> 248
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR 58 Alpha with Codon Optimized Mouse Constant

<400> 74

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

<210> 75

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 75

Met	Met	Ile	Ser	Leu	Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	

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

Ser Ser

<210> 76

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 76

Met	Met	Ile	Ser	Leu	Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Ser	Trp	Val	Trp	Ser	Gln	Arg	Lys	Glu	Val	Glu	Gln	Asp	Pro	Gly	Pro
			20					25					30		

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

<210> 77

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Alpha variable region

<400> 77

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

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

<210> 78
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Alpha CDR1

<400> 78
 Asn Ser Ala Ser Gln Ser
 1 5

<210> 79
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Alpha CDR2

<400> 79
 Val Tyr Ser Ser Gly Asn
 1 5

<210> 80
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Alpha CDR3

<400> 80
 Val Val Asn Arg Asp Asn Tyr Gly Gln Asn Phe Val
 1 5 10

<210> 81
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TCR 58 Alpha Signal peptide

<400> 81

Met Met Ile Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15
Ser Trp Val Trp Ser Gln
20

<210> 82

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Beta Native with Codon Optimized Human
Constant

<400> 82

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca cccccgaag ctcttacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgagggtg ccgtgtttga gccaaagcag gccgagatct cccacacca gaaggccacc 480
ctggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcaactctg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacgga atcacttcag atgccagggt cagttttacg gcctgtctga gaacgacgag 720
tggacccagg atcgggcca gacctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcagggcg tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctggtgctg 900
atggccatgg tgaagagaaa agacttctaa 930

<210> 83

<211> 918

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Beta Native with Codon Optimized Mouse
Constant

<400> 83

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120

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cgctgtgtcc ccatctctaa tcacttatac ttctattggt acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgccagca ccccccgaag ctcttacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgcgcaa tgtgaccccc 420
cctaagggtgt ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
ggcaaggagg tgcactccgg cgtgtgcacc gacccacagg cctacaagga gtccaactac 600
tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcacia ccctcggaat 660
cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
tccccaaagc ccgtgaccca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tggtggtcat ggccatggtg 900
aagcgcaaga acagctaa                                     918

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<210> 84

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Beta with Codon Optimized Human Constant

<400> 84

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

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Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln
210						215				220					
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly
225					230					235					240
Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			245						250					255	
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
		260					265						270		
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys
	275					280						285			
Asp	Phe														
290															

<210> 85

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Beta with Codon Optimized Mouse Constant

<400> 85

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

210	215	220
Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys		
225	230	235
Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile		240
	245	250
Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val		255
	260	265
Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser		270
	275	280
		285

<210> 86
 <211> 309
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Beta with Codon Optimized Human Constant
 and signal peptide

<400> 86

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

225		230		235		240									
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
		245		250		255									
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
		260		265		270									
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275		280		285									
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
		290		295		300									
Lys	Arg	Lys	Asp	Phe											
305															

<210> 87

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 87

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

210	215	220
Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly		
225	230	235
Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg		240
	245	250
Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser		255
	260	265
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala		270
	275	280
Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn		285
	290	300
Ser		
305		

<210> 88
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58 Beta variable region

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

<210> 89
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 58, 59, 60, 61 Beta CDR1

<400> 89

Ser Asn His Leu Tyr
1 5

<210> 90

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58, 59, 60 61 Beta CDR2

<400> 90

Phe Tyr Asn Asn Glu Ile
1 5

<210> 91

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Beta CDR3

<400> 91

Ala Ser Thr Pro Arg Ser Ser Tyr Glu Gln Tyr
1 5 10

<210> 92

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58, 59, 60, 61 Beta signal peptide

<400> 92

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
1 5 10 15
Gly Leu Thr

<210> 93

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Native full sequence with human constant

<400> 93

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atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccactctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaat tcaactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca ccccccgaag ctcttacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgagggtg ccgtgtttga gccaaagcag gccgagatct cccacaccca gaaggccacc 480
ctgggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcactctgg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacgga atcacttcag atgccagggt cagttttacg gcctgtctga gaacgacgag 720
tggacccagg atcggggcaa gcctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcagggcg tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctgggtgctg 900
atggccatgg tgaagagaaa agacttctaa ggctccggag caaccaattt cagcctgctg 960
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gatcctggac ctttcaatgt tccagaggga gccactgtcg ctttcaactg tacttacagc 1140
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ctctgtgtgg tgaacaggga taactatggt cagaattttg tctttgggtc cggaaccaga 1380
ttgtccgtgc tgccaatat ccagaatccg gaccccgagg tatatcaact gcgcgactca 1440
aaatcatccg ataagagtgt ctgtttgttt actgacttcg acagtcaaac taatgtctct 1500
cagagcaaaag attccgatgt ctacatcact gacaagtgcg ttctggatat gcggagcatg 1560
gatttttaagt ccaactccgc cgtagcctgg tccaacaagt cagactttgc ctgtgcaaat 1620
gctttcaaca actcaattat ccctgaggac actttctttc cttaccgga gtcctcatgc 1680
gatgttaaac tggctgaaaa atcttttgag acggatacga acctcaactt ccaaaatttg 1740
agcgttattg gctttaggat tctgcttctc aaggttgcgg ggttcaatct cctgatgacg 1800
ttcgggcttt ggagcagcta a                                     1821
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<210> 94

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Nativefull sequence with mouse constant

<400> 94

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atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccactctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
```

```

gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca ccccccgaag ctcttacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgcgcaa tgtgaccccc 420
cctaagggtg ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
ggcaaggagg tgcactccgg cgtgtgcacc gaccacaggg cctacaagga gtccaactac 600
tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcaca ccctcggaat 660
cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
tcccaaaagc ccgtgacca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tgggtggtcat ggccatggtg 900
aagcgcaaga acagctaagg ctccggagca accaatttca gcctgctgaa gcaggccggc 960
gatgtggagg agaatcctgg cccaatgatg atatccttga gagttttact ggtgatcctg 1020
tggcttcagt taagctgggt ttggagccaa cggaaggagg tggagcagga tcctggaccc 1080
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cagtctttct tctggtacag acaggattgc aggaaagaac ctaagttgct gatgtccgta 1200
tactccagtg gtaatgaaga tggagggtt acagcacagc tcaatagagc cagccagtat 1260
atttccctgc tcatcagaga ctccaagctc agtgattcag ccacctacct ctgtgtggtg 1320
aacagggata actatggtca gaattttgtc tttggtcccg gaaccagatt gtccgtgctg 1380
cccaatatcc agaatccgga gcctgccgtg taccagctga aggaccacg gagccaggat 1440
agcacctgt gcctgttcac cgactttgat tctcagatca acgtgccc aa gaccatggag 1500
agcggcacct tcatcacaga caagtgcgtg ctggatatga aggccatgga cagcaagtcc 1560
aacggcgcca tcgcctggtc caatcagaca tctttcacct gccaggatat ctttaaggag 1620
acaaatgcca cctatccttc ctctgacgtg ccatgtgatg ccaccctgac agagaagagc 1680
ttcgagaccg acatgaacct gaattttcag aatctgctcg tgattgtcct gagaatcctg 1740
ctgctgaagg tggccggcct taacctgctg atgaccctga ggctgtggag ctctga 1797

```

<210> 95

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Full sequence with human constant

<400> 95

```

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

```

Ser	Thr	Pro	Arg	Ser	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Thr	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
		130					135					140			
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170						175
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro
			180					185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
		210				215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225				230						235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
			245						250						255
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265						270	
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
		290				295					300				
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305				310						315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Met	Ile	Ser	Leu
			325						330					335	
Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ser	Trp	Val	Trp	Ser
		340					345						350		
Gln	Arg	Lys	Glu	Val	Glu	Gln	Asp	Pro	Gly	Pro	Phe	Asn	Val	Pro	Glu
		355					360					365			
Gly	Ala	Thr	Val	Ala	Phe	Asn	Cys	Thr	Tyr	Ser	Asn	Ser	Ala	Ser	Gln
		370				375					380				
Ser	Phe	Phe	Trp	Tyr	Arg	Gln	Asp	Cys	Arg	Lys	Glu	Pro	Lys	Leu	Leu
385				390						395					400
Met	Ser	Val	Tyr	Ser	Ser	Gly	Asn	Glu	Asp	Gly	Arg	Phe	Thr	Ala	Gln
			405						410					415	
Leu	Asn	Arg	Ala	Ser	Gln	Tyr	Ile	Ser	Leu	Leu	Ile	Arg	Asp	Ser	Lys
			420					425					430		
Leu	Ser	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Val	Val	Asn	Arg	Asp	Asn	Tyr
		435					440					445			
Gly	Gln	Asn	Phe	Val	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val	Leu	Pro
		450				455					460				
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
465				470						475					480
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
			485						490					495	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys
			500					505					510		

Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
		515					520					525			
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
		530				535					540				
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp
545					550					555					560
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe
				565					570					575	
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
			580				585						590		
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
		595					600					605			

<210> 96

<211> 597

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 Full sequence with mouse constant

<400> 96

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

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

<210> 97
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 59 Alpha Native with Codon Optimized Human
Constant

<400> 97
atgaagagggg agaggggagat gctactcatc acatcaatgt tggctttatg gatgcaattg 60
tcacaggtga atggacaaca ggtaatgcaa attcctcagt accagcatgt acaagaagga 120
gaggacttca ccacgtactg caattcctca actactttta gcaatataca gtggtataag 180
caaaggcctg gtggacatcc cgtttttttg atacagttag tgaagagtgg agaagtgaag 240
aagcagaaaa gactgacatt tcagtttgga gaagcaaaaa agaacagctc cctgcacatc 300
acagccaccc agactacaga tgtaggaacc tacttctgtg cacccaagcg ggaatatgga 360
aacaaactgg tctttggcgc aggaaccatt ctgagagtca agtccaatat ccagaatccg 420
gaccccgcggt tatatcaact gcgcgactca aaatcatccg ataagagtgt ctgtttgttt 480
actgacttcg acagtcaaac taatgtctct cagagcaaag attccgatgt ctacatcact 540
gacaagtgcg ttctggatat gcggagcatg gattttaagt ccaactccgc cgtagcctgg 600
tccaacaagt cagactttgc ctgtgcaaat gctttcaaca actcaattat ccctgaggac 660
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acggatacga acctcaactt ccaaaaattt agcgttattg gctttaggat tctgcttctc 780
aaggttgcggt ggttcaatct cctgatgacg ttgcggcttt ggagcagcta a 831

<210> 98
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 59 Alpha Native with Codon Optimized Mouse
Constant

<400> 98
atgaagagggg agaggggagat gctactcatc acatcaatgt tggctttatg gatgcaattg 60
tcacaggtga atggacaaca ggtaatgcaa attcctcagt accagcatgt acaagaagga 120
gaggacttca ccacgtactg caattcctca actactttta gcaatataca gtggtataag 180
caaaggcctg gtggacatcc cgtttttttg atacagttag tgaagagtgg agaagtgaag 240
aagcagaaaa gactgacatt tcagtttgga gaagcaaaaa agaacagctc cctgcacatc 300
acagccaccc agactacaga tgtaggaacc tacttctgtg cacccaagcg ggaatatgga 360
aacaaactgg tctttggcgc aggaaccatt ctgagagtca agtccaatat ccagaatccg 420
gagcctgccg tgtaccagct gaaggaccca cggagccagg atagcaccct gtgcctgttc 480
accgactttg attctcagat caacgtgccc aagaccatgg agagcggcac cttcatcaca 540
gacaagtgcg tgctggatat gaaggccatg gacagcaagt ccaacggcgc catcgcttgg 600
tccaatcaga catctttcac ctgccaggat atctttaagg agacaaatgc cacctatcct 660
tcctctgacg tgccatgtga tgccaccctg acagagaaga gcttcgagac cgacatgaac 720
ctgaattttc agaattctgct cgtgattgtc ctgagaatcc tgctgctgaa ggtggccggc 780
tttaacctgc tgatgaccct gaggctgtgg agctcctga 819

<210> 99
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 59 Alpha with Codon Optimized Human Constant

<400> 99
Gly Gln Gln Val Met Gln Ile Pro Gln Tyr Gln His Val Gln Glu Gly
1 5 10 15
Glu Asp Phe Thr Thr Tyr Cys Asn Ser Ser Thr Thr Leu Ser Asn Ile
20 25 30
Gln Trp Tyr Lys Gln Arg Pro Gly Gly His Pro Val Phe Leu Ile Gln
35 40 45
Leu Val Lys Ser Gly Glu Val Lys Lys Gln Lys Arg Leu Thr Phe Gln
50 55 60
Phe Gly Glu Ala Lys Lys Asn Ser Ser Leu His Ile Thr Ala Thr Gln
65 70 75 80
Thr Thr Asp Val Gly Thr Tyr Phe Cys Ala Pro Lys Arg Glu Tyr Gly
85 90 95
Asn Lys Leu Val Phe Gly Ala Gly Thr Ile Leu Arg Val Lys Ser Asn
100 105 110
Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
115 120 125
Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
130 135 140
Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
145 150 155 160
Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
165 170 175
Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
180 185 190
Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
195 200 205
Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
210 215 220
Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
225 230 235 240
Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
245 250

<210> 100
<211> 248
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR 59 Alpha with Codon Optimized Mouse Constant

<400> 100

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Gly Gln Gln Val Met Gln Ile Pro Gln Tyr Gln His Val Gln Glu Gly
 1          5          10          15
Glu Asp Phe Thr Thr Tyr Cys Asn Ser Ser Thr Thr Leu Ser Asn Ile
 20          25          30
Gln Trp Tyr Lys Gln Arg Pro Gly Gly His Pro Val Phe Leu Ile Gln
 35          40          45
Leu Val Lys Ser Gly Glu Val Lys Lys Gln Lys Arg Leu Thr Phe Gln
 50          55          60
Phe Gly Glu Ala Lys Lys Asn Ser Ser Leu His Ile Thr Ala Thr Gln
 65          70          75          80
Thr Thr Asp Val Gly Thr Tyr Phe Cys Ala Pro Lys Arg Glu Tyr Gly
 85          90          95
Asn Lys Leu Val Phe Gly Ala Gly Thr Ile Leu Arg Val Lys Ser Asn
100          105          110
Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser
115          120          125
Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
130          135          140
Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val
145          150          155          160
Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
165          170          175
Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
180          185          190
Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu
195          200          205
Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Leu Val
210          215          220
Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
225          230          235          240
Met Thr Leu Arg Leu Trp Ser Ser
245
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<210> 101

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 101

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Met Lys Arg Glu Arg Glu Met Leu Leu Ile Thr Ser Met Leu Val Leu
 1          5          10          15
Trp Met Gln Leu Ser Gln Val Asn Gly Gln Gln Val Met Gln Ile Pro
```

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

<210> 102

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 102

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

Thr	Thr	Asp	Val	Gly	Thr	Tyr	Phe	Cys	Ala	Pro	Lys	Arg	Glu	Tyr	Gly
				85					90					95	
Asn	Lys	Leu	Val	Phe	Gly	Ala	Gly	Thr	Ile	Leu	Arg	Val	Lys	Ser	
			100					105					110		

<210> 104
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 59 Alpha CDR1

<400> 104
 Thr Thr Leu Ser Asn
 1 5

<210> 105
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 59 Alpha CDR2

<400> 105
 Leu Val Lys Ser Gly Glu Val
 1 5

<210> 106
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 59 Alpha CDR3

<400> 106
 Ala Pro Lys Arg Glu Tyr Gly Asn Lys Leu Val
 1 5 10

<210> 107
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TCR 59 Alpha Signal peptide

<400> 107

Met Lys Arg Glu Arg Glu Met Leu Leu Ile Thr Ser Met Leu Val Leu
1 5 10 15
Trp Met Gln Leu Ser Gln Val Asn
20

<210> 108

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 59 Beta Native with Codon Optimized Human
Constant

<400> 108

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattctctaa tcacttatac ttctatttgt acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgcctatt cgggcagggc ctccctacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgagggtgg ccgtgtttga gccaaagcgag gccgagatct cccacaccca gaaggccacc 480
ctgggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcactctgg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacagga atcacttcag atgccagggt cagttttacg gcctgtctga gaacgacgag 720
tggacccagg atcggggcaa gcctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcagggcg tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctgggtgctg 900
atggccatgg tgaagagaaa agacttctaa 930

<210> 109

<211> 918

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 59 Beta Native with Codon Optimized Mouse
Constant

<400> 109

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattctctaa tcacttatac ttctatttgt acagacaaat cttggggcag 180

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aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgcctatt cgggcagggc ctcctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgcgcaa tgtgaccccc 420
cctaagggtgt ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
ggcaaggagg tgcactccgg cgtgtgcacc gaccacagg cctacaagga gtccaactac 600
tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcacia ccctcggaat 660
cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
tccccaaagc ccgtgacca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tgggtggtcat ggccatggtg 900
aagcgcaaga acagctaa                                     918

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<210> 110

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta with Codon Optimized Human Constant

<400> 110

```

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

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210		215		220
Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly				
225		230		235
Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu				
	245		250	
Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr				
	260		265	
Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys				
	275		280	
Asp Phe				
290				

<210> 111

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta with Codon Optimized Mouse Constant

<400> 111

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

Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys
225					230					235					240
Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile
			245						250					255	
Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val
		260					265						270		
Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser		
	275						280					285			

<210> 112

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta with Codon Optimized Human Constant
and signal peptide

<400> 112

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

Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
				245					250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
	290					295					300				
Lys	Arg	Lys	Asp	Phe											
305															

<210> 113

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 113

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

Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly
225					230					235					240
Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg
				245					250					255	
Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser
			260					265					270		
Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala
		275					280					285			
Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn
	290					295					300				
Ser															
305															

<210> 114

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta variable region

<400> 114

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

<210> 115

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Beta CDR3

<400> 115

Ala Tyr Ser Gly Arg Ala Ser Tyr Glu Gln Tyr
1 5 10

<210> 116
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 59 Native full sequence with human constant

<400> 116
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgcctatt cgggcagggc ctcctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgaggtgg ccgtgtttga gccaaagcgag gccgagatct cccacaccca gaaggccacc 480
ctggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcactctgg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacagga atcacttcag atgccagggtg cagttttacg gcctgtctga gaacgacgag 720
tggaaccagg atcggggcaa gcctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcagggcg tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctggtgctg 900
atggccatgg tgaagagaaa agacttctaa ggctccggag caaccaattt cagcctgctg 960
aagcaggccg gcgatgtgga ggagaatcct ggcccaatga agaggagagag ggagatgcta 1020
ctcatcacat caatgttggg cttatggatg caattgtcac aggtgaatgg acaacaggta 1080
atgcaaatc ctcagtacca gcatgtacaa gaaggagagg acttcaccac gtactgcaat 1140
tcctcaacta ctttaagcaa tatacagtgg tataagcaaa ggcctggtgg acatcccgtt 1200
tttttgatac agttagttaa gaggggagaa gtgaagaagc agaaaagact gacatttcag 1260
tttgagaag caaaaaagaa cagctccctg cacatcacag ccaccagac tacagatgta 1320
ggaacctact tctgtgcacc caagcgggaa tatggaaaca aactggtctt tggcgcagga 1380
accattctga gagtcaagtc caatatccag aatccggacc ccgcggtata tcaactgcgc 1440
gactcaaaat catccgataa gagtgtctgt ttgtttactg acttcgacag tcaaactaat 1500
gtctctcaga gcaaagattc cgatgtctac atcactgaca agtgcgttct ggatatgcgg 1560
agcatggatt ttaagtccaa ctccgccgta gcctggtcca acaagtcaga ctttgcctgt 1620
gcaaatgctt tcaacaactc aattatccct gaggacactt tctttccttc accggagtcc 1680
tcatgcgatg ttaaaactgg cgaaaaatct tttgagacgg atacgaacct caacttccaa 1740
aatgtgagcg ttattggctt taggattctg cttctcaagg ttgcgggggt caatctcctg 1800
atgacgttgc ggctttggag cagctaa 1827

<210> 117
<211> 1803
<212> DNA
<213> Artificial Sequence

<220>

<223> TCR 59 Nativefull sequence with mouse constant

<400> 117

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atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaat tcaacttgaa gatccgggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgcctatt cgggcagggc ctcctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgcgcaa tgtgaccccc 420
cctaagggtgt ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
ggcaaggagg tgcactccgg cgtgtgcacc gaccacagg cctacaagga gtccaactac 600
tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcacia ccctcggaat 660
cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
tcccaaaagc ccgtgaccca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccacctgtga tgccgtgctg gtgtccacac tggtggtcat ggccatgggtg 900
aagcgcaaga acagctaagg ctccggagca accaatttca gcctgctgaa gcaggccggc 960
gatgtggagg agaatcctgg cccaatgaag agggagaggg agatgctact catcacatca 1020
atgttggtct tatggatgca attgtcacag gtgaatggac aacaggtaat gcaaattcct 1080
cagtaccagc atgtacaaga aggagaggac ttcaccacgt actgcaattc ctcaactact 1140
ttaagcaata tacagtggta taagcaaagg cctgggtggac atcccgtttt tttgatacag 1200
ttagtgaaga gtggagaagt gaagaagcag aaaagactga catttcagtt tggagaagca 1260
aaaaagaaca gctccctgca catcacagcc acccagacta cagatgtagg aacctacttc 1320
tgtgcaccca agcgggaata tggaaacaaa ctggtctttg gcgcaggaac cattctgaga 1380
gtcaagtcca atatccagaa tccggagcct gccgtgtacc agctgaagga cccacggagc 1440
caggatagca ccctgtgcct gttcaccgac tttgattctc agatcaacgt gccaagacc 1500
atggagagcg gcaccttcat cacagacaag tgcgtgctgg atatgaaggc catggacagc 1560
aagtccaacg gcgccatcgc ctgggtccaat cagacatctt tcacctgcca ggatatcttt 1620
aaggagacaa atgccaccta tccttctctc gacgtgccat gtgatgccac cctgacagag 1680
aagagcttcg agaccgacat gaacctgaat tttcagaatc tgctcgtgat tgtcctgaga 1740
atcctgctgc tgaagggtggc cggctttaac ctgctgatga ccctgaggct gtggagctcc 1800
tga 1803
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<210> 118

<211> 607

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 Full sequence with human constant

<400> 118

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

Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170						175
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro
			180					185						190	
Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu
		195					200					205			
Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys
	210					215					220				
Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly
225					230					235					240
Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg
				245					250					255	
Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser
			260					265					270		
Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala
		275					280					285			
Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn
	290					295					300				
Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp
305					310					315					320
Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Arg	Glu	Arg	Glu	Met	Leu	Leu
				325					330					335	
Ile	Thr	Ser	Met	Leu	Val	Leu	Trp	Met	Gln	Leu	Ser	Gln	Val	Asn	Gly
			340					345					350		
Gln	Gln	Val	Met	Gln	Ile	Pro	Gln	Tyr	Gln	His	Val	Gln	Glu	Gly	Glu
		355					360					365			
Asp	Phe	Thr	Thr	Tyr	Cys	Asn	Ser	Ser	Thr	Thr	Leu	Ser	Asn	Ile	Gln
	370					375					380				
Trp	Tyr	Lys	Gln	Arg	Pro	Gly	Gly	His	Pro	Val	Phe	Leu	Ile	Gln	Leu
385					390					395					400
Val	Lys	Ser	Gly	Glu	Val	Lys	Lys	Gln	Lys	Arg	Leu	Thr	Phe	Gln	Phe
				405					410					415	
Gly	Glu	Ala	Lys	Lys	Asn	Ser	Ser	Leu	His	Ile	Thr	Ala	Thr	Gln	Thr
			420					425					430		
Thr	Asp	Val	Gly	Thr	Tyr	Phe	Cys	Ala	Pro	Lys	Arg	Glu	Tyr	Gly	Asn
		435					440					445			
Lys	Leu	Val	Phe	Gly	Ala	Gly	Thr	Ile	Leu	Arg	Val	Lys	Ser	Asn	Ile
	450					455					460				
Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser	Gln
465					470					475					480
Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn	Val
				485					490					495	
Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys	Val	Leu
			500					505					510		
Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp	Ser
		515					520					525			
Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn	Ala
	530					535					540				

Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu	Lys
545					550					555					560
Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu	Val	Ile
				565					570					575	
Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met
			580					585					590		
Thr	Leu	Arg	Leu	Trp	Ser	Ser									
			595												

<210> 120
 <211> 837
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 60 Alpha Native with Codon Optimized Human
 Constant

<400> 120
 atgatgaaat ccttgagagt tttagtagtg atcctgtggc ttcagttgag ctgggttttg 60
 agccaacaga aggaggtgga gcagaattct ggacccctca gtgttccaga gggagccatt 120
 gcctctctca actgcactta cagtgaccga ggttcccagt ctttcttctg gtacagacaa 180
 tattctggga aaagccctga gttgataatg ttcataact ccaatgggta caaagaagat 240
 ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac 300
 tcccagccca gtgattcagc cacctacctc tgtgccgtga acatgttggg gagggtggag 360
 agcaactata aactgacatt tggaaaagga actctcttaa ccgtgaatcc aaatatccag 420
 aatccggacc ccgcggtata tcaactgcgc gactcaaaat catccgataa gagggtctgt 480
 ttgtttactg acttcgacag tcaaaactaat gtctctcaga gcaaagattc cgatgtctac 540
 atcactgaca agtgcgttct ggatatgcgg agcatggatt ttaagtccaa ctccgccgta 600
 gcctgggtcca acaagtcaga ctttgctgtg gcaaatgctt tcaacaactc aattatccct 660
 gaggacactt tctttccttc accggagtcc tcatgcatg ttaaaactgg cgaaaaatct 720
 tttagacggg atacgaacct caacttccaa aatttgagcg ttattggctt taggattctg 780
 cttctcaagg ttgcgggggt caatctcctg atgacgttgc ggctttggag cagctaa 837

<210> 121
 <211> 825
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 60 Alpha Native with Codon Optimized Mouse
 Constant

<400> 121
 atgatgaaat ccttgagagt tttagtagtg atcctgtggc ttcagttgag ctgggttttg 60
 agccaacaga aggaggtgga gcagaattct ggacccctca gtgttccaga gggagccatt 120
 gcctctctca actgcactta cagtgaccga ggttcccagt ctttcttctg gtacagacaa 180
 tattctggga aaagccctga gttgataatg ttcataact ccaatgggta caaagaagat 240
 ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac 300

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tcccagccca gtgattcagc cacctacctc tgtgccgtga acatgttggg gagtggaggt 360
agcaactata aactgacatt tggaaaagga actctcttaa cctgtaatcc aaatatccag 420
aatccggagc ctgccgtgta ccagctgaag gacccacgga gccaggatag caccctgtgc 480
ctgttcaccg actttgattc tcagatcaac gtgcccaga ccatggagag cggcaccttc 540
atcacagaca agtgcgtgct ggatatgaag gccatggaca gcaagtccaa cggcgccatc 600
gcctgggtcca atcagacatc tttcacctgc caggatatct ttaaggagac aaatgccacc 660
tatccttcct ctgacgtgcc atgtgatgcc accctgacag agaagagctt cgagaccgac 720
atgaacctga attttcagaa tctgctcgtg attgtcctga gaatcctgct gctgaagggtg 780
gccggcttta acctgctgat gaccctgagg ctgtggagct cctga 825

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<210> 122

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha with Codon Optimized Human Constant

<400> 122

```

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

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245

250

255

<210> 123

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha with Codon Optimized Mouse Constant

<400> 123

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

<210> 124

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 124

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

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 125

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

Ser Ser

<210> 126

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha variable region

<400> 126

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

<210> 127

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60, 61 Alpha CDR1

<400> 127

Asp	Arg	Gly	Ser	Gln	Ser
1				5	

<210> 128

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60, 61 Alpha CDR2

<400> 128

Ile	Tyr	Ser	Asn	Gly	Asp
1				5	

<210> 129

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Alpha CDR3

<400> 129

Ala	Val	Asn	Met	Leu	Gly	Ser	Gly	Gly	Ser	Asn	Tyr	Lys	Leu	Thr
1				5					10					15

<210> 130

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60, 61 Alpha Signal peptide

<400> 130

Met	Met	Lys	Ser	Leu	Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Ser	Trp	Val	Trp	Ser	Gln										
				20											

<210> 131

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 60 Beta Native with Codon Optimized Human
Constant

<400> 131

atggatacct	ggctcgtatg	ctgggcaatt	tttagtctct	tgaaagcagg	actcacagaa	60
cctgaagtca	cccagactcc	cagccatcag	gtcacacaga	tgggacagga	agtgatcttg	120
cgctgtgtcc	ccatctctaa	tcacttatac	ttctattggg	acagacaaat	cttggggcag	180
aaagtcgagt	ttctggtttc	cttttataat	aatgaaatct	cagagaagtc	tgaaatattc	240
gatgatcaat	tctcagttga	aaggcctgat	ggatcaaatt	tactctgaa	gatccgggcc	300
acaaaagctg	aggactcagc	catgtacttc	tgtgccatca	gtcggacagt	ctcctacgag	360
cagtacttcg	ggccggggcac	caggctcacg	gtcacagagg	acctgaataa	ggtgttcccc	420
cctgaggtgg	ccgtgtttga	gccaagcgag	gccgagatct	cccacaccca	gaaggccacc	480
ctggtgtgcc	tggcaaccgg	cttctttccc	gatcacgtgg	agctgtcctg	gtgggtgaac	540
ggcaaggagg	tgcactctgg	cgtgtgcaca	gaccacagc	ccctgaagga	gcagcctgcc	600
ctgaatgatt	cccgtatttg	tctgtcctct	cggctgagag	tgtctgccac	cttttggcag	660
aaccacgga	atcacttcag	atgccagggt	cagttttacg	gcctgtctga	gaacgacgag	720
tggacccagg	atcggggcaa	gcctgtgaca	cagatcgtga	gcgcggaagc	atggggcaga	780
gccgactgtg	gcttcaccag	cgtgtcctat	cagcagggcg	tgctgtccgc	caccatcctg	840
tacgagatcc	tgctgggcaa	ggccacactg	tatgccgtgc	tggtgtctgc	cctgggtgctg	900
atggccatgg	tgaagagaaa	agacttctaa				930

<210> 132
 <211> 918
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 60 Beta Native with Codon Optimized Mouse
 Constant

<400> 132
 atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
 cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
 cgctgtgtcc ccactctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
 aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
 gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
 acaaaagctgg aggactcagc catgtacttc tgtgccatca gtcggacagt ctcctacgag 360
 cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgcgcaa tgtgaccccc 420
 cctaagggtg ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
 ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
 ggcaaggagg tgcactccgg cgtgtgcacc gaccacagg cctacaagga gtccaactac 600
 tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcaca ccctcggaat 660
 cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
 tcccaaagc ccgtgacca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
 atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
 ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tgggtggtcat ggccatggtg 900
 aagcgcaaga acagctaa 918

<210> 133
 <211> 290
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 60 Beta with Codon Optimized Human Constant

<400> 133
 Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr Gln Met Gly
 1 5 10 15
 Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His Leu Tyr Phe
 20 25 30
 Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe Leu Val Ser
 35 40 45
 Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe Asp Asp Gln
 50 55 60
 Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu Lys Ile Arg
 65 70 75 80
 Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala Ile Ser Arg
 85 90 95
 Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
 100 105 110

Thr	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu
		115					120					125			
Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys
	130					135					140				
Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val
145					150					155					160
Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu
			165						170					175	
Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg
		180						185						190	
Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg
	195						200					205			
Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln
	210					215					220				
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly
225					230					235					240
Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			245						250					255	
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
		260						265						270	
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys
	275						280					285			
Asp	Phe														
	290														

<210> 134

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Beta with Codon Optimized Mouse Constant

<400> 134

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

115	120	125
Pro Ser Lys Ala Glu Ile	Ala Asn Lys Gln Lys	Ala Thr Leu Val Cys
130	135	140
Leu Ala Arg Gly Phe Phe	Pro Asp His Val Glu	Leu Ser Trp Trp Val
145	150	155
Asn Gly Lys Glu Val His	Ser Gly Val Cys Thr	Asp Pro Gln Ala Tyr
165	170	175
Lys Glu Ser Asn Tyr Ser	Tyr Cys Leu Ser Ser	Arg Leu Arg Val Ser
180	185	190
Ala Thr Phe Trp His Asn	Pro Arg Asn His Phe	Arg Cys Gln Val Gln
195	200	205
Phe His Gly Leu Ser Glu	Glu Asp Lys Trp Pro	Glu Gly Ser Pro Lys
210	215	220
Pro Val Thr Gln Asn Ile	Ser Ala Glu Ala Trp	Gly Arg Ala Asp Cys
225	230	235
Gly Ile Thr Ser Ala Ser	Tyr Gln Gln Gly Val	Leu Ser Ala Thr Ile
245	250	255
Leu Tyr Glu Ile Leu Leu	Gly Lys Ala Thr Leu	Tyr Ala Val Leu Val
260	265	270
Ser Thr Leu Val Val Met	Ala Met Val Lys Arg	Lys Asn Ser
275	280	285

<210> 135

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Beta with Codon Optimized Human Constant
and signal peptide

<400> 135

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

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

<210> 136

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 136

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala	
1	15
Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr	
20	30
Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His	
35	45
Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe	
50	60
Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe	
65	80
Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu	
85	95
Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala	
100	110
Ile Ser Arg Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg	

115	120	125
Leu Thr Val Thr Glu Asp	Leu Arg Asn Val Thr Pro	Pro Lys Val Ser
130	135	140
Leu Phe Glu Pro Ser Lys	Ala Glu Ile Ala Asn Lys	Gln Lys Ala Thr
145	150	155
Leu Val Cys Leu Ala Arg	Gly Phe Phe Pro Asp His	Val Glu Leu Ser
165	170	175
Trp Trp Val Asn Gly Lys	Glu Val His Ser Gly Val	Cys Thr Asp Pro
180	185	190
Gln Ala Tyr Lys Glu Ser	Asn Tyr Ser Tyr Cys Leu	Ser Ser Arg Leu
195	200	205
Arg Val Ser Ala Thr Phe	Trp His Asn Pro Arg Asn	His Phe Arg Cys
210	215	220
Gln Val Gln Phe His Gly	Leu Ser Glu Glu Asp Lys	Trp Pro Glu Gly
225	230	235
Ser Pro Lys Pro Val Thr	Gln Asn Ile Ser Ala Glu	Ala Trp Gly Arg
245	250	255
Ala Asp Cys Gly Ile Thr	Ser Ala Ser Tyr Gln Gln	Gly Val Leu Ser
260	265	270
Ala Thr Ile Leu Tyr Glu	Ile Leu Leu Gly Lys Ala	Thr Leu Tyr Ala
275	280	285
Val Leu Val Ser Thr Leu	Val Val Met Ala Met Val	Lys Arg Lys Asn
290	295	300
Ser		
305		

<210> 137

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Beta variable region

<400> 137

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

Thr

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 60 Beta CDR3

<400> 138
Ala Ile Ser Arg Thr Val Ser Tyr Glu Gln Tyr
1 5 10

<210> 139
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 60 Native full sequence with human constant

<400> 139
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgccatca gtcggacagt ctcctacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgaggtgg ccgtgtttga gccaaagcag gccgagatct cccacacca gaaggccacc 480
ctgggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcactctgg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacagga atcacttcag atgccagggtg cagttttacg gcctgtctga gaacgacgag 720
tggaacccagg atcggggcaa gcctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcagggcg tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctggtgctg 900
atggccatgg tgaagagaaa agacttctaa ggctccggag caaccaatit cagcctgctg 960
aagcaggccg gcgatgtgga ggagaatcct ggccaatga tgaaatcctt gagagtttta 1020
ctagtgatcc tgtggcttca gttgagctgg gtttgagacc aacagaagga ggtggagcag 1080
aattctggac ccctcagtggt tccagaggga gccattgcct ctctcaactg cacttacagt 1140
gaccgaggtt cccagtcctt cttctggtac agacaatatt ctgggaaaag ccctgagttg 1200
ataatgttca tatactccaa tgggtgacaaa gaagatggaa gggtttacagc acagctcaat 1260
aaagccagcc agtatgtttc tctgtcatc agagactccc agcccagtga ttcagccacc 1320
tacctctgtg ccgtgaacat gttggggagt ggaggtagca actataaact gacatttgga 1380
aaaggaactc tcttaaccgt gaatccaaat atccagaatc cggaccccg cgtatatcaa 1440

ctgcgcgact	caaaatcatc	cgataagagt	gtctgtttgt	ttactgactt	cgacagtcaa	1500
actaatgtct	ctcagagcaa	agattccgat	gtctacatca	ctgacaagtg	cgttctggat	1560
atgcggagca	tggattttta	gtccaactcc	gccgtagcct	ggccaacaa	gtcagacttt	1620
gcctgtgcaa	atgctttcaa	caactcaatt	atccctgagg	acactttctt	tccttcaccg	1680
gagtcctcat	gcgatgttaa	actggtcgaa	aaatcttttg	agacggatac	gaacctcaac	1740
ttccaaaatt	tgagcgttat	tggctttagg	attctgcttc	tcaaggttgc	gggggttcaat	1800
ctcctgatga	cgttgcggct	ttggagcagc	taa			1833

<210> 140

<211> 1809

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 60 Nativefull sequence with mouse constant

<400> 140

atggatacct	ggctcgtatg	ctgggcaatt	tttagtctct	tgaaagcagg	actcacagaa	60
cctgaagtca	cccagactcc	cagccatcag	gtcacacaga	tgggacagga	agtgatcttg	120
cgctgtgtcc	ccatctctaa	tcacttatac	ttctattggg	acagacaaat	cttggggcag	180
aaagtcgagt	ttctggtttc	cttttataat	aatgaaatct	cagagaagtc	tgaaatattc	240
gatgatcaat	tctcagttga	aaggcctgat	ggatcaaatt	tcactctgaa	gatccgggtcc	300
acaaagctgg	aggactcagc	catgtacttc	tgtgccatca	gtcggacagt	ctcctacgag	360
cagtacttcg	ggccgggcac	caggctcacg	gtcacagagg	acctgcgcaa	tgtgaccccc	420
cctaagggtg	ccctgtttga	gccctctaag	gccgagatcg	ccaacaagca	gaaggccacc	480
ctgggtgtgcc	tggccagagg	cttcttccct	gatcacgtgg	agctgagctg	gtgggtgaat	540
ggcaaggagg	tgactccggg	cgtgtgcacc	gaccacaggg	cctacaagga	gtccaactac	600
tcttattgtc	tgtcctctag	gctgcgcgtg	agcgccacat	tctggcacia	ccctcggaat	660
cacttcagat	gccaggtgca	gtttcacggc	ctgagcgagg	aggataagtg	gccagagggc	720
tcccaaaagc	ccgtgaccca	gaatatctct	gccgaggcat	ggggcagggc	cgactgtgga	780
atcacctccg	cctcttatca	gcagggcgtg	ctgtccgcca	caatcctgta	cgagatcctg	840
ctgggcaagg	ccaccctgta	tgccgtgctg	gtgtccacac	tggtgggtcat	ggccatgggtg	900
aagcgcaaga	acagctaagg	ctccggagca	accaatttca	gcctgctgaa	gcaggccggc	960
gatgtggagg	agaatcctgg	cccaatgatg	aaatccttga	gagttttact	agtgatcctg	1020
tggcttcagt	tgagctgggt	ttggagccaa	cagaaggagg	tggagcagaa	ttctggaccc	1080
ctcagtgttc	cagagggagc	cattgcctct	ctcaactgca	cttacagtga	ccgaggttcc	1140
cagtccttct	tctggtacag	acaatattct	gggaaaagcc	ctgagttgat	aatgttcata	1200
tactccaatg	gtgacaaaaga	agatggaagg	tttacagcac	agctcaataa	agccagccag	1260
tatgtttctc	tgctcatcag	agactcccag	cccagtgatt	cagccaccta	cctctgtgcc	1320
gtgaacatgt	tggggagtg	aggtagcaac	tataaactga	catttgga	aggaaactctc	1380
ttaaccgtga	atccaaatat	ccagaatccg	gagcctgccg	tgtaccagct	gaaggaccca	1440
cggagccagg	atagcaccct	gtgcctgttc	accgactttg	attctcagat	caacgtgccc	1500
aagaccatgg	agagcggcac	cttcatcaca	gacaagtgcg	tgctggatat	gaaggccatg	1560
gacagcaagt	ccaacggcgc	catcgcctgg	tccaatcaga	catctttcac	ctgccaggat	1620
atctttaagg	agacaaatgc	cacctatcct	tcctctgacg	tgccatgtga	tgccaccctg	1680
acagagaaga	gcttcgagac	cgacatgaac	ctgaattttc	agaatctgct	cgtagttgtc	1740
ctgagaatcc	tgctgctgaa	ggtggccggc	tttaacctgc	tgatgaccct	gaggctgtgg	1800
agctcctga						1809

<210> 141

<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 60 Full sequence with human constant

<400> 141

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

Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu Ser Trp Val Trp Ser
 340 345 350
 Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu
 355 360 365
 Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln
 370 375 380
 Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile
 385 390 395 400
 Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala
 405 410 415
 Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser
 420 425 430
 Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Asn Met Leu Gly
 435 440 445
 Ser Gly Gly Ser Asn Tyr Lys Leu Thr Phe Gly Lys Gly Thr Leu Leu
 450 455 460
 Thr Val Asn Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
 465 470 475 480
 Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
 485 490 495
 Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
 500 505 510
 Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
 515 520 525
 Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
 530 535 540
 Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
 545 550 555 560
 Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
 565 570 575
 Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
 580 585 590
 Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
 595 600 605
 Ser

<210> 142

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 Full sequence with mouse constant

<400> 142

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
 1 5 10 15
 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr

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

	420		425		430										
Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Asn	Met	Leu	Gly	Ser	Gly	Gly	Ser
	435						440					445			
Asn	Tyr	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Leu	Leu	Thr	Val	Asn	Pro
	450					455					460				
Asn	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg
465					470					475					480
Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile
			485						490					495	
Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys
		500						505					510		
Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala
	515						520					525			
Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr
	530					535					540				
Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr
545					550					555					560
Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu
			565					570						575	
Val	Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu
		580						585					590		
Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser							
	595						600								

<210> 143

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Alpha Native with Codon Optimized Human
Constant

<400> 143

```

atgatgaaat ccttgagagt tttactagtg atcctgtggc ttcagttgag ctgggttttg 60
agccaacaga aggaggtgga gcagaattct ggaccctca gtgttccaga gggagccatt 120
gccttcttca actgcactta cagtgaccga gggtcccagt ccttcttctg gtacagacaa 180
tattctggga aaagccctga gttgataatg ttcataact ccaatgggta caaagaagat 240
ggaagggtta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac 300
tcccagccca gtgattcagc cacctacctc tgtgccgtga acatagagaa taacaatgcc 360
agactcatgt ttggagatgg aactcagctg gtggtgaagc ccaatatcca gaatccggac 420
cccgcggtat atcaactgcg cgactcaaaa tcatccgata agagtgtctg tttgtttact 480
gacttcgaca gtcaaaactaa tgtctctcag agcaaagatt ccgatgtcta catcactgac 540
aagtgcgttc tggatatgcg gagcatggat tttaagtcca actccgccgt agcctgggtcc 600
aacaagtcag actttgcctg tgcaaatgct ttcaacaact caattatccc tgaggacact 660
ttctttcctt caccggagtc ctcatgcat gttaaaactgg tcgaaaaatc ttttgagacg 720
gatacgaacc tcaacttcca aaatttgagc gttattggct ttaggattct gcttctcaag 780
gttgcggggt tcaatctcct gatgacgttg cggctttgga gcagctaa 828

```

<210> 144
<211> 816
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 61 Alpha Native with Codon Optimized Mouse
Constant

<400> 144
atgatgaaat ccttgagagt ttctactagt atcctgtggc ttcagttgag ctgggtttgg 60
agccaacaga aggagggtgga gcagaattct ggacccctca gtgttccaga gggagccatt 120
gcctctctca actgcactta cagtgaccga gggtcccagt ccttcttctg gtacagacaa 180
tattctggga aaagccctga gttgataatg ttcatatact ccaatgggtga caaagaagat 240
ggaagggtta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac 300
tcccagccca gtgattcagc cacctacctc tgtgccgtga acatagagaa taacaatgcc 360
agactcatgt ttggagatgg aactcagctg gtggtgaagc ccaatatcca gaatccggag 420
cctgccgtgt accagctgaa ggaccacagg agccaggata gcaccctgtg cctgttcacc 480
gactttgatt ctcatagcaa cgtgccaag accatggaga gcggcacctt catcacagac 540
aagtgcgtgc tggatatgaa ggccatggac agcaagtcca acggcgccat cgcttggtcc 600
aatcagacat ctttcacctg ccaggatatc ttttaaggaga caaatgccac ctatccttcc 660
tctgacgtgc catgtgatgc caccctgaca gagaagagct tcgagaccga catgaacctg 720
aattttcaga atctgtctgt gattgtcctg agaatcctgc tgctgaaggt ggccggcttt 780
aacctgctga tgaccctgag gctgtggagc tcctga 816

<210> 145
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 61 Alpha with Codon Optimized Human Constant

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

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

<210> 146

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Alpha with Codon Optimized Mouse Constant

<400> 146

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

				180				185				190				
Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	
		195					200					205				
Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu	
	210					215					220					
Val	Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	
225					230					235					240	
Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser								
				245												

<210> 147

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 147

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

225		230		235		240									
Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile
		245		250		255									
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu
		260		265		270									
Trp	Ser	Ser													
		275													

<210> 148
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 61 Alpha with Codon Optimized Mouse Constant
 and signal peptide

<400> 148

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

				245					250					255
Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser
			260					265					270	

<210> 149
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 61 Alpha variable region

<400> 149
 Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu Gly
 1 5 10 15
 Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser
 20 25 30
 Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
 35 40 45
 Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
 50 55 60
 Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser Gln
 65 70 75 80
 Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Asn Ile Glu Asn Asn
 85 90 95
 Asn Ala Arg Leu Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro
 100 105 110

<210> 150
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 61 Alpha CDR3

<400> 150
 Ala Val Asn Ile Glu Asn Asn Asn Ala Arg Leu Met
 1 5 10

<210> 151
 <211> 930
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR 61 Beta Native with Codon Optimized Human

Constant

<400> 151

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atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca ccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattcttaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca ccaaactgtt tagctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgaataa ggtgttcccc 420
cctgagggtg ccgtgtttga gccaaagcag gccgagatct cccacaccca gaaggccacc 480
ctgggtgtgcc tggcaaccgg cttctttccc gatcacgtgg agctgtcctg gtgggtgaac 540
ggcaaggagg tgcactctgg cgtgtgcaca gaccacagc ccctgaagga gcagcctgcc 600
ctgaatgatt cccgctattg tctgtcctct cggctgagag tgtctgccac cttttggcag 660
aaccacgga atcacttcag atgccagggt cagttttacg gcctgtctga gaacgacgag 720
tggaccagg atcggggcaa gcctgtgaca cagatcgtga gcgcggaagc atggggcaga 780
gccgactgtg gcttcaccag cgtgtcctat cagcaggggc tgctgtccgc caccatcctg 840
tacgagatcc tgctgggcaa ggccacactg tatgccgtgc tgggtgtctgc cctgggtgctg 900
atggccatgg tgaagagaaa agacttctaa 930
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<210> 152

<211> 918

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Beta Native with Codon Optimized Mouse

Constant

<400> 152

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atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca ccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattcttaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca ccaaactgtt tagctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagagg acctgacgaa tgtgaccccc 420
cctaagggtg ccctgtttga gccctctaag gccgagatcg ccaacaagca gaaggccacc 480
ctgggtgtgcc tggccagagg cttcttccct gatcacgtgg agctgagctg gtgggtgaat 540
ggcaaggagg tgcactccgg cgtgtgcacc gaccacagc cctacaagga gtccaactac 600
tcttattgtc tgtcctctag gctgcgcgtg agcgccacat tctggcacia ccctcggaat 660
cacttcagat gccagggtgca gtttcacggc ctgagcgagg aggataagtg gccagagggc 720
tcccaaagc ccgtgaccca gaatatctct gccgaggcat ggggcagggc cgactgtgga 780
atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tgggtggtcat ggccatggtg 900
aagcgcaaga acagctaa 918
```

<210> 153

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta with Codon Optimized Human Constant

<400> 153

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

<210> 154

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta with Codon Optimized Mouse Constant

<400> 154

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

<210> 155

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta with Codon Optimized Human Constant

and signal peptide

<400> 155

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

<210> 156

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 156

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

<210> 157

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta variable region

<400> 157

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

<210> 158

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Beta CDR3

<400> 158

```
Ala Ser Thr Lys Arg Phe Ser Tyr Glu Gln Tyr
 1              5              10
```

<210> 159

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Native full sequence with human constant

<400> 159

```
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccactctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
```

gatgatcaat	tctcagttga	aaggcctgat	ggatcaaatt	tcactctgaa	gatccgggtcc	300
acaaaagctgg	aggactcagc	catgtacttc	tgtgccagca	ccaaacgttt	tagctacgag	360
cagtacttcg	ggccggggcac	caggctcacg	gtcacagagg	acctgaataa	ggtgttcccc	420
cctgagggtgg	ccgtgtttga	gccaaagcgag	gccgagatct	cccacaccca	gaaggccacc	480
ctgggtgtgcc	tggcaaccgg	cttctttccc	gatcacgtgg	agctgtcctg	gtgggtgaac	540
ggcaaggagg	tgcactctgg	cgtgtgcaca	gaccacagc	ccctgaagga	gcagcctgcc	600
ctgaatgatt	cccgtctattg	tctgtcctct	cggctgagag	tgtctgccac	cttttggcag	660
aaccacgga	atcacttcag	atgccagggtg	cagttttacg	gcctgtctga	gaacgacgag	720
tggacccagg	atcggggcaa	gcctgtgaca	cagatcgtga	gcgcggaagc	atggggcaga	780
gccgactgtg	gcttcaccag	cgtgtcctat	cagcagggcg	tgctgtccgc	caccatcctg	840
tacgagatcc	tgctgggcaa	ggccacactg	tatgccgtgc	tggtgtctgc	cctgggtgctg	900
atggccatgg	tgaagagaaa	agacttctaa	ggctccggag	caaccaatit	cagcctgctg	960
aagcaggccg	gcgatgtgga	ggagaatcct	ggcccaatga	tgaaatcctt	gagagtitta	1020
ctagtgatcc	tgtggcttca	gttgagctgg	gtttggagcc	aacagaagga	ggtggagcag	1080
aattctggac	ccctcagtgt	tccagaggga	gccattgcct	ctctcaactg	cacttacagt	1140
gaccgaggtt	cccagtcctt	cttctggtac	agacaatatt	ctgggaaaag	ccctgagttg	1200
ataatgttca	tatactccaa	tggtgacaaa	gaagatggaa	ggtttacagc	acagctcaat	1260
aaagccagcc	agtatgtttc	tctgctcatc	agagactccc	agcccagtga	ttcagccacc	1320
tacctctgtg	ccgtgaacat	agagaataac	aatgccagac	tcatgtttgg	agatggaact	1380
cagctgggtgg	tgaagcccaa	tatccagaat	ccggaccccg	cggtatatca	actgcgcgac	1440
tcaaaatcat	ccgataagag	tgtctgtttg	tttactgact	tcgacagtca	aactaatgtc	1500
tctcagagca	aagattccga	tgtctacatc	actgacaagt	gcgttctgga	tatgcggagc	1560
atggatttta	agtccaactc	cgccgtagcc	tggtccaaca	agtcagactt	tgctgtgca	1620
aatgctttca	acaactcaat	tatccctgag	gacactttct	ttccttcacc	ggagtcctca	1680
tgcatgttta	aactggtcga	aaaatctttt	gagacggata	cgaacctcaa	cttccaaaat	1740
ttgagcgta	ttggctttag	gattctgctt	ctcaagggtg	cgggggttcaa	tctcctgatg	1800
acgttgcggc	tttggagcag	ctaa				1824

<210> 160

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Nativefull sequence with mouse constant

<400> 160

atggatacct	ggctcgtatg	ctgggcaatt	tttagtctct	tgaaagcagg	actcacagaa	60
cctgaagtca	cccagactcc	cagccatcag	gtcacacaga	tgggacagga	agtgatcttg	120
cgctgtgtcc	ccatctctaa	tcacttatac	ttctattggg	acagacaaat	cttggggcag	180
aaagtcgagt	ttctggtttc	cttttataat	aatgaaatct	cagagaagtc	tgaaatattc	240
gatgatcaat	tctcagttga	aaggcctgat	ggatcaaatt	tcactctgaa	gatccgggtcc	300
acaaaagctgg	aggactcagc	catgtacttc	tgtgccagca	ccaaacgttt	tagctacgag	360
cagtacttcg	ggccggggcac	caggctcacg	gtcacagagg	acctgcgcaa	tgtgaccccc	420
cctaagggtgt	ccctgtttga	gccctctaag	gccgagatcg	ccaacaagca	gaaggccacc	480
ctgggtgtgcc	tggccagagg	cttcttccct	gatcacgtgg	agctgagctg	gtgggtgaat	540
ggcaaggagg	tgcactccgg	cgtgtgcacc	gaccacagg	cctacaagga	gtccaactac	600
tcttattgtc	tgtcctctag	gctgcgcgtg	agcgccacat	tctggcacia	ccctcggaat	660
cacttcagat	gccagggtgca	gtttcacggc	ctgagcgagg	aggataagtg	gccagagggc	720
tccccaaagc	ccgtgaccca	gaatatctct	gccgaggcat	ggggcagggc	cgactgtgga	780

```

atcacctccg cctcttatca gcagggcgtg ctgtccgcca caatcctgta cgagatcctg 840
ctgggcaagg ccaccctgta tgccgtgctg gtgtccacac tgggtggcat ggccatgggtg 900
aagcgcaaga acagctaagg ctccggagca accaatttca gcctgctgaa gcaggccggc 960
gatgtggagg agaatcctgg cccaatgatg aaatccttga gagttttact agtgatcctg 1020
tggcttcagt tgagctgggt ttggagccaa cagaaggagg tggagcagaa ttctggaccc 1080
ctcagtgttc cagagggagc cattgcctct ctcaactgca cttacagtga ccgaggttcc 1140
cagtccttct tctggtacag acaatattct gggaaaagcc ctgagttgat aatgttcata 1200
tactccaatg gtgacaaaga agatggaagg tttacagcac agctcaataa agccagccag 1260
tatgtttctc tgctcatcag agactcccag cccagtgtt cagccaccta cctctgtgcc 1320
gtgaacatag agaataacaa tgccagactc atgtttggag atggaactca gctgggtgggtg 1380
aagcccaata tccagaatcc ggagcctgcc gtgtaccagc tgaaggaccc acggagccag 1440
gatagcacc cgtgcctgtt caccgacttt gattctcaga tcaacgtgcc caagaccatg 1500
gagagcggca cttcatcac agacaagtgc gtgctggata tgaaggccat ggacagcaag 1560
tccaacggcg ccacgcctg gtccaatcag acatctttca cctgccagga tatctttaag 1620
gagacaaatg ccacctatcc ttctctgac gtgccatgtg atgccaccct gacagagaag 1680
agcttcgaga ccgacatgaa cctgaatttt cagaatctgc tcgtgattgt cctgagaatc 1740
ctgctgctga aggtggccgg ctttaacctg ctgatgaccc tgaggctgtg gagctcctga 1800

```

<210> 161

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 Full sequence with human constant

<400> 161

```

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

```

Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	180	185	190
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	195	200	205
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	210	215	220
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	225	230	235
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	245	250	255
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	260	265	270
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	275	280	285
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	290	295	300
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	305	310	315
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Met	Lys	Ser	Leu	325	330	335
Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ser	Trp	Val	Trp	Ser	340	345	350
Gln	Gln	Lys	Glu	Val	Glu	Gln	Asn	Ser	Gly	Pro	Leu	Ser	Val	Pro	Glu	355	360	365
Gly	Ala	Ile	Ala	Ser	Leu	Asn	Cys	Thr	Tyr	Ser	Asp	Arg	Gly	Ser	Gln	370	375	380
Ser	Phe	Phe	Trp	Tyr	Arg	Gln	Tyr	Ser	Gly	Lys	Ser	Pro	Glu	Leu	Ile	385	390	395
Met	Phe	Ile	Tyr	Ser	Asn	Gly	Asp	Lys	Glu	Asp	Gly	Arg	Phe	Thr	Ala	405	410	415
Gln	Leu	Asn	Lys	Ala	Ser	Gln	Tyr	Val	Ser	Leu	Leu	Ile	Arg	Asp	Ser	420	425	430
Gln	Pro	Ser	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Asn	Ile	Glu	Asn	435	440	445
Asn	Asn	Ala	Arg	Leu	Met	Phe	Gly	Asp	Gly	Thr	Gln	Leu	Val	Val	Lys	450	455	460
Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	465	470	475
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	485	490	495
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	500	505	510
Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	515	520	525
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	530	535	540
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	545	550	555
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	565	570	575

Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val
			580					585						590	
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
			595				600						605		

<210> 162
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 61 Full sequence with mouse constant

<400> 162

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

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

<210> 163

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha Native with Codon Optimized Human

Constant

<400> 163

```
atgacacgag ttagcttgct gtgggcagtc gtggtctcca cctgtcttga atccggcatg 60
gccagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gactgtgacc 120
ctgagttgca catatgacac cagtgagaat aattattatt tgttctggta caagcagcct 180
cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaacg 240
gagaatcggt tctctgtgaa cttccagaaa gcagccaaat ctttcagtct caagatctca 300
gactcacagc tgggggacac tgcgatgtat ttctgtgctc tctataccta caaatacatc 360
tttggaaacag gcaccaggct gaaggtttta gcaaatatcc agaatccgga ccccgcggtg 420
tatcaactgc gcgactcaaa atcatccgat aagagtgtct gtttgtttac tgacttcgac 480
agtcaaaacta atgtctctca gagcaaagat tccgatgtct acatcactga caagtgcgtt 540
ctggatatgc ggagcatgga ttttaagtcc aactccgccg tagcctgggtc caacaagtca 600
gactttgcct gtgcaaatgc tttcaacaac tcaattatcc ctgaggacac tttctttcct 660
tcaccggagt cctcatgcga tgttaaaactg gtcgaaaaat cttttgagac ggatacgaac 720
ctcaacttcc aaaaatttgag cgttattggc tttaggattc tgcttctcaa ggttgcgggg 780
ttcaatctcc tgatgacgtt gcggctttgg agcagctaa 819
```

<210> 164

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha Native with Codon Optimized Mouse
Constant

<400> 164

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atgacacgag ttagcttgct gtgggcagtc gtggtctcca cctgtcttga atccggcatg 60
gccagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gactgtgacc 120
ctgagttgca catatgacac cagtgagaat aattattatt tgttctggta caagcagcct 180
cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaacg 240
gagaatcggt tctctgtgaa cttccagaaa gcagccaaat ctttcagtct caagatctca 300
gactcacagc tgggggacac tgcgatgtat ttctgtgctc tctataccta caaatacatc 360
tttggaaacag gcaccaggct gaaggtttta gcaaatatcc agaatccgga gcctgccgtg 420
taccagctga aggaccacg gagccaggat agcaccctgt gcctgttcac cgactttgat 480
tctcagatca acgtgccccaa gaccatggag agcggcacct tcatcacaga caagtgcgtg 540
ctggatatga aggccatgga cagcaagtcc aacggcgcca tcgcctgggtc caatcagaca 600
tctttcacct gccaggatat ctttaaggag acaaatgcc aatcctcttc ctctgacgtg 660
ccatgtgatg ccaccctgac agagaagagc ttcgagaccg acatgaacct gaattttcag 720
aatctgctcg tgattgtcct gagaatcctg ctgctgaagg tggccggctt taacctgctg 780
atgaccctga ggctgtggag ctctga 807
```

<210> 165

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha with Codon Optimized Human Constant

<400> 165

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

<210> 166

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha with Codon Optimized Mouse Constant

<400> 166

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

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

<210> 167

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 167

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

				85				90					95			
Leu	Lys	Ile	Ser	Asp	Ser	Gln	Leu	Gly	Asp	Thr	Ala	Met	Tyr	Phe	Cys	
			100					105					110			
Ala	Leu	Tyr	Thr	Tyr	Lys	Tyr	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Lys	
		115					120						125			
Val	Leu	Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	
	130					135					140					
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	
145					150				155						160	
Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	
			165						170					175		
Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	
			180					185					190			
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	
	195						200					205				
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	
	210					215					220					
Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	
225					230					235					240	
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	
			245						250				255			
Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser	
			260					265					270			

<210> 168

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 168

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

<220>

<223> TCR 62 Alpha CDR1

<400> 170

Thr Ser Glu Asn Asn Tyr Tyr

1 5

<210> 171

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha CDR2

<400> 171

Gln Glu Ala Tyr Lys Gln Gln Asn

1 5

<210> 172

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha CDR3

<400> 172

Ala Leu Tyr Thr Tyr Lys Tyr Ile

1 5

<210> 173

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Alpha Signal peptide

<400> 173

Met Thr Arg Val Ser Leu Leu Trp Ala Val Val Val Ser Thr Cys Leu

1 5 10 15

Glu Ser Gly Met

20

<210> 174
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 62 Beta Native with Codon Optimized Human
Constant

<400> 174
atggggcacca ggctcctctg ctggggcggcc ctctgtctcc tgggagcaga actcacagaa 60
gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt 120
tggtgcaatc ctatatctgg ccatgctacc ctttactggg accagcagat cctgggacag 180
ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct 240
aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct 300
gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttagatac ccggggctcc 360
tcctacaatg agcagttctt cgggccaggg acacggctca ccgtgctaga ggacctgaat 420
aagggtgttcc cccctgaggt ggccgtgttt gagccaagcg aggccgagat ctcccacacc 480
cagaaggcca ccctggtgtg cctggcaacc ggcttctttc ccgatcacgt ggagctgtcc 540
tggtgggtga acggcaagga ggtgcactct ggctgtgtga cagaccaca gccctgaag 600
gagcagcctg ccctgaatga ttcccgtat tgtctgtcct ctcggctgag agtgtctgcc 660
accttttggc agaaccacg gaatcacttc agatgccagg tgcagtttta cggcctgtct 720
gagaacgacg agtggacca ggatcgggcc aagcctgtga cacagatcgt gagcgcgga 780
gcatggggca gagccgactg tggcttcacc agcgtgtcct atcagcaggg cgtgctgtcc 840
gccaccatcc tgtacgagat cctgctgggc aaggccacac tgtatgccgt gctgggtgtct 900
gccctggtgc tgatggccat ggtgaagaga aaagacttct aa 942

<210> 175
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 62 Beta Native with Codon Optimized Mouse
Constant

<400> 175
atggggcacca ggctcctctg ctggggcggcc ctctgtctcc tgggagcaga actcacagaa 60
gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt 120
tggtgcaatc ctatatctgg ccatgctacc ctttactggg accagcagat cctgggacag 180
ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct 240
aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct 300
gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttagatac ccggggctcc 360
tcctacaatg agcagttctt cgggccaggg acacggctca ccgtgctaga ggacctgcgc 420
aatgtgaccc cccctaaggt gtccctgttt gagccctcta aggccgagat cgccaacaag 480
cagaaggcca ccctggtgtg cctggccaga ggcttcttcc ctgatcacgt ggagctgagc 540
tggtgggtga atggcaagga ggtgcactcc ggctgtgtga ccgaccaca ggccctacaag 600
gagtccaact actcttattg tctgtcctct aggcgtgcgc tgagcgccac attctggcac 660
aaccctcggg atcacttcag atgccagggt cagtttcacg gcctgagcga ggaggataag 720
tgccagagg gctcccaaaa gccctgacc cagaatatct ctgccaggc atggggcagg 780

```

gccgactgtg gaatcacctc cgcctcttat cagcagggcg tgctgtccgc cacaatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tatgccgtgc tggtgtccac actggtggtc 900
atggccatgg tgaagcgcaa gaacagctaa                               930

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<210> 176

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta with Codon Optimized Human Constant

<400> 176

```

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

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<210> 177

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta with Codon Optimized Mouse Constant

<400> 177

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

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<210> 178

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta with Codon Optimized Human Constant
and signal peptide

<400> 178

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

Met Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 179

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 179

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

Thr Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val
 290 295 300
 Lys Arg Lys Asn Ser
 305

<210> 180
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 62 Beta variable region

<400> 180
 Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile Glu Lys Arg
 1 5 10 15
 Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His Ala Thr Leu
 20 25 30
 Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu Leu Ile Gln
 35 40 45
 Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro Lys Asp Arg
 50 55 60
 Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu Lys Ile Gln
 65 70 75 80
 Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Leu
 85 90 95
 Asp Thr Arg Gly Ser Ser Tyr Asn Glu Gln Phe Phe Gly Pro Gly Thr
 100 105 110
 Arg Leu Thr Val Leu
 115

<210> 181
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 62 Beta CDR1

<400> 181
 Ser Gly His Ala Thr
 1 5

<210> 182
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TCR 62 Beta CDR2

<400> 182

Phe Gln Asn Asn Gly Val

1 5

<210> 183

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta CDR3

<400> 183

Ala Ser Ser Leu Asp Thr Arg Gly Ser Ser Tyr Asn Glu Gln Phe

1 5 10 15

<210> 184

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Beta signal peptide

<400> 184

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala

1 5 10 15

Glu Leu Thr

<210> 185

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Native full sequence with human constant

<400> 185

atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa 60

gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt 120

tggtgcaatc ctatatctgg ccatgctacc ctttactggt accagcagat cctgggacag 180

ggcccaaagc ttctgattca gtttcagaat aacggtgtag tggatgattc acagttgcct 240

aaggatcgat	tttctgcaga	gaggctcaaa	ggagtagact	ccactctcaa	gatccagcct	300
gcaaagcttg	aggactcggc	cgtgtatctc	tgtgccagca	gcttagatac	ccggggctcc	360
tcctacaatg	agcagttctt	cgggccaggg	acacggctca	ccgtgctaga	ggacctgaat	420
aagggtgttcc	cccctgaggt	ggccgtgttt	gagccaagcg	aggccgagat	ctccacaccc	480
cagaaggcca	ccctgggtgtg	cctggcaacc	ggcttctttc	ccgatcacgt	ggagctgtcc	540
tgggtgggtga	acggcaagga	ggtgcactct	ggcgtgtgca	cagaccaca	gcccctgaag	600
gagcagcctg	ccctgaatga	ttcccgtat	tgtctgtcct	ctcggctgag	agtgtctgcc	660
accttttggc	agaaccacg	gaatcacttc	agatgccagg	tgcagtttta	cggcctgtct	720
gagaacgacg	agtggacca	ggatcgggcc	aagcctgtga	cacagatcgt	gagcgcggaa	780
gcatggggca	gagccgactg	tggcttcacc	agcgtgtcct	atcagcaggg	cgtgctgtcc	840
gccaccatcc	tgtacgagat	cctgctgggc	aaggccacac	tgtatgccgt	gctgggtgtct	900
gccctgggtgc	tgatggccat	ggtgaagaga	aaagacttct	aaggctccgg	agcaaccaat	960
ttcagcctgc	tgaagcaggc	cggcgatgtg	gaggagaatc	ctggcccaat	gacacgagtt	1020
agcttgctgt	gggcagtcgt	ggtctccacc	tgtcttgaat	ccggcatggc	ccagacagtc	1080
actcagtctc	aaccagagat	gtctgtgcag	gaggcagaga	ctgtgaccct	gagttgcaca	1140
tatgacacca	gtgagaataa	ttattatttg	ttctggtaca	agcagcctcc	cagcaggcag	1200
atgattctcg	ttattcgcca	agaagcttat	aagcaacaga	atgcaacgga	gaatcgtttc	1260
tctgtgaact	tccagaaaagc	agccaaaatcc	ttcagttctca	agatctcaga	ctcacagctg	1320
ggggacactg	cgatgtatit	ctgtgctctc	tataacctaca	aatacatctt	tggaacaggc	1380
accaggctga	aggtttttagc	aaatatccag	aatccggacc	ccgcggtata	tcaactgcgc	1440
gactcaaaaat	catccgataa	gagtgtctgt	ttgtttactg	acttcgacag	tcaaactaat	1500
gtctctcaga	gcaaagattc	cgatgtctac	atcactgaca	agtgcgttct	ggatatgcgg	1560
agcatggatt	ttaagtccaa	ctccgccgta	gcctgggtcca	acaagtcaga	ctttgcctgt	1620
gcaaatgctt	tcaacaactc	aattatccct	gaggacactt	tctttccttc	accggagtcc	1680
tcatgcatg	ttaaactggg	cgaaaaatct	tttgagacgg	atacgaacct	caacttccaa	1740
aatttgagcg	ttattggctt	taggattctg	cttctcaagg	ttgcgggggtt	caatctcctg	1800
atgacgttgc	ggctttggag	cagctaa				1827

<210> 186

<211> 1803

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Nativefull sequence with mouse constant

<400> 186

atggggacca	ggctcctctg	ctgggcggcc	ctctgtctcc	tgggagcaga	actcacagaa	60
gctggagttg	cccagtctcc	cagatataag	attatagaga	aaaggcagag	tgtggctttt	120
tgggtgcaatc	ctatatctgg	ccatgctacc	ctttactggg	accagcagat	cctgggacag	180
ggcccaaagc	ttctgattca	gtttcagaat	aacgggtgtag	tggatgattc	acagttgcct	240
aaggatcgat	tttctgcaga	gaggctcaaa	ggagtagact	ccactctcaa	gatccagcct	300
gcaaagcttg	aggactcggc	cgtgtatctc	tgtgccagca	gcttagatac	ccggggctcc	360
tcctacaatg	agcagttctt	cgggccaggg	acacggctca	ccgtgctaga	ggacctgcgc	420
aatgtgaccc	cccctaaggt	gtcccgtgtt	gagccctcta	aggccgagat	cgccaacaag	480
cagaaggcca	ccctgggtgtg	cctggccaga	ggcttcttcc	ctgatcacgt	ggagctgagc	540
tgggtgggtga	atggcaagga	ggtgcactcc	ggcgtgtgca	ccgaccaca	ggcctacaag	600
gagtccaact	actcttattg	tctgtcctct	aggctgcgcg	tgagcgccac	attctggcac	660
aaccctcggg	atcacttcag	atgccagggtg	cagtttcacg	gcctgagcga	ggaggataag	720
tggccagagg	gctcccaaaa	gcccgtgacc	cagaatatct	ctgccgaggc	atggggcagg	780

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gccgactgtg gaatcacctc cgcctcttat cagcagggcg tgctgtccgc cacaatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tatgccgtgc tggtgtccac actggtgggc 900
atggccatgg tgaagcgcaa gaacagctaa ggctccggag caaccaatct cagcctgctg 960
aagcaggccg gcgatgtgga ggagaatcct ggcccaatga cacgagttag cttgctgtgg 1020
gcagtcgtgg tctccacctg tcttgaatcc ggcatggccc agacagtcac tcagtctcaa 1080
ccagagatgt ctgtgcagga ggcagagact gtgaccctga gttgcacata tgacaccagt 1140
gagaataatt attatttggt ctggtacaag cagcctcca gcaggcagat gattctcgtt 1200
attcgccaag aagcttataa gcaacagaat gcaacggaga atcgtttctc tgtgaacttc 1260
cagaaagcag ccaaactcct cagtctcaag atctcagact cacagctggg ggacactgcg 1320
atgtatttct gtgctctcta tacctacaaa tacatctttg gaacaggcac caggctgaag 1380
gttttagcaa atatccagaa tccggagcct gccgtgtacc agctgaagga cccacggagc 1440
caggatagca ccctgtgcct gttcaccgac tttgattctc agatcaacgt gcccagacc 1500
atggagagcg gcaccctcat cacagacaag tgcgtgctgg atatgaaggc catggacagc 1560
aagtccaacg gcgccatcgc ctggtccaat cagacatctt tcacctgcca ggatatcttt 1620
aaggagacaa atgccaccta tccttctctc gacgtgccat gtgatgccac cctgacagag 1680
aagagcttcg agaccgacat gaacctgaat tttcagaatc tgctcgtgat tgtcctgaga 1740
atcctgctgc tgaagggtggc cggctttaac ctgctgatga ccctgaggct gtggagctcc 1800
tga

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<210> 187

<211> 607

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Full sequence with human constant

<400> 187

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

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Val 180	Glu 185	Leu 190	Ser 195	Trp 200	Trp 205	Val 210	Asn 215	Gly 220	Lys 225	Glu 230	Val 235	His 240	Ser 245	Gly 250	Val 255
Cys 195	Thr 200	Asp 205	Pro 210	Gln 215	Pro 220	Leu 225	Lys 230	Glu 235	Gln 240	Pro 245	Ala 250	Leu 255	Asn 260	Asp 265	Ser 270
Arg 210	Tyr 215	Cys 220	Leu 225	Ser 230	Ser 235	Arg 240	Leu 245	Arg 250	Val 255	Ser 260	Ala 265	Thr 270	Phe 275	Trp 280	Gln 285
Asn 225	Pro 230	Arg 235	Asn 240	His 245	Phe 250	Arg 255	Cys 260	Gln 265	Val 270	Gln 275	Phe 280	Tyr 285	Gly 290	Leu 295	Ser 300
Glu 240	Asn 245	Asp 250	Glu 255	Trp 260	Thr 265	Gln 270	Asp 275	Arg 280	Ala 285	Lys 290	Pro 295	Val 300	Thr 305	Gln 310	Ile 315
Val 260	Ser 265	Ala 270	Glu 275	Ala 280	Trp 285	Gly 290	Arg 295	Ala 300	Asp 305	Cys 310	Gly 315	Phe 320	Thr 325	Ser 330	Val 335
Ser 275	Tyr 280	Gln 285	Gln 290	Gly 295	Val 300	Leu 305	Ser 310	Ala 315	Thr 320	Ile 325	Leu 330	Tyr 335	Glu 340	Ile 345	Leu 350
Leu 290	Gly 295	Lys 300	Ala 305	Thr 310	Leu 315	Tyr 320	Ala 325	Val 330	Leu 335	Val 340	Ser 345	Ala 350	Leu 355	Val 360	Leu 365
Met 305	Ala 310	Met 315	Val 320	Lys 325	Arg 330	Lys 335	Asp 340	Phe 345	Gly 350	Ser 355	Gly 360	Ala 365	Thr 370	Asn 375	Phe 380
Ser 320	Leu 325	Leu 330	Lys 335	Gln 340	Ala 345	Gly 350	Asp 355	Val 360	Glu 365	Asn 370	Pro 375	Gly 380	Pro 385	Met 390	
Thr 335	Arg 340	Val 345	Ser 350	Leu 355	Leu 360	Trp 365	Ala 370	Val 375	Val 380	Val 385	Ser 390	Thr 395	Cys 400	Leu 405	Glu 410
Ser 350	Gly 355	Met 360	Ala 365	Gln 370	Thr 375	Val 380	Thr 385	Gln 390	Ser 395	Gln 400	Pro 405	Glu 410	Met 415	Ser 420	Val 425
Gln 365	Glu 370	Ala 375	Glu 380	Thr 385	Val 390	Thr 395	Leu 400	Ser 405	Cys 410	Thr 415	Tyr 420	Asp 425	Thr 430	Ser 435	Glu 440
Asn 385	Asn 390	Tyr 395	Tyr 400	Leu 405	Phe 410	Trp 415	Tyr 420	Lys 425	Gln 430	Pro 435	Pro 440	Ser 445	Arg 450	Gln 455	Met 460
Ile 400	Leu 405	Val 410	Ile 415	Arg 420	Gln 425	Glu 430	Ala 435	Tyr 440	Lys 445	Gln 450	Gln 455	Asn 460	Ala 465	Thr 470	Glu 475
Asn 415	Arg 420	Phe 425	Ser 430	Val 435	Asn 440	Phe 445	Gln 450	Lys 455	Ala 460	Ala 465	Lys 470	Ser 475	Phe 480	Ser 485	Leu 490
Lys 430	Ile 435	Ser 440	Asp 445	Ser 450	Gln 455	Leu 460	Gly 465	Asp 470	Thr 475	Ala 480	Met 485	Tyr 490	Phe 495	Cys 500	Ala 505
Leu 445	Tyr 450	Thr 455	Tyr 460	Lys 465	Tyr 470	Ile 475	Phe 480	Gly 485	Thr 490	Gly 495	Thr 500	Arg 505	Leu 510	Lys 515	Val 520
Leu 460	Ala 465	Asn 470	Ile 475	Gln 480	Asn 485	Pro 490	Asp 495	Pro 500	Ala 505	Val 510	Tyr 515	Gln 520	Leu 525	Arg 530	Asp 535
Ser 475	Lys 480	Ser 485	Ser 490	Asp 495	Lys 500	Ser 505	Val 510	Cys 515	Leu 520	Phe 525	Thr 530	Asp 535	Phe 540	Asp 545	Ser 550
Gln 490	Thr 495	Asn 500	Val 505	Ser 510	Gln 515	Ser 520	Lys 525	Asp 530	Ser 535	Asp 540	Val 545	Tyr 550	Ile 555	Thr 560	Asp 565
Lys 505	Cys 510	Val 515	Leu 520	Asp 525	Met 530	Arg 535	Ser 540	Met 545	Asp 550	Phe 555	Lys 560	Ser 565	Asn 570	Ser 575	Ala 580
Val 520	Ala 525	Trp 530	Ser 535	Asn 540	Lys 545	Ser 550	Asp 555	Phe 560	Ala 565	Cys 570	Ala 575	Asn 580	Ala 585	Phe 590	Asn 595
Asn 535	Ser 540	Ile 545	Ile 550	Pro 555	Glu 560	Asp 565	Thr 570	Phe 575	Phe 580	Pro 585	Ser 590	Pro 595	Glu 600	Ser 605	Ser 610
Cys 550	Asp 555	Val 560	Lys 565	Leu 570											

Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys
			580					585					590		
Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser	
		595					600					605			

<210> 188

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 Full sequence with mouse constant

<400> 188

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

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

<210> 189

<211> 816

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha Native with Codon Optimized Human

Constant

<400> 189

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atggagactg ttctgcacgt actcctaggg atattgggggt tccaagcagc ctgggtcagt 60
agccaagaac tggagcagag tcctcagtcc ttgatcgtcc aagagggaaa gaatctcacc 120
ataaactgca cgtcatcaaa gacgttatat ggcttatact ggtataagca aaagtatggt 180
gaaggcttta tcttcttgat gatgctacag aaagggtgggg aagagaaaaag tcatgaaaaag 240
ataactgcca agttggatga gaaaaagcag caaagttccc tgcataatcac agcctcccag 300
cccagccatg caggcatcta cctctgtgga gcagacatag acgactacaa gctcagcttt 360
ggagccggaa ccacagtaac tgtaagagca aatatccaga atccggaccc cgcggtatat 420
caactgcgcg actcaaaaatc atccgataag agtgtctgtt tgtttactga cttcgacagt 480
caaactaatg tctctcagag caaagattcc gatgtctaca tctactgacaa gtgcgttctg 540
gatatgcgga gcatggattt taagtccaac tccgccgtag cctggtccaa caagtcagac 600
tttgctgtg caaatgcttt caacaactca attatccctg aggacacttt ctttctttca 660
ccggagtcct catgcgatgt taaactgggtc gaaaaatctt ttgagacgga tacgaacctc 720
aacttccaaa atttgagcgt tattggcttt aggattctgc ttctcaaggt tgcggggttc 780
aatctcctga tgacgttgcg gctttggagc agctaa 816
```

<210> 190

<211> 804

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha Native with Codon Optimized Mouse
Constant

<400> 190

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atggagactg ttctgcacgt actcctaggg atattgggggt tccaagcagc ctgggtcagt 60
agccaagaac tggagcagag tcctcagtcc ttgatcgtcc aagagggaaa gaatctcacc 120
ataaactgca cgtcatcaaa gacgttatat ggcttatact ggtataagca aaagtatggt 180
gaaggcttta tcttcttgat gatgctacag aaagggtgggg aagagaaaaag tcatgaaaaag 240
ataactgcca agttggatga gaaaaagcag caaagttccc tgcataatcac agcctcccag 300
cccagccatg caggcatcta cctctgtgga gcagacatag acgactacaa gctcagcttt 360
ggagccggaa ccacagtaac tgtaagagca aatatccaga atccggagcc tgccgtgtac 420
cagctgaagg acccacggag ccaggatagc accctgtgcc tgttcaccga ctttgattct 480
cagatcaacg tgcccaagac catggagagc ggacacctca tcacagacaa gtgcgtgctg 540
gatatgaagg ccatggacag caagtccaac ggcgccatcg cctggtccaa tcagacatct 600
ttcacctgcc aggatatctt taaggagaca aatgccacct atccttcctc tgacgtgcca 660
tgtgatgcca ccctgacaga gaagagcttc gagaccgaca tgaacctgaa ttttcagaat 720
ctgctcgtga ttgtcctgag aatcctgctg ctgaagggtgg ccggctttta cctgctgatg 780
accctgagggc tgtggagctc ctga 804
```

<210> 191

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha with Codon Optimized Human Constant

<400> 191

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

<210> 192

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha with Codon Optimized Mouse Constant

<400> 192

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

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

<210> 193

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 193

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

				85					90					95			
Thr	Ala	Ser	Gln	Pro	Ser	His	Ala	Gly	Ile	Tyr	Leu	Cys	Gly	Ala	Asp		
			100					105					110				
Ile	Asp	Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val		
		115					120					125					
Arg	Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp		
	130					135					140						
Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser		
145					150					155					160		
Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp		
			165					170					175				
Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala		
			180					185					190				
Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn		
	195						200					205					
Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser		
	210					215					220						
Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu		
225					230					235					240		
Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys		
			245					250						255			
Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
		260						265					270				

<210> 194

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 194

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

<220>

<223> TCR 63 Alpha CDR1

<400> 196

Lys Thr Leu Tyr Gly

1 5

<210> 197

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha CDR2

<400> 197

Leu Gln Lys Gly Gly Glu Glu

1 5

<210> 198

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha CDR3

<400> 198

Gly Ala Asp Ile Asp Asp Tyr Lys Leu Ser

1 5 10

<210> 199

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Alpha Signal peptide

<400> 199

Met Glu Thr Val Leu His Val Leu Leu Gly Ile Leu Gly Phe Gln Ala

1 5 10 15

Ala Trp Val Ser

20

<210> 200
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 63 Beta Native with Codon Optimized Human
Constant

<400> 200
atggggcacca ggctcctctg ctgggtgggtc ctgggtttcc tagggacaga tcacacaggt 60
gctggagtct cccagtcccc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc 120
aggtgtgatc caatttcggg tcatgtatcc cttttttggg accaacaggc cctggggcag 180
gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc 240
agtgatcgct tctttgcaga aaggcctgag ggatccgtct ccactctgaa gatccagcgc 300
acacagcagg aggactccgc cgtgtatctc tgtgccagca gaccaagaca ggggtataat 360
gacaatgagc agttcttcgg gccagggaca cggctcaccg tgctagagga cctgaataag 420
gtgttcccc ctgagggtggc cgtgtttgag ccaagcgagg ccgagatctc ccacaccag 480
aaggccaccc tgggtgtgcct ggcaaccggc ttctttcccg atcacgtgga gctgtcctgg 540
tgggtgaacg gcaaggaggt gcaactctggc gtgtgcacag acccacagcc cctgaaggag 600
cagcctgccc tgaatgattc ccgctattgt ctgtcctctc ggctgagagt gtctgccacc 660
ttttggcaga acccacggaa tcacttcaga tgccagggtgc agttttacgg cctgtctgag 720
aacgacgagt ggacccagga tcgggccaag cctgtgacac agatcgtgag cgcggaagca 780
tggggcagag ccgactgtgg cttcaccagc gtgtcctatc agcagggcgt gctgtccgcc 840
accatcctgt acgagatcct gctgggcaag gccacactgt atgccgtgct ggtgtctgcc 900
ctgggtgctga tggccatggt gaagagaaaa gacttctaa 939

<210> 201
<211> 927
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 63 Beta Native with Codon Optimized Mouse
Constant

<400> 201
atggggcacca ggctcctctg ctgggtgggtc ctgggtttcc tagggacaga tcacacaggt 60
gctggagtct cccagtcccc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc 120
aggtgtgatc caatttcggg tcatgtatcc cttttttggg accaacaggc cctggggcag 180
gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc 240
agtgatcgct tctttgcaga aaggcctgag ggatccgtct ccactctgaa gatccagcgc 300
acacagcagg aggactccgc cgtgtatctc tgtgccagca gaccaagaca ggggtataat 360
gacaatgagc agttcttcgg gccagggaca cggctcaccg tgctagagga cctgcgcaat 420
gtgaccccc ctaagggtgc cctgtttgag ccctctaagg ccgagatcgc caacaagcag 480
aaggccaccc tgggtgtgcct ggccagaggc ttcttccctg atcacgtgga gctgagctgg 540
tgggtgaatg gcaaggaggt gcaactccggc gtgtgcacag acccacaggc ctacaaggag 600
tccaactact cttattgtct gtcctctagg ctgcgcgtga gcgccacatt ctggcacaac 660
cctcggaatc acttcagatg ccagggtgcag tttcacggcc tgagcgagga ggataagtgg 720
ccagaggggct ccccaaagcc cgtgaccagc aatatctctg ccgaggcatg gggcagggcc 780

gactgtggaa tcacctccgc ctcttatcag cagggcgtgc tgtccgccac aatcctgtac 840
gagatcctgc tgggcaaggc caccctgtat gccgtgctgg tgtccacact ggtgggtcatg 900
gccatggtga agcgcaagaa cagctaa 927

$\langle 210 \rangle$ 202

<211> 293

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> TCR 63 Beta with Codon Optimized Human Constant

<400> 202

Gly 1	Ala	Gly	Val	Ser 5	Gln	Ser	Pro	Arg	Tyr 10	Lys	Val	Ala	Lys	Arg 15	Gly
Gln	Asp	Val	Ala 20	Leu	Arg	Cys	Asp	Pro 25	Ile	Ser	Gly	His	Val 30	Ser	Leu
Phe	Trp	Tyr 35	Gln	Gln	Ala	Leu	Gly 40	Gln	Gly	Pro	Glu	Phe 45	Leu	Thr	Tyr
Phe 50	Gln	Asn	Glu	Ala	Gln	Leu 55	Asp	Lys	Ser	Gly	Leu 60	Pro	Ser	Asp	Arg
Phe 65	Phe	Ala	Glu	Arg	Pro 70	Glu	Gly	Ser	Val	Ser 75	Thr	Leu	Lys	Ile	Gln 80
Arg	Thr	Gln	Gln	Glu 85	Asp	Ser	Ala	Val	Tyr 90	Leu	Cys	Ala	Ser	Arg 95	Pro
Arg	Gln	Gly	Tyr 100	Asn	Asp	Asn	Glu	Gln 105	Phe	Phe	Gly	Pro	Gly 110	Thr	Arg
Leu	Thr	Val	Leu	Glu	Asp	Leu	Asn 120	Lys	Val	Phe	Pro	Pro	Glu 125	Val	Ala
Val	Phe 130	Glu	Pro	Ser	Glu	Ala 135	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
Leu 145	Val	Cys	Leu	Ala	Thr	Gly 150	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser 160
Trp	Trp	Val	Asn 165	Gly	Lys	Glu	Val	His	Ser 170	Gly	Val	Cys	Thr	Asp	Pro
Gln	Pro	Leu	Lys 180	Glu	Gln	Pro	Ala	Leu 185	Asn	Asp	Ser	Arg	Tyr 190	Cys	Leu
Ser	Ser	Arg 195	Leu	Arg	Val	Ser	Ala 200	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
His	Phe 210	Arg	Cys	Gln	Val	Gln	Phe 215	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
Trp 225	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu 240
Ala	Trp	Gly	Arg	Ala 245	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
Gly	Val	Leu	Ser 260	Ala	Thr	Ile	Leu	Tyr 265	Glu	Ile	Leu	Leu	Gly	Lys	Ala
Thr	Leu	Tyr 275	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
Lys	Arg	Lys	Asp	Phe				280				285			

<210> 203

<211> 289

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Beta with Codon Optimized Mouse Constant

<400> 203

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

Ser

<210> 204
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 63 Beta with Codon Optimized Human Constant
 and signal peptide

<400> 204
 Met Gly Thr Arg Leu Leu Cys Trp Val Val Leu Gly Phe Leu Gly Thr
 1 5 10 15
 Asp His Thr Gly Ala Gly Val Ser Gln Ser Pro Arg Tyr Lys Val Ala
 20 25 30
 Lys Arg Gly Gln Asp Val Ala Leu Arg Cys Asp Pro Ile Ser Gly His
 35 40 45
 Val Ser Leu Phe Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Glu Phe
 50 55 60
 Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Asp Lys Ser Gly Leu Pro
 65 70 75 80
 Ser Asp Arg Phe Phe Ala Glu Arg Pro Glu Gly Ser Val Ser Thr Leu
 85 90 95
 Lys Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala
 100 105 110
 Ser Arg Pro Arg Gln Gly Tyr Asn Asp Asn Glu Gln Phe Phe Gly Pro
 115 120 125
 Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
 130 135 140
 Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
 145 150 155 160
 Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
 165 170 175
 Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys
 180 185 190
 Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
 195 200 205
 Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
 210 215 220
 Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
 225 230 235 240
 Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
 245 250 255
 Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
 260 265 270
 Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
 275 280 285
 Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
 290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 205

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 205

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

Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys
290 295 300
Arg Lys Asn Ser
305

<210> 206
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 63 Beta variable region

<400> 206
Gly Ala Gly Val Ser Gln Ser Pro Arg Tyr Lys Val Ala Lys Arg Gly
1 5 10 15
Gln Asp Val Ala Leu Arg Cys Asp Pro Ile Ser Gly His Val Ser Leu
20 25 30
Phe Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr
35 40 45
Phe Gln Asn Glu Ala Gln Leu Asp Lys Ser Gly Leu Pro Ser Asp Arg
50 55 60
Phe Phe Ala Glu Arg Pro Glu Gly Ser Val Ser Thr Leu Lys Ile Gln
65 70 75 80
Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Arg Pro
85 90 95
Arg Gln Gly Tyr Asn Asp Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg
100 105 110
Leu Thr Val Leu
115

<210> 207
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 63 Beta CDR1

<400> 207
Ser Gly His Val Ser
1 5

<210> 208
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR 63 Beta CDR2

<400> 208

Phe Gln Asn Glu Ala Gln

1

5

<210> 209

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Beta CDR3

<400> 209

Ala Ser Arg Pro Arg Gln Gly Tyr Asn Asp Asn Glu Gln Phe

1

5

10

<210> 210

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Beta signal peptide

<400> 210

Met Gly Thr Arg Leu Leu Cys Trp Val Val Leu Gly Phe Leu Gly Thr

1

5

10

15

Asp His Thr

<210> 211

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Native full sequence with human constant

<400> 211

atgggcacca ggctcctctg ctgggtgggtc ctgggtttcc tagggacaga tcacacaggt 60
gctggagtct cccagtcccc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc 120
aggtgtgatc caatttcggg tcatgtatcc cttttttggt accaacaggc cctggggcag 180
gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc 240

agtgatcgct	tctttgcaga	aaggcctgag	ggatccgtct	ccactctgaa	gatccagcgc	300
acacagcagg	aggactccgc	cgtgtatctc	tgtgccagca	gaccaagaca	gggggtataat	360
gacaatgagc	agttcttcgg	gccagggaca	cggctcaccg	tgctagagga	cctgaataag	420
gtgttcccc	ctgagggtggc	cgtgtttgag	ccaagcgagg	ccgagatctc	ccacacccag	480
aaggccaccc	tgggtgtgcct	ggcaaccggc	ttctttcccg	atcacgtgga	gctgtcctgg	540
tgggtgaacg	gcaaggaggt	gcaactctggc	gtgtgcacag	acccacagcc	cctgaaggag	600
cagcctgccc	tgaatgattc	ccgctattgt	ctgtcctctc	ggctgagagt	gtctgccacc	660
ttttggcaga	acccacggaa	tcacttcaga	tgccagggtgc	agttttacgg	cctgtctgag	720
aacgacgagt	ggacccagga	tcgggccaag	cctgtgacac	agatcgtgag	cgcggaagca	780
tggggcagag	ccgactgtgg	cttcaccagc	gtgtcctatc	agcagggcgt	gctgtccgcc	840
accatcctgt	acgagatcct	gctgggcaag	gccacactgt	atgccgtgct	ggtgtctgcc	900
ctgggtgctga	tggccatggt	gaagagaaaa	gacttctaag	gctccggagc	aaccaatttc	960
agcctgctga	agcaggccgg	cgatgtggag	gagaatcctg	gccaatgga	gactgttctg	1020
cacgtactcc	tagggatatt	gggggttcaa	gcagcctggg	tcagtagcca	agaactggag	1080
cagagtcctc	agtccttgat	cgtccaagag	ggaaagaatc	tcaccataaa	ctgcacgtca	1140
tcaaagacgt	tatatggctt	atactggtat	aagcaaaaagt	atggtgaagg	tcttatcttc	1200
ttgatgatgc	tacagaaaagg	tggggaagag	aaaagtcatg	aaaagataac	tgccaagttg	1260
gatgagaaaa	agcagcaaaag	ttccctgcat	atcacagcct	cccagcccag	ccatgcaggc	1320
atctacctct	gtggagcaga	catagacgac	tacaagctca	gctttggagc	cggaaccaca	1380
gtaactgtaa	gagcaaatat	ccagaatccg	gacccgcg	tatatcaact	gcgcgactca	1440
aaatcatccg	ataagagtgt	ctgtttgttt	actgacttcg	acagtcaaac	taatgtctct	1500
cagagcaaaag	attccgatgt	ctacatcact	gacaagtgcg	ttctggatat	gcggagcatg	1560
gattttaagt	ccaactccgc	cgtagcctgg	tccaacaagt	cagactttgc	ctgtgcaaat	1620
gctttcaaca	actcaattat	ccctgaggac	actttctttc	cttcaccgga	gtcctcatgc	1680
gatgttaaac	tggtcgaaaa	atctttttgag	acggatacga	acctcaactt	ccaaaatttg	1740
agcgttattg	gctttaggat	tctgcttctc	aagggtgcgg	ggttcaatct	cctgatgacg	1800
ttgcggcttt	ggagcagcta	a				1821

<210> 212

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Nativefull sequence with mouse constant

<400> 212

atggggcacca	ggctcctctg	ctgggtgggtc	ctgggtttcc	tagggacaga	tcacacaggt	60
gctggagtct	cccagtcccc	taggtacaaa	gtcgcaaaaga	gaggacagga	tgtagctctc	120
aggtgtgatc	caatttcggg	tcatgtatcc	cttttttggg	accaacaggc	cctggggcag	180
gggcccagagt	ttctgactta	tttccagaat	gaagctcaac	tagacaaatc	ggggctgccc	240
agtgatcgct	tctttgcaga	aaggcctgag	ggatccgtct	ccactctgaa	gatccagcgc	300
acacagcagg	aggactccgc	cgtgtatctc	tgtgccagca	gaccaagaca	gggggtataat	360
gacaatgagc	agttcttcgg	gccagggaca	cggctcaccg	tgctagagga	cctgcgcaat	420
gtgaccccc	ctaagggtgc	cctgtttgag	ccctctaagg	ccgagatcgc	caacaagcag	480
aaggccaccc	tgggtgtgcct	ggccagaggc	ttcttccctg	atcacgtgga	gctgagctgg	540
tgggtgaatg	gcaaggaggt	gcaactccggc	gtgtgcaccg	acccacaggc	ctacaaggag	600
tccaactact	cttattgtct	gtcctctagg	ctgcgcgtga	gcgccacatt	ctggcacaac	660
cctcggaatc	acttcagatg	ccagggtgcag	tttcacggcc	tgagcgagga	ggataagtg	720
ccagaggggct	ccccaaagcc	cgtgaccagg	aatatctctg	ccgaggcatg	gggcagggcc	780

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gactgtggaa tcacctccgc ctcttatcag cagggcgtgc tgtccgccac aatcctgtac 840
gagatcctgc tgggcaaggc caccctgtat gccgtgctgg tgtccacact ggtgggtcatg 900
gccatggtga agcgcaagaa cagctaaggc tccggagcaa ccaatttcag cctgctgaag 960
cagggccggcg atgtggagga gaatcctggc ccaatggaga ctgttctgca cgtactccta 1020
gggatattgg gggtccaagc agcctgggtc agtagccaag aactggagca gagtcctcag 1080
tccttgatcg tccaagaggg aaagaatctc accataaact gcacgtcatc aaagacgtta 1140
tatggccttat actggtataa gcaaaagtat ggtgaaggtc ttatcttctt gatgatgcta 1200
cagaaaagggtg gggaagagaa aagtcatgaa aagataactg ccaagttgga tgagaaaaaag 1260
cagcaaaagt ccctgcatat cacagcctcc cagcccagcc atgcaggcat ctacctctgt 1320
ggagcagaca tagacgacta caagctcagc tttggagccg gaaccacagt aactgtaaga 1380
gcaaatatcc agaatccgga gcctgccgtg taccagctga aggaccacag gagccaggat 1440
agcaccctgt gcctgttcac cgactttgat tctcagatca acgtgcccac gaccatggag 1500
agcggcacct tcatcacaga caagtgcgtg ctggatatga aggccatgga cagcaagtcc 1560
aacggcgcca tcgctgggtc caatcagaca tctttcacct gccaggatat ctttaaggag 1620
acaaatgcca cctatccttc ctctgacgtg ccatgtgatg ccaccctgac agagaagagc 1680
ttcgagaccg acatgaacct gaattttcag aatctgctcg tgattgtcct gagaatcctg 1740
ctgctgaagg tggccggcct taacctgctg atgaccctga ggctgtggag ctcctga 1797

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<210> 213

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 Full sequence with human constant

<400> 213

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

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			180					185				190			
Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg
		195					200					205			
Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn
	210					215					220				
Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu
225					230					235					240
Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val
				245					250					255	
Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser
			260					265						270	
Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu
		275					280					285			
Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met
	290					295					300				
Ala	Met	Val	Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser
305					310					315					320
Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu
				325					330					335	
Thr	Val	Leu	His	Val	Leu	Leu	Gly	Ile	Leu	Gly	Phe	Gln	Ala	Ala	Trp
			340					345					350		
Val	Ser	Ser	Gln	Glu	Leu	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Val	Gln
		355					360					365			
Glu	Gly	Lys	Asn	Leu	Thr	Ile	Asn	Cys	Thr	Ser	Ser	Lys	Thr	Leu	Tyr
	370					375					380				
Gly	Leu	Tyr	Trp	Tyr	Lys	Gln	Lys	Tyr	Gly	Glu	Gly	Leu	Ile	Phe	Leu
385					390					395					400
Met	Met	Leu	Gln	Lys	Gly	Gly	Glu	Glu	Lys	Ser	His	Glu	Lys	Ile	Thr
				405					410					415	
Ala	Lys	Leu	Asp	Glu	Lys	Lys	Gln	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala
			420					425					430		
Ser	Gln	Pro	Ser	His	Ala	Gly	Ile	Tyr	Leu	Cys	Gly	Ala	Asp	Ile	Asp
		435					440					445			
Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg	Ala
	450					455					460				
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
465					470					475					480
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
				485					490					495	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys
			500					505					510		
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
		515					520					525			
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
	530														

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

<210> 215

<211> 840

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha Native with Codon Optimized Human
Constant

<400> 215

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atgaacatgc tgactgccag cctgttgagg gcagtcatag cctccatctg tgttgatatcc 60
agcatggctc agaaggtaac tcaagcgcag actgaaatct ctgtgggtgga gaaggaggat 120
gtgaccttgg actgtgtgta tgaaacccgt gatactactt attacttatt ctggtacaag 180
caaccaccaa gtggagaatt ggttttcctt attcgtcggg actcttttga tgagcaaaat 240
gaaataagtg gtcgggtattc ttggaacttc cagaaatcca ccagttcctt caacttcacc 300
atcacagcct cacaagtcgt ggactcagca gtatacttct gtgctctgag tgggggtcgat 360
aactatgggc agaattttgt ctttgggtccc ggaaccagat tgtccgtgct gcccaatatc 420
cagaatccgg accccgcggg atatcaactg cgcgactcaa aatcatccga taagagtgtc 480
tgtttgttta ctgacttcga cagtcaaaact aatgtctctc agagcaaaga ttccgatgtc 540
tacatcactg acaagtgcgt tctggatatg cggagcatgg attttaagtc caactccgcc 600
gtagcctggg ccaacaagtc agactttgcc tgtgcaaatg ctttcaacaa ctcaattatc 660
cctgaggaca ctttctttcc ttcaccggag tcctcatgcg atgttaaact ggtcgaaaaa 720
tcttttgaga cggatacga cctcaacttc caaaatttga gcgttattgg ctttaggatt 780
ctgcttctca aggttgcggg gttcaatctc ctgatgacgt tgcggctttg gagcagctaa 840
```

<210> 216

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha Native with Codon Optimized Mouse
Constant

<400> 216

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atgaacatgc tgactgccag cctgttgagg gcagtcatag cctccatctg tgttgatatcc 60
agcatggctc agaaggtaac tcaagcgcag actgaaatct ctgtgggtgga gaaggaggat 120
gtgaccttgg actgtgtgta tgaaacccgt gatactactt attacttatt ctggtacaag 180
caaccaccaa gtggagaatt ggttttcctt attcgtcggg actcttttga tgagcaaaat 240
gaaataagtg gtcgggtattc ttggaacttc cagaaatcca ccagttcctt caacttcacc 300
atcacagcct cacaagtcgt ggactcagca gtatacttct gtgctctgag tgggggtcgat 360
aactatgggc agaattttgt ctttgggtccc ggaaccagat tgtccgtgct gcccaatatc 420
cagaatccgg agcctgccgt gtaccagctg aaggaccac ggagccagga tagcaccctg 480
tgctgttca ccgactttga ttctcagatc aacgtgccca agaccatgga gagcggcacc 540
ttcatcacag acaagtgcgt gctggatatg aaggccatgg acagcaagtc caacggcgcc 600
atcgcttggg ccaatcagac atctttcacc tgccaggata tctttaagga gacaaatgcc 660
acctatcctt cctctgacgt gccatgtgat gccaccctga cagagaagag cttcgagacc 720
gacatgaacc tgaattttca gaatctgctc gtgattgtcc tgagaatcct gctgctgaag 780
gtggccggct ttaacctgct gatgaccctg aggctgtgga gctcctga 828
```

<210> 217

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha with Codon Optimized Human Constant

<400> 217

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

Ser

<210> 218

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha with Codon Optimized Mouse Constant

<400> 218

Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser	Val	Val	Glu	Lys
1				5					10					15	
Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg	Asp	Thr	Thr	Tyr

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

<210> 219

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 219

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

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

<210> 220

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 220

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

				85				90					95			
Phe	Asn	Phe	Thr	Ile	Thr	Ala	Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	
			100					105					110			
Phe	Cys	Ala	Leu	Ser	Gly	Val	Asp	Asn	Tyr	Gly	Gln	Asn	Phe	Val	Phe	
	115						120					125				
Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val	Leu	Pro	Asn	Ile	Gln	Asn	Pro	Glu	
	130					135					140					
Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	
145				150				155							160	
Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	
			165					170						175		
Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Lys	Ala	
			180					185					190			
Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	
	195					200						205				
Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	
	210					215					220					
Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	
225				230						235					240	
Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu	Val	Ile	Val	Leu	Arg	Ile	
			245					250						255		
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	
			260					265						270		
Trp	Ser	Ser														
			275													

<210> 221

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Alpha variable region

<400> 221

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

Ser Val Leu Pro
115

<210> 222
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Alpha CDR1

<400> 222
Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 223
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Alpha CDR2

<400> 223
Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 224
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Alpha CDR3

<400> 224
Ala Leu Ser Gly Val Asp Asn Tyr Gly Gln Asn Phe Val
1 5 10

<210> 225
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Alpha Signal peptide

<400> 225

Met Asn Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile
1 5 10 15
Cys Val Val Ser Ser Met
20

<210> 226

<211> 933

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Beta Native with Codon Optimized Human
Constant

<400> 226

atgggctgca ggctcctctg ctgtgtgggc ttctgcctcc tccaagcagg tcccttggac 60
acagctgttt cccagactcc aaaatacctg gtcacacaga tgggaaacga caagtccatt 120
aaatgtgaac aaaatctggg ccatgatact atgtattggg ataaacagga ctctaagaaa 180
tttctgaaga taatgttttag ctacaataat aaggagctca ttataaatga aacagttcca 240
aatcgcttct cacctaaatc tccagacaaa gctcacttaa atcttcacat caattccctg 300
gagcttgggtg actctgctgt gtatttctgt gccagcagcc agggggaagc tggggccaac 360
gtcctgactt tgggggccgg cagcaggctg accgtgctgg aggacctgaa taagggtgttc 420
ccccctgagg tggccgtgtt tgagccaagc gaggccgaga tctcccacac ccagaaggcc 480
accctgggtg gcctggcaac cggcttcttt cccgatcacg tggagctgtc ctggtgggtg 540
aacggcaagg aggtgcactc tggcgtgtgc acagaccac agcccctgaa ggagcagcct 600
gccctgaatg attcccgcta ttgtctgtcc tctcggctga gagtgtctgc caccttttgg 660
cagaaccac ggaatcactt cagatgccag gtgcagtttt acggcctgtc tgagaacgac 720
gagtggaccc aggatcgggc caagcctgtg acacagatcg tgagcgcgga agcatggggc 780
agagccgact gtggcttcac cagcgtgtcc tatcagcagg gcgtgctgtc cgccaccatc 840
ctgtacgaga tcctgtctggg caaggccaca ctgtatgccg tgctgggtgtc tggcctgggtg 900
ctgatggcca tgggtgaagag aaaagacttc taa 933

<210> 227

<211> 921

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Beta Native with Codon Optimized Mouse
Constant

<400> 227

atgggctgca ggctcctctg ctgtgtgggc ttctgcctcc tccaagcagg tcccttggac 60
acagctgttt cccagactcc aaaatacctg gtcacacaga tgggaaacga caagtccatt 120
aaatgtgaac aaaatctggg ccatgatact atgtattggg ataaacagga ctctaagaaa 180
tttctgaaga taatgttttag ctacaataat aaggagctca ttataaatga aacagttcca 240
aatcgcttct cacctaaatc tccagacaaa gctcacttaa atcttcacat caattccctg 300

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gagcttggtg actctgctgt gtatttctgt gccagcagcc agggggaagc tggggccaac 360
gtcctgactt tcggggccgg cagcaggctg accgtgctgg aggacctgcg caatgtgacc 420
ccccctaagg tgtccctgtt tgagccctct aaggccgaga tcgccaacaa gcagaaggcc 480
accctggtgt gcctggccag aggcttcttc cctgatcacg tggagctgag ctggtgggtg 540
aatggcaagg aggtgcactc cggcgtgtgc accgaccac aggccataca ggagtccaac 600
tactcttatt gtctgtcctc taggctgcgc gtgagcgcca cattctggca caaccctcgg 660
aatcacttca gatgccaggt gcagtttcac ggcttgagcg aggaggataa gtggccagag 720
ggctcccaa agcccgtgac ccagaatatc tctgccgagg catggggcag ggccgactgt 780
ggaatcacct ccgcctctta tcagcagggc gtgctgtccg ccacaatcct gtacgagatc 840
ctgctgggca aggccaccct gtatgccgtg ctggtgtcca cactggtggt catggccatg 900
gtgaagcgca agaacagcta a                                     921

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<210> 228

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Beta with Codon Optimized Human Constant

<400> 228

```

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

```

225					230					235				240
Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly
				245					250					255
Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr
			260					265					270	
Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys
		275					280					285		Arg
Lys	Asp	Phe												
	290													

<210> 229
 <211> 287
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 64 Beta with Codon Optimized Mouse Constant

<400> 229

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

Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr
				245					250					255	
Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu
			260					265					270		
Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser	
		275					280					285			

<210> 230

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Beta with Codon Optimized Human Constant
and signal peptide

<400> 230

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

Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln
			260					265					270		
Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys
		275					280					285			
Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met
	290					295					300				
Val	Lys	Arg	Lys	Asp	Phe										
305					310										

<210> 231

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 231

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

Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly
				245					250					255	
Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			260					265					270		
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
		275					280					285			
Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys
	290					295					300				
Asn	Ser														
305															

<210> 232
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 64 Beta variable region

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

<210> 233
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 64 Beta CDR1

Leu	Gly	His	Asp	Thr
1			5	

<210> 234
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Beta CDR2

<400> 234
Tyr Asn Asn Lys Glu Leu
1 5

<210> 235
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Beta CDR3

<400> 235
Ala Ser Ser Gln Gly Glu Ala Gly Ala Asn Val Leu Thr
1 5 10

<210> 236
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR 64 Beta signal peptide

<400> 236
Met Gly Cys Arg Leu Leu Cys Cys Val Val Phe Cys Leu Leu Gln Ala
1 5 10 15
Gly Pro Leu

<210> 237
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 64 Native full sequence with human constant

<400> 237

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atgggctgca ggctcctctg ctgtgtgggc ttctgcctcc tccaagcagg tcccttggac 60
acagctgttt cccagactcc aaaatacctg gtcacacaga tgggaaacga caagtccatt 120
aaatgtgaac aaaatctggg ccatgatact atgtattggg ataaacagga ctctaagaaa 180
tttctgaaga taatgttttag ctacaataat aaggagctca ttataaatga aacagttcca 240
aatcgcttct cacctaaatc tccagacaaa gctcacttaa atcttcacat caattccctg 300
gagcttgggtg actctgctgt gtatttctgt gccagcagcc agggggaagc tggggccaac 360
gtcctgactt tcggggccgg cagcaggctg accgtgctgg aggacctgaa taagggtgtc 420
ccccctgagg tggccgtgtt tgagccaagc gaggccgaga tctcccacac ccagaaggcc 480
accctgggtg gcctggcaac cggcttcttt ccgatcacg tggagctgtc ctggtgggtg 540
aacggcaagg aggtgcactc tggcgtgtgc acagaccac agcccctgaa ggagcagcct 600
gccctgaatg attcccgtca ttgtctgtcc tctcggctga gagtgtctgc caccttttgg 660
cagaaccac ggaatcactt cagatgccag gtgcagtttt acggcctgtc tgagaacgac 720
gagtggaccc aggatcgggc caagcctgtg acacagatcg tgagcgcgga agcatggggc 780
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ctgaagcagg ccggcgatgt ggaggagaat cctggcccaa tgaacatgct gactgccagc 1020
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caagcgcaga ctgaaatttc tgtggtggag aaggaggatg tgaccttga ctgtgtgtat 1140
gaaaccctgt atactactta ttacttattc tggtaacaag aaccaccaag tggagaattg 1200
gttttcctta ttcgtcggaa ctcttttgat gagcaaaatg aaataagtgg tcggtattct 1260
tggaacttcc agaaatccac cagttccttc aacttcacca tcacagcctc acaagtcgtg 1320
gactcagcag tatacttctg tgctctgagt ggggtcgata actatggtca gaattttgtc 1380
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tatcaactgc gcgactcaaa atcatccgat aagagtgtct gtttgtttac tgacttcgac 1500
agtcaaaacta atgtctctca gagcaaagat tccgatgtct acatcactga caagtgcgtt 1560
ctggatatgc ggagcatgga ttttaagtcc aactccgccg tagcctgggtc caacaagtca 1620
gactttgcct gtgcaaatgc tttcaacaac tcaattatcc ctgaggacac tttctttcct 1680
tcaccggagt cctcatgcga tgttaaaactg gtcgaaaaat cttttgagac ggatacgaac 1740
ctcaacttcc aaaatttgag cgttattggc tttaggattc tgcttctcaa ggttgcgggg 1800
ttcaatctcc tgatgacgtt gcggctttgg agcagctaa 1839
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<210> 238

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Nativefull sequence with mouse constant

<400> 238

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acagctgttt cccagactcc aaaatacctg gtcacacaga tgggaaacga caagtccatt 120
aaatgtgaac aaaatctggg ccatgatact atgtattggg ataaacagga ctctaagaaa 180
tttctgaaga taatgttttag ctacaataat aaggagctca ttataaatga aacagttcca 240
aatcgcttct cacctaaatc tccagacaaa gctcacttaa atcttcacat caattccctg 300
gagcttgggtg actctgctgt gtatttctgt gccagcagcc agggggaagc tggggccaac 360
gtcctgactt tcggggccgg cagcaggctg accgtgctgg aggacctgcg caatgtgacc 420
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ccccctaagg tgtccctgtt tgagccctct aaggccgaga tcgccaacaa gcagaaggcc 480
accctggtgt gcctggccag aggcttcttc cctgatcacg tggagctgag ctggtgggtg 540
aatggcaagg aggtgcactc cggcgtgtgc accgaccac aggctacaa ggagtccaac 600
tactcttatt gtctgtcctc taggctgcgc gtgagcgcca cattctggca caaccctcgg 660
aatcacttca gatgccaggt gcagtttcac ggcctgagcg aggaggataa gtggccagag 720
ggctcccaa agcccgtgac ccagaatatc tctgccgagg catggggcag ggccgactgt 780
ggaatcacct ccgcctctta tcagcagggc gtgctgtccg ccacaatcct gtacgagatc 840
ctgctgggca aggccaccct gtatgccgtg ctggtgtcca cactggtggt catggccatg 900
gtgaagcgca agaacagcta aggctccgga gcaaccaatt tcagcctgct gaagcaggcc 960
ggcgatgtgg aggagaatcc tggcccaatg aacatgctga ctgccagcct gttgagggca 1020
gtcatagcct ccatctgtgt tgtatccagc atggctcaga aggtaactca agcgcagact 1080
gaaatttctg tgggtggagaa ggaggatgtg accttggaact gtgtgtatga aaccctgat 1140
actacttatt acttattctg gtacaagcaa ccaccaagtg gagaattggt tttccttatt 1200
cgtcggaaact cttttgatga gcaaaatgaa ataagtggtc ggtattcttg gaacttccag 1260
aaatccacca gttccttcaa cttcaccatc acagcctcac aagtcgtgga ctcagcagta 1320
tacttctgtg ctctgagtgg ggtcgataac tatggtcaga attttgtctt tgggtcccga 1380
accagattgt ccgtgctgcc caatatccag aatccggagc ctgccgtgta ccagctgaag 1440
gaccacgga gccaggatag caccctgtgc ctgttcaccg actttgattc tcagatcaac 1500
gtgccaaga ccatggagag cggcaccttc atcacagaca agtgcgtgct ggatatgaag 1560
gccatggaca gcaagtccaa cggcgccatc gcctgggtcca atcagacatc tttcacctgc 1620
caggatatct ttaaggagac aaatgccacc tatccttcct ctgacgtgcc atgtgatgcc 1680
accctgacag agaagagctt cgagaccgac atgaacctga attttcagaa tctgctcgtg 1740
attgtcctga gaatcctgct gctgaagggtg gccggcttta acctgctgat gaccctgagg 1800
ctgtggagct cctga 1815

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<210> 239

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Full sequence with human constant

<400> 239

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

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Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val
130						135					140				
Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala
145					150					155					160
Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu
				165					170					175	
Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp
			180					185					190		
Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys
		195					200					205			
Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg
	210					215					220				
Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp
225					230					235					240
Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala
				245					250					255	
Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln
			260					265					270		
Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys
		275					280					285			
Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met
	290					295					300				
Val	Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu
305					310					315					320
Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Asn	Met	Leu
				325					330					335	
Thr	Ala	Ser	Leu	Leu	Arg	Ala	Val	Ile	Ala	Ser	Ile	Cys	Val	Val	Ser
			340					345					350		
Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser	Val	Val
		355					360					365			
Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg	Asp	Thr
	370					375					380				
Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu	Leu	Val
385					390					395					400
Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile	Ser	Gly
				405					410					415	
Arg	Tyr	Ser	Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	Asn	Phe	Thr
			420					425					430		
Ile	Thr	Ala	Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Leu
		435					440					445			
Ser	Gly	Val	Asp	Asn	Tyr	Gly	Gln	Asn	Phe	Val	Phe	Gly	Pro	Gly	Thr
	450					455					460				
Arg	Leu	Ser	Val	Leu	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr
465					470					475					480
Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr
				485					490					495	
Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val
			500					505					510		
Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys
		515					520					525			

Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala
530						535					540				
Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser
545					550					555					560
Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr
				565					570						575
Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile
			580					585					590		
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu
		595					600					605			
Trp	Ser	Ser													
610															

<210> 240

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 Full sequence with mouse constant

<400> 240

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

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

<210> 241
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 65 Alpha Native with Codon Optimized Human
Constant

<400> 241
atggagaaaa tgttggagtg tgcattcata gtcttgtggc ttcagcttgg ctggttgagt 60
ggagaagacc aggtgacgca gagtcccag gccctgagac tccaggaggg agagagtagc 120
agtcttaact gcagttacac agtcagcggg ttaagagggc tgttctggta taggcaagat 180
cctgggaaaag gccctgaatt cctcttcacc ctgtattcag ctggggaaga aaaggagaaa 240
gaaaggctaa aagccacatt aacaaagaag gaaagctttc tgcacatcac agcccctaaa 300
cctgaagact cagccactta tctctgtgct gtgcaggcag aaagaggctc aaccctgggg 360
aggctatact ttggaagagg aactcagttg actgtctggc ctaatatcca gaatccggac 420
cccgcggtat atcaactgcg cgactcaaaa tcatccgata agagtgtctg tttgtttact 480
gacttcgaca gtcaaaactaa tgtctctcag agcaaagatt ccgatgtcta catcactgac 540
aagtgcgttc tggatatgcg gagcatggat tttaaagtcca actccgccgt agcctgggtcc 600
aacaagtcag actttgcctg tgcaaatgct ttcaacaact caattatccc tgaggacact 660
ttctttcctt caccggagtc ctcatgcatg gttaaactgg tcgaaaaatc ttttgagacg 720
gatacgaacc tcaacttcca aaatttgagc gttattggct ttaggattct gcttctcaag 780
gttgcggggt tcaatctcct gatgacgttg cggttttggg gcagctaa 828

<210> 242
<211> 816
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 65 Alpha Native with Codon Optimized Mouse
Constant

<400> 242
atggagaaaa tgttggagtg tgcattcata gtcttgtggc ttcagcttgg ctggttgagt 60
ggagaagacc aggtgacgca gagtcccag gccctgagac tccaggaggg agagagtagc 120
agtcttaact gcagttacac agtcagcggg ttaagagggc tgttctggta taggcaagat 180
cctgggaaaag gccctgaatt cctcttcacc ctgtattcag ctggggaaga aaaggagaaa 240
gaaaggctaa aagccacatt aacaaagaag gaaagctttc tgcacatcac agcccctaaa 300
cctgaagact cagccactta tctctgtgct gtgcaggcag aaagaggctc aaccctgggg 360
aggctatact ttggaagagg aactcagttg actgtctggc ctaatatcca gaatccggag 420
cctgccgtgt accagctgaa ggaccacagg agccaggata gcaccctgtg cctgttcacc 480
gactttgatt ctcatatcaa cgtgcccagg accatggaga gcggcacctt catcacagac 540
aagtgcgtgc tggatatgaa ggccatggac agcaagtcca acggcgccat cgcttgggtcc 600
aatcagacat ctttcacctg ccaggatatc tttaaaggaga caaatgccac ctatccttcc 660
tctgacgtgc catgtgatgc caccctgaca gagaagagct tcgagaccga catgaacctg 720
aattttcaga atctgtcctg gattgtcctg agaatcctgc tgctgaagggt ggccggcctt 780
aacctgctga tgaccctgag gctgtggagc tcctga 816

<210> 243
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 65 Alpha with Codon Optimized Human Constant

<400> 243
 Glu Asp Gln Val Thr Gln Ser Pro Glu Ala Leu Arg Leu Gln Glu Gly
 1 5 10 15
 Glu Ser Ser Ser Leu Asn Cys Ser Tyr Thr Val Ser Gly Leu Arg Gly
 20 25 30
 Leu Phe Trp Tyr Arg Gln Asp Pro Gly Lys Gly Pro Glu Phe Leu Phe
 35 40 45
 Thr Leu Tyr Ser Ala Gly Glu Glu Lys Glu Lys Glu Arg Leu Lys Ala
 50 55 60
 Thr Leu Thr Lys Lys Glu Ser Phe Leu His Ile Thr Ala Pro Lys Pro
 65 70 75 80
 Glu Asp Ser Ala Thr Tyr Leu Cys Ala Val Gln Ala Glu Arg Gly Ser
 85 90 95
 Thr Leu Gly Arg Leu Tyr Phe Gly Arg Gly Thr Gln Leu Thr Val Trp
 100 105 110
 Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 115 120 125
 Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
 130 135 140
 Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 145 150 155 160
 Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
 165 170 175
 Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 180 185 190
 Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
 195 200 205
 Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
 210 215 220
 Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
 225 230 235 240
 Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 245 250

<210> 244
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TCR 65 Alpha with Codon Optimized Mouse Constant

<400> 244

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

<210> 245

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Alpha with Codon Optimized Human Constant
and signal peptide

<400> 245

Met	Glu	Lys	Met	Leu	Glu	Cys	Ala	Phe	Ile	Val	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Gly	Trp	Leu	Ser	Gly	Glu	Asp	Gln	Val	Thr	Gln	Ser	Pro	Glu	Ala	Leu

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

<210> 246

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Alpha with Codon Optimized Mouse Constant
and signal peptide

<400> 246

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

Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Gln	Ala	Glu	Arg	Gly	Ser
				85					90					95	
Thr	Leu	Gly	Arg	Leu	Tyr	Phe	Gly	Arg	Gly	Thr	Gln	Leu	Thr	Val	Trp
			100					105						110	
Pro															

<210> 248
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 65 Alpha CDR1

<400> 248
 Val Ser Gly Leu Arg Gly
 1 5

<210> 249
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 65 Alpha CDR2

<400> 249
 Leu Tyr Ser Ala Gly Glu Glu
 1 5

<210> 250
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR 65 Alpha CDR3

<400> 250
 Ala Val Gln Ala Glu Arg Gly Ser Thr Leu Gly Arg Leu Tyr
 1 5 10

<210> 251
 <211> 21
 <212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Alpha Signal peptide

<400> 251

Met	Glu	Lys	Met	Leu	Glu	Cys	Ala	Phe	Ile	Val	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Gly	Trp	Leu	Ser	Gly											
			20												

<210> 252

<211> 936

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Beta Native with Codon Optimized Human
Constant

<400> 252

atgggaatca	ggctcctctg	tcgtgtggcc	ttttgtttcc	tggctgtagg	cctcgtagat	60
gtgaaagtaa	cccagagctc	gagatatcta	gtcaaaagga	cgggagagaa	agtttttctg	120
gaatgtgtcc	aggatatgga	ccatgaaaaat	atgttcttgg	atcgacaaga	cccagggtctg	180
gggctacggc	tgatctatit	ctcatatgat	gttaaaaatga	aagaaaaagg	agatattcct	240
gaggggtaca	gtgtctctag	agagaagaag	gagcgcttct	ccctgattct	ggagtccgcc	300
agcaccaacc	agacatctat	gtacctctgt	gccagcagtt	tatggggacg	gcgaaacacc	360
ggggagctgt	tttttggaga	aggctctagg	ctgaccgtac	tggaggacct	gaataagggtg	420
ttccccctg	aggtggccgt	gtttgagcca	agcgaggccg	agatctccca	caccagaag	480
gccaccctgg	tgtgcctggc	aaccggcttc	tttcccgatc	acgtggagct	gtcctgggtgg	540
gtgaacggca	aggagggtgca	ctctggcggtg	tgcacagacc	cacagcccct	gaaggagcag	600
cctgcccctga	atgattcccg	ctattgtctg	tcctctcggc	tgagagtgtc	tgccaccttt	660
tggcagaacc	cacggaatca	cttcagatgc	cagggtgcagt	tttacggcct	gtctgagaac	720
gacgagtgga	cccaggatcg	ggccaagcct	gtgacacaga	tcgtgagcgc	ggaagcatgg	780
ggcagagccg	actgtggctt	caccagcgtg	tcctatcagc	agggcgtgct	gtccgccacc	840
atcctgtacg	agatcctgct	gggcaaggcc	acactgtatg	ccgtgctggt	gtctgccctg	900
gtgctgatgg	ccatggtgaa	gagaaaagac	ttctaa			936

<210> 253

<211> 924

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Beta Native with Codon Optimized Mouse
Constant

<400> 253

atgggaatca	ggctcctctg	tcgtgtggcc	ttttgtttcc	tggctgtagg	cctcgtagat	60
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gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg 120
gaatgtgtcc aggatatgga ccatgaaaat atgttctggt atcgacaaga cccagggtctg 180
gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct 240
gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgt gccagcagtt tatggggacg gcgaaacacc 360
ggggagctgt tttttggaga aggctctagg ctgaccgtac tggaggacct gcgcaatgtg 420
accccccta aggtgtccct gtttgagccc tctaaggccg agatcgccaa caagcagaag 480
gccaccctgg tgtgcctggc cagaggcttc ttccctgac acgtggagct gagctggtgg 540
gtgaatggca aggaggtgca ctccggcgtg tgcaccgacc cacaggccta caaggagtcc 600
aactactctt attgtctgtc ctctaggctg cgcgtgagcg ccacattctg gcacaaccct 660
cggaatcact tcagatgccg ggtgcagttt cacggcctga gcgaggagga taagtggcca 720
gagggctccc caaagcccgt gacccagaat atctctgccg aggcattgggg cagggccgac 780
tgtggaatca cctccgctc ttatcagcag ggcgtgctgt ccgccacaat cctgtacgag 840
atcctgctgg gcaaggccac cctgtatgcc gtgctggtgt ccacactggt ggtcatggcc 900
atggtgaagc gcaagaacag ctaa 924

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<210> 254

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta with Codon Optimized Human Constant

<400> 254

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

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		195				200				205					
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp
	210					215					220				
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala
225					230					235					240
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly
				245					250					255	
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr
			260					265					270		
Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys
		275					280					285			
Arg	Lys	Asp	Phe												
	290														

<210> 255

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta with Codon Optimized Mouse Constant

<400> 255

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

Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser
210						215					220				
Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala
225					230					235					240
Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala
				245					250					255	
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val
			260					265					270		
Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser
		275					280					285			

<210> 256

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta with Codon Optimized Human Constant
and signal peptide

<400> 256

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

Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn
225					230				235						240
Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser
				245				250						255	
Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr
			260				265						270		
Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly
	275					280					285				
Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala
290					295					300					
Met	Val	Lys	Arg	Lys	Asp	Phe									
305					310										

<210> 257

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta with Codon Optimized Mouse Constant
and signal peptide

<400> 257

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

Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe
210						215					220				
Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro
225					230					235					240
Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp
				245					250					255	
Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val
			260					265					270		
Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu
		275					280					285			
Tyr	Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg
	290					295					300				
Lys	Asn	Ser													
305															

<210> 258

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta variable region

<400> 258

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

<210> 259

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta CDR1

<400> 259

Met Asp His Glu Asn

1 5

<210> 260

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta CDR2

<400> 260

Ser Tyr Asp Val Lys Met

1 5

<210> 261

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta CDR3

<400> 261

Ala Ser Ser Leu Trp Gly Arg Arg Asn Thr Gly Glu Leu Phe

1 5 10

<210> 262

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Beta signal peptide

<400> 262

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val

1 5 10 15

Gly Leu Val

<210> 263

<211> 1830

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Native full sequence with human constant

<400> 263

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gaatgtgtcc aggatatgga ccatgaaaat atgttctggg atcgacaaga cccagggtctg 180
gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct 240
gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgt gccagcagtt tatggggacg gcgaaacacc 360
ggggagctgt tttttggaga aggctctagg ctgaccgtac tggaggacct gaataagggtg 420
ttccccctg aggtggccgt gtttgagcca agcgaggccg agatctcca caccagaag 480
gccaccctgg tgtgcctggc aaccggcttc tttccgatc acgtggagct gtcctgggtg 540
gtgaacggca aggaggtgca ctctggcgtg tgcacagacc cacagcccct gaaggagcag 600
cctgccctga atgattcccc ctattgtctg tcctctcggc tgagagtgtc tgccaccttt 660
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ttcctcttca ccctgtattc agctggggaa gaaaaggaga aagaaaggct aaaagccaca 1260
ttaacaaaga aggaaagctt tctgcacatc acagccccta aacctgaaga ctcagccact 1320
tatctctgtg ctgtgcaggc agaaagaggc tcaaccctgg ggaggctata ctttgggaaga 1380
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cgcgactcaa aatcatccga taagagtgtc tgtttgttta ctgacttcga cagtcaaact 1500
aatgtctctc agagcaaaga ttccgatgtc tacatcactg acaagtgcgt tctggatatg 1560
cggagcatgg attttaagtc caactccgcc gtagcctggg ccaacaagtc agactttgcc 1620
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tcctcatgcg atgttaaaact ggtcgaaaaa tcttttgaga cggatacgaa cctcaacttc 1740
caaaatttga gcgttattgg ctttaggatt ctgcttctca aggttgcggg gttcaatctc 1800
ctgatgacgt tgcggctttg gagcagctaa 1830
```

<210> 264

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Nativefull sequence with mouse constant

<400> 264

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gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg 120
gaatgtgtcc aggatatgga ccatgaaaat atgttctggg atcgacaaga cccagggtctg 180
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gggctacggc tgatctatct ctcatatgat gttaaaaatga aagaaaaaagg agatattcct 240
gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgt gccagcagtt tatggggacg gcgaaacacc 360
ggggagctgt tttttggaga aggctctagg ctgaccgtac tggaggacct gcgcaatgtg 420
accccccta aggtgtccct gtttgagccc tctaaggccg agatcgccaa caagcagaag 480
gccaccctgg tgtgcctggc cagaggcttc ttccctgata acgtggagct gagctggtgg 540
gtgaatggca aggaggtgca ctccggcgtg tgcaccgacc cacaggccta caaggagtcc 600
aactactctt attgtctgtc ctctaggctg cgcgtgagcg ccacattctg gcacaaccct 660
cggaatcact tcagatgcca ggtgcagttt cacggcctga gcgaggagga taagtggcca 720
gagggctccc caaagcccgt gacccagaat atctctgccc aggcatgggg cagggccgac 780
tgtggaatca cctccgctc ttatcagcag ggctgtgtgt ccgccacaat cctgtacgag 840
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gtcttgtggc ttcagcttgg ctggttgagt ggagaagacc aggtgacgca gagtcccag 1080
gccctgagac tccaggaggg agagagtagc agtcttaact gcagttacac agtcagcgg 1140
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agccaggata gcaccctgtg cctgttcacc gactttgatt ctcagatcaa cgtgccaag 1500
accatggaga gcggcacctt catcacagac aagtgcgtgc tggatatgaa ggccatggac 1560
agcaagtcca acggcgccat cgcctggtcc aatcagacat ctttcacctg ccaggatatc 1620
tttaaggaga caaatgccac ctatccttcc tctgacgtgc catgtgatgc caccctgaca 1680
gagaagagct tcgagaccga catgaacctg aattttcaga atctgctcgt gattgtcctg 1740
agaatcctgc tgctgaagggt ggccggcttt aacctgctga tgaccctgag gctgtggagc 1800
tcctga 1806

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<210> 265

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Full sequence with human constant

<400> 265

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

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Leu	Glu	Ser	Ala	Ser	Thr	Asn	Gln	Thr	Ser	Met	Tyr	Leu	Cys	Ala	Ser	100	105	110
Ser	Leu	Trp	Gly	Arg	Arg	Asn	Thr	Gly	Glu	Leu	Phe	Phe	Gly	Glu	Gly	115	120	125
Ser	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	130	135	140
Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	145	150	155
Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	165	170	175
Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	180	185	190
Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	195	200	205
Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	210	215	220
Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	225	230	235
Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	245	250	255
Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	260	265	270
Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	275	280	285
Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	290	295	300
Met	Val	Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	305	310	315
Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Lys	325	330	335
Met	Leu	Glu	Cys	Ala	Phe	Ile	Val	Leu	Trp	Leu	Gln	Leu	Gly	Trp	Leu	340	345	350
Ser	Gly	Glu	Asp	Gln	Val	Thr	Gln	Ser	Pro	Glu	Ala	Leu	Arg	Leu	Gln	355	360	365
Glu	Gly	Glu	Ser	Ser	Ser	Leu	Asn	Cys	Ser	Tyr	Thr	Val	Ser	Gly	Leu	370	375	380
Arg	Gly	Leu	Phe	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Pro	Glu	Phe	385	390	395
Leu	Phe	Thr	Leu	Tyr	Ser	Ala	Gly	Glu	Glu	Lys	Glu	Lys	Glu	Arg	Leu	405	410	415
Lys	Ala	Thr	Leu	Thr	Lys	Lys	Glu	Ser	Phe	Leu	His	Ile	Thr	Ala	Pro	420	425	430
Lys	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Gln	Ala	Glu	Arg	435	440	445
Gly	Ser	Thr	Leu	Gly	Arg	Leu	Tyr	Phe	Gly	Arg	Gly	Thr	Gln	Leu	Thr	450	455	460
Val	Trp	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	465	470	475
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	485	490	495

Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr
			500					505					510		
Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser
		515					520					525			
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe
		530				535					540				
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser
545					550					555					560
Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn
			565					570						575	
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu
			580					585					590		
Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser
		595					600						605		

<210> 266

<211> 600

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 Full sequence with mouse constant

<400> 266

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

		195				200				205					
Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe
	210					215					220				
Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro
225					230					235					240
Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp
				245					250					255	
Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val
		260						265					270		
Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu
	275						280					285			
Tyr	Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys	Arg
	290					295					300				
Lys	Asn	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala
305					310					315					320
Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Lys	Met	Leu	Glu	Cys
				325					330					335	
Ala	Phe	Ile	Val	Leu	Trp	Leu	Gln	Leu	Gly	Trp	Leu	Ser	Gly	Glu	Asp
			340					345					350		
Gln	Val	Thr	Gln	Ser	Pro	Glu	Ala	Leu	Arg	Leu	Gln	Glu	Gly	Glu	Ser
		355					360					365			
Ser	Ser	Leu	Asn	Cys	Ser	Tyr	Thr	Val	Ser	Gly	Leu	Arg	Gly	Leu	Phe
	370					375					380				
Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Pro	Glu	Phe	Leu	Phe	Thr	Leu
385					390					395					400
Tyr	Ser	Ala	Gly	Glu	Glu	Lys	Glu	Lys	Glu	Arg	Leu	Lys	Ala	Thr	Leu
			405						410					415	
Thr	Lys	Lys	Glu	Ser	Phe	Leu	His	Ile	Thr	Ala	Pro	Lys	Pro	Glu	Asp
			420					425					430		
Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Gln	Ala	Glu	Arg	Gly	Ser	Thr	Leu
	435					440						445			
Gly	Arg	Leu	Tyr	Phe	Gly	Arg	Gly	Thr	Gln	Leu	Thr	Val	Trp	Pro	Asn
	450					455					460				
Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser
465					470					475					480
Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn
			485						490					495	
Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys	Val
			500					505					510		
Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp
	515						520					525			
Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn
	530					535					540				
Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu
545					550					555					560
Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu	Val
				565					570					575	
Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu
			580					585					590		
Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser								

<210> 267
<211> 9
<212> PRT
<213> Human papillomavirus

<220>
<223> E6(18-26) peptide

<400> 267
Lys Leu Pro Gln Leu Cys Thr Glu Leu
1 5

<210> 268
<211> 10
<212> PRT
<213> Human papillomavirus

<220>
<223> E6(29-38) peptide

<400> 268
Thr Ile His Asp Ile Ile Leu Glu Cys Val
1 5 10

<210> 269
<211> 9
<212> PRT
<213> Human papillomavirus

<220>
<223> E6(52-60) peptide

<400> 269
Phe Ala Phe Arg Asp Leu Cys Ile Val
1 5

<210> 270
<211> 8
<212> PRT
<213> Human papillomavirus

<220>
<223> E7(86-93) peptide

<400> 270

Thr Leu Gly Ile Val Cys Pro Ile
1 5

<210> 271

<211> 9

<212> PRT

<213> Human papillomavirus

<220>

<223> E7(11-19) peptide

<400> 271

Tyr Met Leu Asp Leu Gln Pro Glu Thr
1 5

<210> 272

<211> 9

<212> PRT

<213> Human papillomavirus

<220>

<223> E7(85-93) peptide

<400> 272

Gly Thr Leu Gly Ile Val Cys Pro Ile
1 5

<210> 273

<211> 9

<212> PRT

<213> Human papillomavirus

<220>

<223> E7(82-90) peptide

<400> 273

Leu Leu Met Gly Thr Leu Gly Ile Val
1 5

<210> 274

<211> 9

<212> PRT

<213> Human papillomavirus

<220>

<223> E7(7-15) peptide

<400> 274

Thr Leu His Glu Tyr Met Leu Asp Leu
1 5

<210> 275

<211> 137

<212> PRT

<213> Mus musculus

<220>

<223> Mouse alpha constant

<400> 275

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> 276

<211> 137

<212> PRT

<213> Mus musculus

<220>

<223> Mouse alpha constant

<400> 276

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

<220>

<223> Mouse alpha constant

<400> 278

Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser
1				5				10						15	
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> 279

<211> 137

<212> PRT

<213> Mus musculus

<220>

<223> Mouse alpha constant

<400> 279

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> 280
 <211> 137
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mouse alpha constant

<220>
 <221> VARIANT
 <222> (48)...(48)
 <223> X = unknown or other

<220>
 <221> VARIANT
 <222> (112)...(112)
 <223> X = unknown or other

<220>
 <221> VARIANT
 <222> (114)...(114)
 <223> X = unknown or other

<220>
 <221> VARIANT
 <222> (115)...(115)
 <223> X = unknown or other

<400> 280
 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 Xaa
 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 Xaa
 100 105 110
 Val Xaa Xaa Leu Arg Ile Leu Leu Lys Val Ala Gly Phe Asn Leu
 115 120 125
 Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135

<210> 281
 <211> 137
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mouse alpha constant

<400> 281
 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 Cys
 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> 282
 <211> 137
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mouse alpha constant

<400> 282
 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	Leu
			100					105					110		
Val	Ile	Val	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> 283
 <211> 172
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mouse beta constant

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

<210> 284
 <211> 173
 <212> PRT
 <213> Mus musculus

<220>
 <223> Mouse beta constant

<400> 284

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
		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			
				165					170						

<210> 285

<211> 173

<212> PRT

<213> Mus musculus

<220>

<223> Mouse beta constant

<220>

<221> VARIANT

<222> (57)...(57)

<223> X = unknown or other

<400> 285

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	Xaa	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			
				165					170						

<210> 286
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal Sequence

<400> 286
 Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
 1 5 10 15
 Asp Cys Met Ser Arg
 20

<210> 287
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<220>
 <221> REPEAT
 <222> (5)...(9)
 <223> SGGGG is repeated 5 or 6 times

<400> 287
 Pro Gly Gly Gly Ser Gly Gly Gly Gly Pro
 1 5 10

<210> 288
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 288

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
1 5 10 15
Ser

<210> 289

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR E7(11-19) beta overall CDR3 consensus

<220>

<221> VARIANT

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

<223> Xaa = A or S

<220>

<221> VARIANT

<222> (2)...(2)

<223> Xaa = A, I, S, or Y

<220>

<221> VARIANT

<222> (3)...(3)

<223> Xaa = S, T, or R

<220>

<221> VARIANT

<222> (4)...(4)

<223> Xaa = G, K, R, L, P, S, or Q

<220>

<221> VARIANT

<222> (5)...(5)

<223> Xaa = D, G, R, T, or W

<220>

<221> VARIANT

<222> (6)...(6)

<223> Xaa = A, E, F, R, S, Q, T or V

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = A, R, G, Y, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = G, N, S, or null

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = A, D, G, S, or Y

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = L, N, or Y

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = E or V

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = L or Q

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa = F, Y, or T

<400> 289
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 290
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR E7(11-19) beta CDR3 consensus

<220>

<221> VARIANT
<222> (1)...(1)
<223> Xaa = A or S

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = A or S

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = S or R

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = S, L, or P

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = W, D, or R

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = R, T, or Q

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = R, G, Y, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = G, N, or S

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = G, D, or Y

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = N or L

<400> 290

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Gln Phe
1 5 10

<210> 291
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR E7(11-19) beta CDR3 consensus

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = A or S

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = I, S, or Y

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = S or T

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = G, P, R, or T

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = R or T

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = F, S, A, or V

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = S or T

<400> 291
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Glu Gln Tyr
1 5 10

<210> 292
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR E7(11-19) alpha overall CDR3 consensus

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = A or G

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = A, G, P, V, or L

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = A, K, N, Y, D, or S

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = R, M, I, T, or G

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = N, E, L, D, V, or null

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Y, G, N, D, or null

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = S, N, G, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = G, N, Y, or null

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = D, F, G, N, or null

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa =A, N, Q, or Y

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = K, R, or N

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = F, L, or Y

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa = I, M, S, T, V, or Y

<400> 292
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 293
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR E7(11-19) alpha CDR3 consensus

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = M or I

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = E or L

<220>
<221> VARIANT

<222> (6)...(6)
<223> Xaa = G or N

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = S, G, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = S or N

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa =Y or A

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = K or R

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa = T or M

<400> 293
Ala Val Asn Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Leu Xaa
1 5 10

<210> 294
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal Sequence

<400> 294
Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
1 5 10 15
Gly Leu Thr

<210> 295
<211> 36

<212> DNA
<213> Homo sapiens

<220>
<223> spacer (IgG4hinge)

<400> 295
gaatctaagt acggaccgcc ctgccccct tgcctt

36

<210> 296
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<223> Hinge-CH3 spacer

<400> 296
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg
1 5 10 15
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
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
100 105 110
Leu Ser Leu Ser Leu Gly Lys
115

<210> 297
<211> 229
<212> PRT
<213> Homo sapiens

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

<400> 297
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

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> 299

<211> 357

<212> PRT

<213> Artificial Sequence

<220>

<223> tEGFR

<400> 299

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	
Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly
		20					25					30			
Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe
		35					40					45			
Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala
		50				55					60				
Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu
65					70				75						80
Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile
			85					90						95	
Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu
		100						105					110		
Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala
		115					120					125			
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
Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys				
	165		170	
Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly				
	180		185	
Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu				
	195		200	
Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys				
	210		215	
Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu				
	225		230	
Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met				
	245		250	
Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala				
	260		265	
His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val				
	275		280	
Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His				
	290		295	
Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro				
	305		310	
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	
Ile Gly Leu Phe Met				
	355			

<210> 300
 <211> 335
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tEGFR

<400> 300
 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> 301

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A

<400> 301

Leu	Glu	Gly	Gly	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp
1				5					10					15	
Val	Glu	Glu	Asn	Pro	Gly	Pro	Arg								
			20												

<210> 302

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

<220>
<223> T2A

<400> 302
Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15
Gly Pro

<210> 303
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> CD28

<400> 303
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> 304
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<223> CD28

<400> 304
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> 305
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<223> CD28

<400> 305
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> 306
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<223> CD28

<400> 306
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> 307
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<223> 4-1BB

<400> 307
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> 308
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> CD3 zeta

<400> 308
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> 309
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> CD3 zeta

<400> 309
Arg Val Lys Phe Ser Arg Ser Ala Glu Pro 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> 310
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> CD3 zeta

<400> 310
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys 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> 311
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A

<400> 311
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15
Pro Gly Pro

<210> 312
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A

<400> 312

Val	Lys	Gln	Thr	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val
1				5					10					15	
Glu	Ser	Asn	Pro	Gly	Pro										
			20												

<210> 313
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E2A

Gln	Cys	Thr	Asn	Tyr	Ala	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser
1				5					10					15	
Asn	Pro	Gly	Pro												
			20												

<210> 314
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <223> spacer (IgG4hinge)

Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
1				5					10		

<210> 315
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P2A

ggctccggcg	ccacaaactt	ttctctgctg	aagcaggcag	gcgatgtgga	ggagaaccct	60
ggacca						66

<210> 316
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>

<223> P2A

<400> 316

ggaagcggag ccaccaactt ttccctgctg aagcaggccg gcgatgtgga ggagaatcct 60
ggccca 66

<210> 317

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 317

ggatctggag ccaccaactt ctccctgctg aagcaggccg gcgatgtgga ggagaatcct 60
ggccca 66

<210> 318

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 318

ggatccggag ctaccaactt ctctctgctg aaacaggcag gcgatgtgga ggaaaatcct 60
gggcca 66

<210> 319

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 319

gggagtggag caacaaactt ttactgctg aagcaggccg gcgatgtgga ggaaaatcct 60
gggcca 66

<210> 320

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 320

gggtccggag ccacaaattt ttctctgctg aaacaggctg gcgatgtgga ggaaaaccct 60
gggccca 66

<210> 321

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 321

ggaagcggcg caacaaactt ttccctgctg aaacaggccg gagatgtgga ggaaaatcct 60
ggccca 66

<210> 322

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 322

ggaagcggcg ccacaaactt ctactgctg aaacaggccg gcgacgtgga ggagaatcct 60
ggccca 66

<210> 323

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 323

ggcagcggcg ccaccaactt cagcctgctt aaacaggcag gcgacgtgga ggagaatcct 60
ggccca 66

<210> 324

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A

<400> 324
ggctctggcg ccaccaactt tagcctgctg aagcaggccg gcgatgtgga ggagaatcct 60
ggccca 66

<210> 325
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> P2A

<400> 325
ggaagcggcg ccacaaactt ctactgctg aaacaggctg gcgacgtgga ggagaatcct 60
ggccca 66

<210> 326
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> P2A

<400> 326
ggcagcggcg ccaccaactt cagcctgctt aaacaagctg gcgacgtgga ggagaatcct 60
ggccca 66

<210> 327
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal Sequence

<300>
<308> NCBI NG_001332.3
<309> 2016-08-31

<400> 327
Met Lys Lys His Leu Thr Thr Phe Leu Val Ile Leu Trp Leu Tyr Phe
1 5 10 15
Tyr Arg Gly Asn Gly
20

<210> 328
<211> 19
<212> PRT

<213> Homo sapiens

<220>

<223> Signal Sequence

<300>

<308> NCBI NG_001333.2

<309> 2016-08-31

<400> 328

Met	Glu	Thr	Leu	Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp
1				5				10				15			
Val	Ser	Ser													

<210> 329

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal Sequence

<400> 329

Met	Ser	Leu	Gly	Leu	Leu	Cys	Cys	Gly	Ala	Phe	Ser	Leu	Leu	Trp	Ala
1				5				10					15		
Gly	Pro	Val													

<210> 330

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal Sequence

<400> 330

Met	Leu	Ser	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Ser	Val	Phe
1				5				10				15	

<210> 331

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal Sequence

<400> 331

Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
1 5 10 15
Gly Thr Arg

<210> 332

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal Sequence

<400> 332

Met Glu Lys Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His
1 5 10 15
Leu Asp Cys Val Ser Ser
20

<210> 333

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR alpha constant region

<400> 333

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> 334

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR alpha constant region

<400> 334

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> 335

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR alpha constant region

<400> 335

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> 336
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Native TCR alpha constant region

<400> 336															
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> 337
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Native TCR alpha constant region

<400> 337															
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> 338

<211> 142

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR alpha constant region

<400> 338

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> 339

<211> 177

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR beta constant region

<400> 339

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> 340

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR beta constant region

<400> 340

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> 341
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Native TCR alpha constant region

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> 342
 <211> 180
 <212> PRT

<213> Homo sapiens

<220>

<223> Native TCR beta constant region

<400> 342

```
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> 343

<211> 180

<212> PRT

<213> Homo sapiens

<220>

<223> Native TCR beta constant region

<400> 343

```
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> 344
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TCR alpha constant region

<400> 344
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> 345
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>

<223> TCR alpha constant region

<400> 345

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> 346

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<223> TCR alpha constant region

<400> 346

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	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> 347
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TCR alpha constant region

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> 348
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TCR alpha constant region

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> 349
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal Sequence

Met	Gly	Ile	Arg	Leu	Leu	Cys	Arg	Val	Ala	Phe	Cys	Phe	Leu	Ala	Val
1				5					10					15	
Gly	Leu	Val													

<210> 350
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TCR beta constant region

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> 351
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TCR beta constant region

<400> 351

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> 352
 <211> 180
 <212> PRT

<213> Homo sapiens

<220>

<223> TCR beta constant region

<400> 352

```
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          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> 353

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal sequence

<400> 353

```
Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
 1          5          10          15
Gly Pro Gly Ile
20
```

<210> 354

<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence

<400> 354
Met Lys Leu Val Thr Ser Ile Thr Val Leu Leu Ser Leu Gly Ile Met
1 5 10 15
Gly

<210> 355
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence

<400> 355
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
Asp His Ala Asp Thr
20

<210> 356
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR E7(11-19) alpha CDR3 consensus

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = A or G

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = A, G, P, V, or L

<220>
<221> VARIANT

<222> (3)...(3)
<223> Xaa = A, K, N, Y, D, or S

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = R, M, I, T, or G

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = N, E, L, V, or null

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Y, G, N, D, or null

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = S, N, G, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = G, N, Y, or null

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = D, F, G, N, or null

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = A, N, Q, or Y

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = K, R, or N

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = F, L, or Y

<220>
<221> VARIANT

<222> (13)...(13)

<223> Xaa = I, M, S, T, V, or Y

<400> 356

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 357

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR E7(11-19) beta CDR3 consensus

<220>

<221> VARIANT

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

<223> Xaa = A or S

<220>

<221> VARIANT

<222> (2)...(2)

<223> Xaa = A, I, S, or Y

<220>

<221> VARIANT

<222> (3)...(3)

<223> Xaa = S, T, or R

<220>

<221> VARIANT

<222> (4)...(4)

<223> Xaa = G, K, R, L, P, S, or Q

<220>

<221> VARIANT

<222> (5)...(5)

<223> Xaa = D, G, T, or W

<220>

<221> VARIANT

<222> (6)...(6)

<223> Xaa = A, E, F, R, S, Q, T or V

<220>

<221> VARIANT

<222> (7)...(7)

<223> Xaa = A, R, G, Y, or null

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = G, N, S, or null

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = A, D, G, S, or Y

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = L, N, or Y

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = E or V

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = L or Q

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa = F, Y, or T

<400> 357
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 358
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<223> TCR beta constant region

<400> 358
gaagatctga agaactgtctt cccacctgag gtggccgtgt tcgagccttc tgaggccgag 60
atcagccaca cacagaaaagc cacactcgtg tgtctggcca ccggcttcta tcccgatcac 120
gtggaactgt cttgggtgggt caacggcaaa gaggtgcaca gcggcgtctg taccgatcct 180
cagcctctga aagagcagcc cgctctgaac gacagcagat actgcctgag cagcagactg 240
agagtgtccg ccaccttctg gcagaacccc agaaaccact tcagatgcca ggtgcagttc 300

```

tacggcctga gcgagaacga tgagtggacc caggatagag ccaagcctgt gacacagatc 360
gtgtctgccg aagcctgggg cagagccgat tgtggcttta ccagcgagag ctaccagcag 420
ggcgtgctgt ctgccacaat cctgtacgag atcctgctgg gcaaagccac tctgtacgcc 480
gtgctggtgt ctgccctggt gctgatggcc atggtcaagc ggaaggatag cagaggc 537

```

<210> 359

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Beta with human constant sequence

<400> 359

```

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

```

Lys Arg Lys Asp Ser Arg Gly
290 295

<210> 360

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Beta with human constant sequence and signal
peptide

<400> 360

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

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg
 290 295 300
 Lys Asp Ser Arg Gly
 305

<210> 361
 <211> 927
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> beta with human constant sequence and signal
 peptide

<400> 361
 atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
 catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
 gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
 atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgctga gaaggacaag 240
 tttctcatca accatgcaag cctgacctg tccactctga cagtgaccag tgcccacatc 300
 gaagacagca gcttctacat ctgcagtgt agatcttggc gggggggcct tgagcagttc 360
 ttcgggccag ggacacggct caccgtgcta gaagatctga agaactgtctt cccacctgag 420
 gtggccgtgt tcgagccttc tgaggccgag atcagccaca cacagaaagc cacactcgtg 480
 tgtctggcca ccggcttcta tcccgatcac gtggaactgt cttggtgggt caacggcaaa 540
 gaggtgcaca gcggcgctctg taccgatcct cagcctctga aagagcagcc cgctctgaac 600
 gacagcagat actgcctgag cagcagactg agagtgtccg ccaccttctg gcagaacccc 660
 agaaaccact tcagatgcca ggtgcagttc tacggcctga gcgagaacga tgagtggacc 720
 caggatagag ccaagcctgt gacacagatc gtgtctgccg aagcctgggg cagagccgat 780
 tgtggcttta ccagcgagag ctaccagcag ggcgtgctgt ctgccacaat cctgtacgag 840
 atcctgctgg gcaaagccac tctgtacgcc gtgctgggtgt ctgccctggt gctgatggcc 900
 atggtcaagc ggaaggatag cagaggc 927

<210> 362
 <211> 600
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR Full sequence with human constant

<400> 362
 Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
 1 5 10 15
 Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
 20 25 30
 Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
 35 40 45
 Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
 50 55 60

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

Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser
465					470					475					480
Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser
				485					490					495	
Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Arg
			500					505					510		
Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser
		515					520					525			
Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp
	530					535					540				
Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu
545					550					555					560
Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val
				565					570					575	
Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu
			580					585						590	
Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser								
		595					600								

<210> 363

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR Full sequence with human constant

<400> 363

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catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgctga gaaggacaag 240
tttctcatca accatgcaag cctgacctg tccactctga cagtgaccag tgcccatcct 300
gaagacagca gcttctacat ctgcagtgt agatcttggc gggggggcct tgagcagttc 360
ttcgggccag ggacacggct caccgtgcta gaagatctga agaactctt cccacctgag 420
gtggccgtgt tcgagccttc tgaggccgag atcagccaca cacagaaagc cacactcgtg 480
tgtctggcca ccggcttcta tcccgatcac gtggaactgt cttggtgggt caacggcaaa 540
gaggtgcaca gcggcgtctg taccgatcct cagcctctga aagagcagcc cgctctgaac 600
gacagcagat actgcctgag cagcagactg agagtgtccg ccaccttctg gcagaacccc 660
agaaaccact tcagatgcca ggtgcagttc tacggcctga gcgagaacga tgagtggacc 720
caggatagag ccaagcctgt gacacagatc gtgtctgccg aagcctgggg cagagccgat 780
tgtggcttta ccagcgagag ctaccagcag ggctgtgctgt ctgccacaat cctgtacgag 840
atcctgctgg gcaaagccac tctgtacgcc gtgtgtgtgt ctgccctggt gctgatggcc 900
atgggtcaagc ggaaggatag cagaggcgga agcggcgcca caaacttctc actgctgaaa 960
caggctggcg acgtggagga gaatcctggc ccaatgggtcc tgaaaattctc cgtgtccatt 1020
ctttggattc agttggcatg ggtgagcacc cagctgctgg agcagagccc tcagtttcta 1080
agcatccaag agggagaaaa tctactgtg tactgcaact cctcaagtgt tttttccagc 1140
ttacaatggt acagacagga gcctggggaa ggtcctgtcc tcctggtgac agtagttacg 1200
gggtggagaag tgaagaagct gaagagacta acctttcagt ttggtgatgc aagaaaggac 1260

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agttctctcc	acatcactgc	agcccagcct	ggtgatacag	gcctctacct	ctgtgcagga	1320
gctcgcaact	tcaacaaaatt	ttacttttga	tctggggacca	aactcaatgt	aaaaccaaatt	1380
atccagaatc	cggaccccg	ggtatatcaa	ctgcgcgact	caaaatcatc	cgataagagt	1440
gtctgtttgt	ttactgactt	cgacagtcaa	actaatgtct	ctcagagcaa	agattccgat	1500
gtctacatca	ctgacaagtg	cgttctggat	atgcggagca	tggattttta	gtccaactcc	1560
gccgtagcct	ggtccaacaa	gtcagacttt	gcctgtgcaa	atgctttcaa	caactcaatt	1620
atccctgagg	acacttttct	tccttcaccg	gagtcctcat	gcgatgttaa	actggtcgaa	1680
aaatcttttg	agacggatac	gaacctcaac	ttccaaaatt	tgagcggtat	tggctttagg	1740
attctgcttc	tcaagggtgc	ggggttcaat	ctcctgatga	cgttgcggtc	ttggagcagc	1800

<210> 364

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Native full sequence with human constant
(nt)

<400> 364

atggccaact	ctgctatgga	caccagagta	ctctgctgtg	cggatcatctg	tcttctgggg	60
gcagggtctct	caaatgccgg	cgatcatgcag	aaccaagac	acctgggtcag	gaggagggga	120
caggaggcaa	gactgagatg	cagcccaatg	aaaggacaca	gtcatgttta	ctggatcgg	180
cagctcccag	aggaagggtct	gaaattcatg	gtttatctcc	agaaaagaaa	tatcatagat	240
gagtcaggaa	tgccaaagga	acgattttct	gctgaatttc	ccaaagagggg	ccccagcatc	300
ctgaggatcc	agcaggtagt	gcgaggagat	tcggcagctt	atttctgtgc	cagctcacca	360
gacgaaagca	gggatagcaa	tcagccccag	cattttggtg	atgggactcg	actctccatc	420
ctagaggacc	tgaataaggt	gttccccct	gagggtggccg	tgtttgagcc	aagcgaggcc	480
gagatctccc	acaccagaa	ggccaccctg	gtgtgcctgg	caaccggctt	ctttcccgat	540
cacgtggagc	tgtcctgggt	ggtgaacggc	aaggagggtgc	actctggcgt	gtgcacagac	600
ccacagcccc	tgaaggagca	gcctgccctg	aatgattccc	gctattgtct	gtcctctcgg	660
ctgagagtgt	ctgccacctt	ttggcagaac	ccacggaatc	acttcagatg	ccagggtgcag	720
ttttacggcc	tgtctgagaa	cgacgagtgg	accaggatc	gggccaagcc	tgtgacacag	780
atcgtgagcg	cggaaagcatg	gggcagagcc	gactgtggct	tcaccagcgt	gtcctatcag	840
cagggcggtg	tgtccgccac	catcctgtac	gagatcctgc	tgggcaaggc	cacactgtat	900
gccgtgctgg	tgtctgccct	ggtgctgatg	gccatgggtga	agagaaaaga	cttctaaggc	960
tccggagcaa	ccaatttcag	cctgctgaag	caggccggcg	atgtggagga	gaatcctggc	1020
ccaatggctc	aggaactggg	aatgcagtgc	caggctcgtg	gtatcctgca	gcagatgtgg	1080
ggagttttcc	ttctttatgt	ttccatgaag	atgggaggca	ctacaggaca	aaacattgac	1140
cagcccactg	agatgacagc	tacggaaggt	gccattgtcc	agatcaactg	cacgtaccag	1200
acatctgggt	tcaacgggct	gttctggtac	cagcaacatg	ctggcgaagc	accacattt	1260
ctgtcttaca	atgttctgga	tggtttgag	gagaaaagtc	gtttttcttc	attccttagt	1320
cggctctaaag	ggtacagtta	cctccttttg	aaggagctcc	agatgaaaga	ctctgcctct	1380
tacctctgtg	ctgtgagaga	ttggggatat	ggtgggtgcta	caaacaagct	catctttgga	1440
actggcactc	tgcttgctgt	ccagccaaat	atccagaatc	cggaccccg	ggtatatcaa	1500
ctgcgcgact	caaaatcatc	cgataagagt	gtctgtttgt	ttactgactt	cgacagtcaa	1560
actaatgtct	ctcagagcaa	agattccgat	gtctacatca	ctgacaagtg	cgttctggat	1620
atgcggagca	tggattttta	gtccaactcc	gccgtagcct	ggtccaacaa	gtcagacttt	1680
gcctgtgcaa	atgctttcaa	caactcaatt	atccctgagg	acactttctt	tccttcaccg	1740

gagtcctcat	gcgatgttaa	actggtcgaa	aaatcttttg	agacggatac	gaacctcaac	1800
ttccaaaatt	tgagcggttat	tggctttagg	attctgcttc	tcaagggtgc	ggggttcaat	1860
ctcctgatga	cgttgcggct	ttggagcagc	taa			1893

<210> 365

<211> 1803

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Full sequence with human constant (nt)

<400> 365

atgctgctgc	ttctgctgct	tctggggcca	ggctccgggc	ttggtgctgt	cgtctctcaa	60
catccgagct	gggttatctg	taagagtgga	acctctgtga	agatcgagtg	ccgttccctg	120
gactttcaag	ccacaactat	gttttgggtat	cgtcagttcc	cgaaacagag	tctcatgctg	180
atggcaactt	ccaatgaggg	ctccaaggcc	acatacgagc	aaggcgtcga	gaaggacaag	240
tttctcatca	accatgcaag	cctgaccttg	tccactctga	cagtgaccag	tgcccatcct	300
gaagacagca	gcttctacat	ctgcagtgtc	agatcttggc	ggggggggcct	tgagcagttc	360
ttcggggccag	ggacacggct	caccgtgcta	gaagatctga	agaacgtctt	cccacctgag	420
gtggccgtgt	tcgagccttc	tgaggccgag	atcagccaca	cacagaaagc	cacactcgtg	480
tgtctggcca	ccggcttcta	tcccgatcac	gtggaactgt	cttgggtgggt	caacggcaaa	540
gaggtccaca	gcggcgtctg	taccgatcct	cagcctctga	aagagcagcc	cgctctgaac	600
gacagcagat	actgcctgag	cagcagactg	agagtgtccg	ccaccttctg	gcagaacccc	660
agaaaccact	tcagatgcc	ggtgcagttc	tacggcctga	gcgagaacga	tgagtggacc	720
caggatagag	ccaagcctgt	gacacagatc	gtgtctgccg	aagcctgggg	cagagccgat	780
tgtggcttta	ccagcgagag	ctaccagcag	ggcgtgctgt	ctgccacaat	cctgtacgag	840
atcctgctgg	gcaaagccac	tctgtacgcc	gtgctgggtg	ctgccctggg	gctgatggcc	900
atggtcaagc	ggaaggatag	cagaggcgga	agcggcgcca	caacttctc	actgctgaaa	960
caggctggcg	acgtggagga	gaatcctggc	ccaatgggtc	tgaaattctc	cgtgtccatt	1020
ctttggattc	agttggcatg	ggtcagcacc	cagctgctgg	agcagagccc	tcagtttcta	1080
agcatccaag	agggagaaaa	tctcactgtg	tactgcaact	cctcaagtgt	tttttcctcc	1140
ttacaatggg	atcgacagga	gcctggggaa	ggtcctgtcc	tcctgggtgac	agtagttacg	1200
ggtggagaag	tgaagaagct	gaagagacta	acctttcagt	ttggtgatgc	aagaaaggac	1260
agttctctcc	acatcactgc	agcccagcct	ggtgatacag	gcctctacct	ctgtgccgga	1320
gctcgcaact	tcaacaaatt	ttactttgga	tctgggacca	aactcaatgt	gaaaccaa	1380
atccagaatc	cggaccccg	ggtatatcaa	ctgcgcgact	caaaatcatc	cgataagagt	1440
gtctgtttgt	ttactgactt	cgacagtcaa	actaatgtct	ctcagagcaa	agattccgat	1500
gtctacatca	ctgacaaaatg	cgttctggat	atgcggagca	tggattttta	gtccaactcc	1560
gccgtagcct	ggtccaacaa	gtcagacttt	gcctgtgcaa	atgctttcaa	caactcaatt	1620
atccctgagg	acactttctt	tccttcaccg	gagtcctcat	gcgatgttaa	actggtcgaa	1680
aaatcttttg	agacggatac	gaacctcaac	ttccaaaatt	tgagcggttat	tggctttcgg	1740
attctgcttc	tcaaagttgc	ggggttcaat	ctcctgatga	cgttgcggct	ttggagcagc	1800
taa						1803

<210> 366

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR alpha constant region, Homo sapiens (nt)

<400> 366

```
ccgcggtata tcaactgcgc gactcaaaat catccgataa gagtgtctgt ttgtttactg 60
acttcgacag tcaaactaat gtctctcaga gcaaagattc cgatgtctac atcactgaca 120
agtgcgttct ggatatgcgg agcatggatt ttaagtccaa ctccgccgta gcctgggtcca 180
acaagtcaga ctttgcctgt gcaaatgctt tcaacaactc aattatccct gaggacactt 240
tctttccttc accggagtcc tcatgcgatg ttaaaactggc cgaaaaatct ttgagacagg 300
atacgaacct caacttccaa aatttgagcg ttattggctt taggattctg cttctcaagg 360
ttgcgggggtt caatctcctg atgacgttgc ggctttggag cagctaa 407
```

<210> 367

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR alpha constant region, Homo sapiens (nt)

<400> 367

```
ccgcggtata tcaactgcgc gactcaaaat catccgataa gagtgtctgt ttgtttactg 60
acttcgacag tcaaactaat gtctctcaga gcaaagattc cgatgtctac atcactgaca 120
aatgcgttct ggatatgcgg agcatggatt ttaagtccaa ctccgccgta gcctgggtcca 180
acaagtcaga ctttgcctgt gcaaatgctt tcaacaactc aattatccct gaggacactt 240
tctttccttc accggagtcc tcatgcgatg ttaaaactggc cgaaaaatct ttgagacagg 300
atacgaacct caacttccaa aatttgagcg ttattggctt tcggattctg cttctcaaag 360
ttgcgggggtt caatctcctg atgacgttgc ggctttggag cagctaa 407
```

<210> 368

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> P2A Artificial (nt)

<400> 368

```
ggaagcggcg ccacaaactt ctactgctg aaacaggctg gcgacgtgga ggagaatcct 60
ggccca 66
```

<210> 369

<211> 296

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 beta with human constant sequence (aa)

<400> 369

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

<210> 370

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 beta with human constant sequence (aa)

<400> 370

Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr Gln Met Gly

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

<210> 371

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 beta with human constant sequence (aa)

<400> 371

Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr	Gln	Met	Gly
1					5				10					15	

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

<210> 372

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 beta with human constant sequence (aa)

<400> 372

Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr Gln Met Gly
 1 5 10 15
 Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His Leu Tyr Phe

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

<210> 373

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 beta with human constant sequence (aa)

<400> 373

Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr	Gln	Met	Gly		
1				5					10					15			
Gln	Glu	Val	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His	Leu	Tyr	Phe		
		20					25					30					

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

<210> 374

<211> 296

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 beta with human constant sequence (aa)

<400> 374

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

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

<210> 375

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 beta with human constant sequence (aa)

<400> 375

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

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

<210> 376

<211> 293

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 beta with human constant sequence (aa)

<400> 376

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

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

<210> 377

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 65 beta with human constant sequence (aa)

<400> 377

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

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

<210> 378

<211> 320

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 56 beta with human constant sequence and
 signal peptide (aa)

<400> 378

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

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

<210> 379

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 58 beta with human constant sequence and
signal peptide (aa)

<400> 379

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

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

<210> 380

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 59 beta with human constant sequence and
 signal peptide (aa)

<400> 380

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

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

<210> 381

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 60 beta with human constant sequence and
signal peptide (aa)

<400> 381

Met	Asp	Thr	Trp	Leu	Val	Cys	Trp	Ala	Ile	Phe	Ser	Leu	Leu	Lys	Ala
1				5				10						15	

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

<210> 382

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 61 beta with human constant sequence and
signal peptide (aa)

<400> 382

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

<210> 383

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 62 beta with human constant sequence and
signal peptide (aa)

<400> 383

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

<210> 384

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 63 beta with human constant sequence and
signal peptide (aa)

<400> 384

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

<210> 385

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR 64 beta with human constant sequence and
signal peptide (aa)

<400> 385

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

<210> 386

<211> 313

<210> 387
<211> 1890
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 56 Native full sequence with human constant
(nt)

<400> 387
atggccaact ctgctatgga caccagagta ctctgctgtg cggtcacatg tcttctgggg 60
gcagggtctct caaatgccgg cgctcatgcag aaccaagac acctgggtcag gaggagggga 120
caggaggcaa gactgagatg cagccaatg aaaggacaca gtcatgttta ctggtatcgg 180
cagctcccag aggaaggctt gaaattcatg gtttatctcc agaaagaaaa tatcatagat 240
gagtcaggaa tgccaaagga acgattttct gctgaatttc ccaaagaggg cccagcatc 300
ctgaggatcc agcaggtagt gcgaggagat tcggcagctt atttctgtgc cagctcacca 360
gacgaaagca gggatagcaa tcagccccag cattttgggtg atgggactcg actctccatc 420
ctagaggacc tgaataaggt gttccccctt gaggtggccg tgtttgagcc aagcagggcc 480
gagatctccc acaccagaa ggccaccctg gtgtgcctgg caaccggctt ctttccgat 540
cacgtggagc tgtcctgggt ggtgaacggc aaggagggtgc actctggcgt gtgcacagac 600
ccacagcccc tgaaggagca gcctgccctg aatgattccc gctattgtct gtcctctcgg 660
ctgagagtgt ctgccacctt ttggcagaac ccacggaatc acttcagatg ccagggtcag 720
ttttacggcc tgtctgagaa cgacgagtgg acccaggatc gggccaagcc tgtgacacag 780
atcgtgagcg cgggaagcatg gggcagagcc gactgtggct tcaccagcgt gtcctatcag 840
cagggcggtc tgtccgccac catcctgtac gagatcctgc tgggcaaggc cacactgtat 900
gccgtgctgg tgtctgccct ggtgctgatg gccatgggtga agagaaaaga cttcggctcc 960
ggagcaacca atttcagcct gctgaagcag gccggcgatg tggaggagaa tcctggccca 1020
atggctcagg aactgggaat gcagtccag gctcgtggta tcctgcagca gatgtgggga 1080
gttttccttc tttatgtttc catgaagatg ggaggcacta caggacaaaa cattgaccag 1140
cccactgaga tgacagctac ggaagggtgcc attgtccaga tcaactgcac gtaccagaca 1200
tctgggttca acgggctgtt ctggtaccag caacatgctg gcgaagcacc cacatttctg 1260
tcttacaatg ttctggatgg tttggaggag aaaggctcgt tttcttcatt ccttagtcgg 1320
tctaaagggg acagttacct cttttgaag gagctccaga tgaaagactc tgcctcttac 1380
ctctgtgctg tgagagattg gggatatggt ggtgctacaa acaagctcat ctttggaaact 1440
ggcactctgc ttgctgtcca gccaaatatc cagaatccgg accccgcggg atatcaactg 1500
cgcgactcaa aatcatccga taagagtgtc tgtttgttta ctgacttcga cagtcaaaact 1560
aatgtctctc agagcaaaga ttccgatgtc tacatcactg acaagtgcgt tctggatatg 1620
cggagcatgg attttaagtc caactccgcc gtagcctggg ccaacaagtc agactttgcc 1680
tgtgcaaatg ctttcaacaa ctcaattatc cctgaggaca ctttctttcc ttcaccggag 1740
tcctcatgcg atgttaaaact ggtcgaaaaa tcttttgaga cggatacgaa cctcaacttc 1800
caaaatttga gcgttattgg ctttaggatt ctgcttctca aggttgcggg gttcaatctc 1860
ctgatgacgt tgcggctttg gagcagctaa 1890

<210> 388
<211> 1899
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR 56 Codon-optimized full sequence with human

constant (nt)

<400> 388

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atgggaccca tggccaatag cgccatggat accagagtgc tgtgctgcgc cgtgatctgt 60
ctgcttggag ccggactgtc taatgccggc gtgatgcaga accccagaca cctcgttcgg 120
agaagaggcc aagaggccag actgagatgc agccctatga agggccacag ccacgtgtac 180
tggtagacag agctgcctga agagggcctg aagttcatgg tgtacctgca gaaagagaac 240
atcatcgacg agagcggcat gcccaaagag cggttctctg ccgagtttcc caaagagggc 300
cccagcatcc tgagaatcca gcaggttgtg cggggagata gcgccgccta cttttgtgcc 360
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ctgtctattc tcgaggacct gaataagggtg ttccccctg aggtggccgt gtttgagcca 480
agcgaggccg agatctccca caccagaag gccaccctgg tgtgcctggc aaccggcttc 540
tttcccgatc acgtggagct gtcttggtgg gtgaacggca aggaggtgca ctctggcgtg 600
tgcacagacc cacagcccct gaaggagcag cctgccctga atgattcccg ctattgtctg 660
tcctctcggc tgagagtgtc tgccaccttt tggcagaacc cacggaatca cttcagatgc 720
caggtgcagt tttacggcct gtctgagaac gacgagtgga cccaggatcg ggccaagcct 780
gtgacacaga tcgtgagcgc ggaagcatgg ggcagagccg actgtggctt caccagcgtg 840
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cctggcccaa tggctcaaga gctgggcatg cagtgtcagg ccagaggaat cctgcagcag 1080
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tatcaactgc gcgactcaaa atcatccgat aagagtgtct gtttgtttac tgacttcgac 1560
agtcaaaacta atgtctctca gagcaaagat tccgatgtct acatcactga caagtgcgtt 1620
ctggatatgc ggagcatgga ttttaagtcc aactccgccg tagcctggtc caacaagtca 1680
gactttgcct gtgcaaatgc tttcaacaac tcaattatcc ctgaggacac tttctttcct 1740
tcaccggagt cctcatgcga tgttaaaactg gtcgaaaaat cttttgagac ggatacgaac 1800
ctcaacttcc aaaatttgag cgttattggc tttaggattc tgcttctcaa ggttgcgggg 1860
ttcaatctcc tgatgacgtt gcggctttgg agcagctaa 1899
```

<210> 389

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Native full sequence with human constant
(nt)

<400> 389

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atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg 120
gactttcagg ccacaactat gttttgggtat cgtcagttcc cgaaacagag tctcatgctg 180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag 240
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tttctcatca	accatgcaag	cctgaccttg	tccactctga	cagtgaccag	tgcccatcct	300
gaagacagca	gcttctacat	ctgcagtgct	agatcttggc	gggggggcct	tgagcagttc	360
ttcgggccag	ggacacggct	caccgtgcta	gaggacctga	ataaggtgtt	ccccctgag	420
gtggccgtgt	ttgagccaag	cgaggccgag	atctcccaca	cccagaaggc	caccctggtg	480
tgcttgga	ccggcttctt	tcccgatcac	gtggagctgt	cctggtgggt	gaacggcaag	540
gaggtgcact	ctggcgtgtg	cacagaccca	cagcccctga	aggagcagcc	tgccctgaat	600
gattccccgct	attgtctgtc	ctctcggctg	agagtgtctg	ccaccttttg	gcagaaccca	660
cggaatcact	tcagatgcca	ggtgcagttt	tacggcctgt	ctgagaacga	cgagtggacc	720
caggatcggg	ccaagcctgt	gacacagatc	gtgagcgcgg	aagcatgggg	cagagccgac	780
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ggcgatgtgg	aggagaatcc	tggccaatg	gtcctgaaat	tctccgtgtc	cattctttgg	1020
attcagttgg	catgggtgag	caccagctg	ctggagcaga	gccctcagtt	tctaagcatc	1080
caagaggggag	aaaatctcac	tgtgtactgc	aactcctcaa	gtgttttttc	cagcttacia	1140
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gaagtgaaga	agctgaagag	actaaccttt	cagtttggtg	atgcaagaaa	ggacagttct	1260
ctccacatca	ctgcagccca	gcctgggtgat	acaggcctct	acctctgtgc	aggagctcgc	1320
aacttcaaca	aattttactt	tggatctggg	acaaaactca	atgtaaaacc	aaatatccag	1380
aatccggacc	ccgcggtata	tcaactgcgc	gactcaaaat	catccgataa	gagtgtctgt	1440
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gcctgggtcca	acaagtcaga	ctttgcctgt	gcaaagtgtt	tcaacaactc	aattatccct	1620
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tttgagacgg	atacgaacct	caacttccaa	aatttgagcg	ttattggctt	taggattctg	1740
cttctcaagg	ttgcgggggt	caatctcctg	atgacgttgc	ggctttggag	cagctaa	1797

<210> 390

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Codon-optimized full sequence with human constant (nt)

<400> 390

atgctcctgc	tgcttctgct	cctcgggccc	ggcagcggtc	tcggcgccgt	cgtgtcgag	60
cacccgtcgt	gggtgatttg	caagagcgga	acgagcgtga	agatcgagtg	ccgctcgctc	120
gacttccagg	ccacaaccat	gttctggtac	cgccagtttc	ccaagcagag	cctcatgctg	180
atggccacaa	gcaatgaagg	cagcaaggcc	acttatgaac	agggcgtgga	gaaggacaag	240
tttctgatca	accacgcctc	cctgaccctg	tccaccctca	ctgtgaccag	cgcccaccct	300
gaggacagca	gcttctacat	ctgcagcgcc	cgcagctgga	ggggcggcct	ggagcagttc	360
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gtggccgtgt	ttgagccaag	cgaggccgag	atctcccaca	cccagaaggc	caccctggtg	480
tgcttgga	ccggcttctt	tcccgatcac	gtggagctgt	cctggtgggt	gaacggcaag	540
gaggtgcact	ctggcgtgtg	cacagaccca	cagcccctga	aggagcagcc	tgccctgaat	600
gattccccgct	attgtctgtc	ctctcggctg	agagtgtctg	ccaccttttg	gcagaaccca	660
cggaatcact	tcagatgcca	ggtgcagttt	tacggcctgt	ctgagaacga	cgagtggacc	720
caggatcggg	ccaagcctgt	gacacagatc	gtgagcgcgg	aagcatgggg	cagagccgac	780

tgtggcttca	ccagcgtgtc	ctatcagcag	ggcgtgctgt	ccgccaccat	cctgtacgag	840
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atgggtgaaga	gaaaagactt	cggctccgga	gcaaccaatt	tcagcctgct	gaagcaggcc	960
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attcagctgg	cctgggtgtc	cacccagctc	ctggagcaga	gccccagtt	cctgtccatc	1080
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gaggtgaaga	agctaaagcg	cctgacgttc	cagttcggag	acgcgcggaa	ggactcgtcg	1260
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atcactgaca	agtgcgttct	ggatatgcgg	agcatggatt	ttaagtccaa	ctccgccgta	1560
gcctgggtcca	acaagtcaga	ctttgcctgt	gcaaatgctt	tcaacaactc	aattatccct	1620
gaggacactt	tctttccttc	accggagtcc	tcatgcgatg	ttaaaactgg	cgaaaaatct	1680
tttgagacgg	atacgaacct	caacttccaa	aatttgagcg	ttattggctt	taggattctg	1740
cttctcaagg	ttgcgggggt	caatctcctg	atgacgttgc	ggctttggag	cagctaa	1797

<210> 391

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Native full sequence with human constant
(nt)

<400> 391

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cctgaagtca	cccagactcc	cagccatcag	gtcacacaga	tgggacagga	agtgatcttg	120
cgctgtgtcc	ccatctctaa	tcacttatac	ttctattggg	acagacaaat	cttggggcag	180
aaagtcgagt	ttctggtttc	cttttataat	aatgaaatct	cagagaagtc	tgaaatattc	240
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cctgaggtgg	ccgtgtttga	gccaagcgag	gccgagatct	cccacaccca	gaaggccacc	480
ctgggtgtgcc	tggcaaccgg	cttctttccc	gatcacgtgg	agctgtcctg	gtgggtgaac	540
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ctgaatgatt	cccgtctattg	tctgtcctct	cggctgagag	tgtctgccac	cttttggcag	660
aaccacgga	atcacttcag	atgccagggtg	cagttttacg	gcctgtctga	gaacgacgag	720
tggacccagg	atcggggcaa	gcctgtgaca	cagatcgtga	gcgcggaagc	atggggcaga	780
gccgactgtg	gcttcaccag	cgtgtcctat	cagcagggcg	tgctgtccgc	caccatcctg	840
tacgagatcc	tgctgggcaa	ggccacactg	tatgccgtgc	tgggtgtctg	cctgggtgctg	900
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agtgtcttct	agtctttctt	ctggtacaga	caggattgca	ggaaagaacc	taagttgctg	1200
atgtccgtat	actccagtgg	taatgaagat	ggaaggttta	cagcacagct	caatagagcc	1260
agccagtata	tttccctgct	catcagagac	tccaagctca	gtgattcagc	cacctacctc	1320

tgtgtggtga	acagggataa	ctatgggtcag	aattttgtct	ttgggtcccgg	aaccagattg	1380
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tcattccgata	agagtgtctg	tttgtttact	gacttcgaca	gtcaaaactaa	tgtctctcag	1500
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cggctttgga	gcagctaa					1818

<210> 392

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 59 Native full sequence with human constant
(nt)

<400> 392

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1824

<210> 393

<211> 1830

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 60 Native full sequence with human constant
(nt)

<400> 393

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```

<210> 394

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Native full sequence with human constant
(nt)

<400> 394

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cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
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cctgagggtg ccgtgtttga gccaaagcgag gccgagatct cccacaccca gaaggccacc 480
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ttgcggcttt ggagcagcta a                                     1821
```

<210> 395

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Native full sequence with human constant
(nt)

<400> 395

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gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt 120
tgggtgcaatc ctatatctgg ccatgctacc ctttactggg accagcagat cctgggacag 180
ggcccaaagc ttctgattca gtttcagaat aacggtgtag tggatgattc acagttgcct 240
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```

aaggatcgat tttctgcaga gaggtcmeta ggagtagact ccactctcaa gatccagcct 300
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acgttgcggc tttggagcag ctaa
1824

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<210> 396

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Native full sequence with human constant
(nt)

<400> 396

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agggtgtgatc caatttcggg tcatgtatcc ctttttttgt accaacaggc cctggggcag 180
gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc 240
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cagcctgccc tgaatgattc ccgctattgt ctgtcctctc ggctgagagt gtctgccacc 660
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cggctttgga	gcagctaa					1818

<210> 397

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Native full sequence with human constant
(nt)

<400> 397

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aaatgtgaac	aaaaatctggg	ccatgatact	atgtattggg	ataaacagga	ctctaagaaa	180
tttctgaaga	taatgttttag	ctacaataat	aaggagctca	ttataaatga	aacagttcca	240
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gagcttgggtg	actctgctgt	gtatttctgt	gccagcagcc	agggggaagc	tggggccaac	360
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<210> 398

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Native full sequence with human constant
(nt)

<400> 398

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<210> 399

<211> 1902

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with human constant (nt)

<400> 399

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<210> 400

<211> 1896

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Native full sequence with human constant
(nt)

<400> 400

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<210> 401

<211> 1905

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with human
constant (nt)

<400> 401

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<210> 402

<211> 1803

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Codon-optimized full sequence with human constant (nt)

<400> 402

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<210> 403

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Native full sequence with human constant
(nt)

<400> 403

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<210> 404

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 59 Native full sequence with human constant
(nt)

<400> 404

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<210> 405

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 60 Native full sequence with human constant
(nt)

<400> 405

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<210> 406

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Native full sequence with human constant
(nt)

<400> 406

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<210> 407

<211> 1830

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Native full sequence with human constant

(nt)

<400> 407

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<210> 408

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Native full sequence with human constant
(nt)

<400> 408

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<210> 409

<211> 1842

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 64 Native full sequence with human constant
(nt)

<400> 409

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<210> 410

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 65 Native full sequence with human constant
(nt)

<400> 410

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<210> 411

<211> 960

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Native full sequence with human constant (nt)

<400> 411

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caggaggcaa	gactgagatg	cagccaatg	aaaggacaca	gtcatgttta	ctggtatcgg	180
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gagtcaggaa	tgccaaagga	acgattttct	gctgaatttc	ccaaagagggg	ccccagcatc	300
ctgaggatcc	agcaggtagt	gcgaggagat	tcggcagctt	atttctgtgc	cagctcacca	360
gacgaaagca	gggatagcaa	tcagccccag	catitttggtg	atgggactcg	actctccatc	420
ctagaagatc	tgaagaacgt	cttcccacct	gagggtggccg	tgttcgagcc	ttctgaggcc	480
gagatcagcc	acacacagaa	agccacactc	gtgtgtctgg	ccaccggctt	ctatcccgat	540
cacgtggaac	tgtcttggtg	ggtcaacggc	aaagaggtgc	acagcggcgt	ctgtaccgat	600
cctcagcctc	tgaagagca	gcccgtcttg	aacgacagca	gatactgcct	gagcagcaga	660
ctgagagtgt	ccgccacctt	ctggcagaac	cccagaaacc	acttcagatg	ccagggtgcag	720
ttctacggcc	tgagcgagaa	cgatgagtgg	acccaggata	gagccaagcc	tgtgacacag	780
atcgtgtctg	ccgaagcctg	gggcagagcc	gattgtggct	ttaccagcga	gagctaccag	840
cagggcggtg	tgtctgccac	aatcctgtac	gagatcctgc	tgggcaaagc	cactctgtac	900
gccgtgctgg	tgtctgccct	ggtgctgatg	gccatggtca	agcgggaagga	tagcagaggc	960

<210> 412

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with human constant (nt)

<400> 412

atgggaccca	tggccaatag	cgccatggat	accagagtgc	tgtgctgcgc	cgtgatctgt	60
------------	------------	------------	------------	------------	------------	----

```

ctgcttggag ccggactgtc taatgccggc gtgatgcaga accccagaca cctcgttcgg 120
agaagaggcc aagaggccag actgagatgc agccctatga agggccacag ccacgtgtac 180
tggtacagac agctgcctga agagggcctg aagttcatgg tgtacctgca gaaagagaac 240
atcatcgacg agagcggcat gccc aaagag cggttctctg ccgagtttcc caaagagggc 300
cccagcatcc tgagaatcca gcaggttgtg cggggagata gcgccgccta cttttgtgcc 360
agctctcccc atgagagccg ggactcta at cagcctcagc actttggcga cggcaccagg 420
ctgtctattc tcgaagatct gaagaacgtc ttcccacctg aggtggccgt gttcgagcct 480
tctgaggccg agatcagcca cacacagaaa gccacactcg tgtgtctggc caccggcttc 540
tatcccgatc acgtggaact gtcttggtgg gtcaacggca aagagggtgca cagcggcgtc 600
tgtaccgatc ctcagcctct gaaagagcag cccgctctga acgacagcag atactgcctg 660
agcagcagac tgagagtgtc cgccaccttc tggcagaacc ccagaaacca cttcagatgc 720
cagggtgcagt tctacggcct gagcgagaa gatgagtgga cccaggatag agccaagcct 780
gtgacacaga tcgtgtctgc cgaagcctgg ggcagagccg attgtggctt taccagcgag 840
agctaccagc agggcggtgt gtctgccaca atcctgtacg agatcctgct gggcaaagcc 900
actctgtacg ccgtgctggt gtctgccctg gtgctgatgg ccatgggtcaa gcggaaggat 960
agcagaggc 969

```

<210> 413

<211> 927

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 57 Codon-optimized full sequence with human constant (nt)

<400> 413

```

atgctcctgc tgcttctgct cctcgggccc ggcagcggtc tcggcgccgt cgtgtcgcag 60
caccgcctgt ggggtgatttg caagagcgga acgagcgtga agatcgagtg ccgctcgtc 120
gacttccagg ccacaaccat gttctggtac cgccagtttc ccaagcagag cctcatgctg 180
atggccacaa gcaatgaagg cagcaaggcc acttatgaac agggcgtgga gaaggacaag 240
tttctgatca accacgcctc cctgaccctg tccaccctca ctgtgaccag cgccccacct 300
gaggacagca gcttctacat ctgcagcgcc cgagctgga ggggcggcct ggagcagttc 360
ttcggccctg gcacccggct gacagtgtg gaagatctga agaacgtctt cccacctgag 420
gtggccgtgt tcgagccttc tgaggccgag atcagccaca cacagaaagc cacactcgtg 480
tgtctggcca ccggcttcta tccgatcac gtggaactgt cttggtgggt caacggcaaa 540
gaggtgcaca gcggcgtctg taccgatcct cagcctctga aagagcagcc cgctctgaac 600
gacagcagat actgcctgag cagcagactg agagtgtccg ccaccttctg gcagaacccc 660
agaaaccact tcagatgcca ggtgcagttc tacggcctga gcgagaacga tgagtggacc 720
caggatagag ccaagcctgt gacacagatc gtgtctgccg aagcctgggg cagagccgat 780
tgtggcttta ccagcgagag ctaccagcag ggcgtgctgt ctgccacaat cctgtacgag 840
atcctgctgg gcaaagccac tctgtacgcc gtgctggtgt ctgccctggt gctgatggcc 900
atggtcaagc ggaaggatag cagaggc 927

```

<210> 414

<211> 933

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 58 Native full sequence with human constant
(nt)

<400> 414

```
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcaactctgaa gatccgggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgccagca cccccgaag ctcctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagaag atctgaagaa cgtcttccca 420
cctgaggtgg ccgtgttcga gccttctgag gccgagatca gccacacaca gaaagccaca 480
ctcgtgtgtc tggccaccgg cttctatccc gatcacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcacagcgg cgtctgtacc gatcctcagc ctctgaaaga gcagcccgt 600
ctgaacgaca gcagatactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aaccacagaa accacttcag atgccaggtg cagtctctac gcctgagcga gaacgatgag 720
tggaccagg atagagccaa gcctgtgaca cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgtg gctttaccag cgagagctac cagcagggcg tgctgtctgc cacaatcctg 840
tacgagatcc tgctgggcaa agccactctg tacgccgtgc tgggtgtctgc cctgggtgctg 900
atggccatgg tcaagcggaa ggatagcaga ggc 933
```

<210> 415

<211> 933

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 59 Native full sequence with human constant
(nt)

<400> 415

```
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcaactctgaa gatccgggtcc 300
acaaaagctgg aggactcagc catgtacttc tgtgcctatt cgggcagggc ctcctacgag 360
cagtacttcg ggccggggcac caggctcacg gtcacagaag atctgaagaa cgtcttccca 420
cctgaggtgg ccgtgttcga gccttctgag gccgagatca gccacacaca gaaagccaca 480
ctcgtgtgtc tggccaccgg cttctatccc gatcacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcacagcgg cgtctgtacc gatcctcagc ctctgaaaga gcagcccgt 600
ctgaacgaca gcagatactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aaccacagaa accacttcag atgccaggtg cagtctctac gcctgagcga gaacgatgag 720
tggaccagg atagagccaa gcctgtgaca cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgtg gctttaccag cgagagctac cagcagggcg tgctgtctgc cacaatcctg 840
tacgagatcc tgctgggcaa agccactctg tacgccgtgc tgggtgtctgc cctgggtgctg 900
atggccatgg tcaagcggaa ggatagcaga ggc 933
```

<210> 416

<211> 933

<212> DNA
<213> Artificial Sequence

<220>

<223> TCR 60 Native full sequence with human constant
(nt)

<400> 416

```
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccatca gtcggacagt ctctacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagaag atctgaagaa cgtcttccca 420
cctgagggtg ccgtgttcga gccttctgag gccgagatca gccacacaca gaaagccaca 480
ctcgtgtgtc tggccaccgg cttctatccc gatcacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcacagcgg cgtctgtacc gatcctcagc ctctgaaaga gcagcccgt 600
ctgaacgaca gcagatactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aaccacagaa accacttcag atgccagggt cagttctacg gcctgagcga gaacgatgag 720
tggaccacag atagagccaa gcctgtgaca cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgtg gctttaccag cgagagctac cagcagggcg tgctgtctgc cacaatcctg 840
tacgagatcc tgctgggcaa agccactctg tacgccgtgc tgggtgtctgc cctggtgtctg 900
atggccatgg tcaagcggaa ggatagcaga ggc 933
```

<210> 417

<211> 933

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 61 Native full sequence with human constant
(nt)

<400> 417

```
atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa 60
cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg 120
cgctgtgtcc ccattctctaa tcacttatac ttctattggg acagacaaat cttggggcag 180
aaagtcgagt ttctggtttc cttttataat aatgaaatct cagagaagtc tgaaatattc 240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc 300
acaaagctgg aggactcagc catgtacttc tgtgccagca ccaaacgttt tagctacgag 360
cagtacttcg ggccgggcac caggctcacg gtcacagaag atctgaagaa cgtcttccca 420
cctgagggtg ccgtgttcga gccttctgag gccgagatca gccacacaca gaaagccaca 480
ctcgtgtgtc tggccaccgg cttctatccc gatcacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcacagcgg cgtctgtacc gatcctcagc ctctgaaaga gcagcccgt 600
ctgaacgaca gcagatactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aaccacagaa accacttcag atgccagggt cagttctacg gcctgagcga gaacgatgag 720
tggaccacag atagagccaa gcctgtgaca cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgtg gctttaccag cgagagctac cagcagggcg tgctgtctgc cacaatcctg 840
tacgagatcc tgctgggcaa agccactctg tacgccgtgc tgggtgtctgc cctggtgtctg 900
```

atggccatgg tcaagcggaa ggatagcaga ggc

933

<210> 418

<211> 945

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 62 Native full sequence with human constant
(nt)

<400> 418

```
atggggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa 60
gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt 120
tggtgcaatc ctatatctgg ccatgtctacc ctttactggg accagcagat cctgggacag 180
ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct 240
aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct 300
gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttagatac ccggggctcc 360
tcctacaatg agcagttctt cgggccaggg acacggctca ccgtgctaga agatctgaag 420
aacgtcttcc cacctgaggt ggccgtgttc gagccttctg aggccgagat cagccacaca 480
cagaaagcca cactcgtgtg tctggccacc ggcttctatc ccgatcacgt ggaactgtct 540
tgggtgggtca acggcaaaga ggtgcacagc ggctgtctgta ccgatcctca gcctctgaaa 600
gagcagcccc ctctgaacga cagcagatac tgcctgagca gcagactgag agtgtccgcc 660
accttctggc agaaccctcag aaaccacttc agatgccagg tgcagttcta cggcctgagc 720
gagaacgatg agtggaccca ggatagagcc aagcctgtga cacagatcgt gtctgccgaa 780
gcctgggggca gagccgattg tggctttacc agcgagagct accagcaggg cgctgtgtct 840
gccacaatcc tgtacgagat cctgtctgggc aaagccactc tgtacgccgt gctgggtgtct 900
gccctggtgc tgatggccat ggtcaagcgg aaggatagca gaggc 945
```

<210> 419

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 63 Native full sequence with human constant
(nt)

<400> 419

```
atggggcacca ggctcctctg ctgggtgggtc ctgggtttcc tagggacaga tcacacaggt 60
gctggagtct cccagtcccc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc 120
aggtgtgatc caatttcggg tcatgtatcc cttttttggg accaacaggc cctggggcag 180
gggacagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc 240
agtgtatcgt tctttgcaga aaggcctgag ggatccgtct ccactctgaa gatccagcgc 300
acacagcagg aggactccgc cgtgtatctc tgtgccagca gaccaagaca ggggtataat 360
gacaatgagc agttcttcgg gccagggaca cggctcaccg tgctagaaga tctgaagaac 420
gtcttccac ctgagggtggc cgtgttcgag ccttctgagg ccgagatcag ccacacacag 480
aaagccacac tcgtgtgtct ggccaccggc ttctatcccg atcacgtgga actgtcttgg 540
tgggtcaacg gcaaagaggt gcacagcggc gtctgtaccg atcctcagcc tctgaaagag 600
cagcccgtc tgaacgacag cagatactgc ctgagcagca gactgagagt gtccgccacc 660
```

ttctggcaga	accccagaaa	ccacttcaga	tgccagggtgc	agttctacgg	cctgagcgag	720
aacgatgagt	ggacccagga	tagagccaag	cctgtgacac	agatcgtgtc	tgccgaagcc	780
tggggcagag	ccgattgtgg	ctttaccagc	gagagctacc	agcagggcgt	gctgtctgcc	840
acaatcctgt	acgagatcct	gctgggcaaa	gccactctgt	acgccgtgct	ggtgtctgcc	900
ctggtgctga	tggccatggt	caagcggaag	gatagcagag	gc		942

<210> 420

<211> 870

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Codon-Optimized with Codon Optimized
Human Constant (nt)

<400> 420

atggctcaag	agctgggcat	gcagtgtcag	gccagaggaa	tcctgcagca	gatgtgggga	60
gtgttcctgc	tgtacgtgtc	catgaagatg	ggcggcacca	ccggccagaa	catcgatcag	120
cctacagaga	tgaccgccac	cgagggcgcc	atcgtgcaga	tcaattgcac	ctaccagacc	180
agcggcttca	acggcctgtt	ctggtatcag	cagcatgccg	gcgaggcccc	taccttcctg	240
agctacaatg	tgctggacgg	cctggaagag	aagggcagat	tcagcagctt	cctgtccaga	300
agcaagggct	acagctacct	gctgctgaaa	gaactgcaga	tgaaggacag	cgcttcctac	360
ctgtgcgccg	ttagagattg	gggatacggc	ggagccacca	acaagctgat	ctttggcaca	420
ggcacactgc	tggccgtgca	gcctaataatc	cagaatccgg	accccgcggt	atatcaactg	480
cgcgactcaa	aatcatccga	taagagtgtc	tgtttgttta	ctgacttcga	cagtcaaaact	540
aatgtctctc	agagcaaaga	ttccgatgtc	tacatcactg	acaagtgcgt	tctggatatg	600
cggagcatgg	attttaagtc	caactccgcc	gtagcctggg	ccaacaagtc	agactttgcc	660
tgtgcaaattg	ctttcaacaa	ctcaattatc	cctgaggaca	ctttctttcc	ttcaccggag	720
tcctcatgcg	atgttaaact	ggtcgaaaaa	tcttttgaga	cggatacgaa	cctcaacttc	780
caaaaatttga	gcgttattgg	ctttaggatt	ctgcttctca	aggttgcggg	gttcaatctc	840
ctgatgacgt	tgcggctttg	gagcagctaa				870

<210> 421

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Alpha Codon-Optimized with Codon Optimized
Mouse Constant (nt)

<400> 421

atggctcaag	agctgggcat	gcagtgtcag	gccagaggaa	tcctgcagca	gatgtgggga	60
gtgttcctgc	tgtacgtgtc	catgaagatg	ggcggcacca	ccggccagaa	catcgatcag	120
cctacagaga	tgaccgccac	cgagggcgcc	atcgtgcaga	tcaattgcac	ctaccagacc	180
agcggcttca	acggcctgtt	ctggtatcag	cagcatgccg	gcgaggcccc	taccttcctg	240
agctacaatg	tgctggacgg	cctggaagag	aagggcagat	tcagcagctt	cctgtccaga	300
agcaagggct	acagctacct	gctgctgaaa	gaactgcaga	tgaaggacag	cgcttcctac	360
ctgtgcgccg	ttagagattg	gggatacggc	ggagccacca	acaagctgat	ctttggcaca	420
ggcacactgc	tggccgtgca	gcctaataatc	cagaatccgg	agcctgccgt	gtaccagctg	480

aaggacccac	ggagccagga	tagcaccctg	tgctgttca	ccgactttga	ttctcagatc	540
aacgtgcca	agaccatgga	gagcggcacc	ttcatcacag	acaagtgcgt	gctggatatg	600
aaggccatgg	acagcaagtc	caacggcgcc	atcgcttgg	ccaatcagac	atctttcacc	660
tgccaggata	tctttaagga	gacaaatgcc	acctatcctt	cctctgacgt	gcatgtgat	720
gccaccctga	cagagaagag	cttcgagacc	gacatgaacc	tgaattttca	gaatctgctc	780
gtgattgtcc	tgagaatcct	gctgctgaag	gtggccggct	ttaacctgct	gatgaccctg	840
aggctgtgga	gctcctga					858

<210> 422

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR 56 Codon-optimized full sequence with mouse
constant (nt)

<400> 422

atgggaccca	tggccaatag	cgccatggat	accagagtgc	tgtgctgcgc	cgatgatctgt	60
ctgcttgagg	ccggactgtc	taatgccggc	gtgatgcaga	accccagaca	cctcgttcgg	120
agaagaggcc	aagaggccag	actgagatgc	agccctatga	agggccacag	ccacgtgtac	180
tggtacagac	agctgcctga	agagggcctg	aagttcatgg	tgtacctgca	gaaagagaac	240
atcatcgacg	agagcggcat	gccc aaagag	cggttctctg	ccgagtttcc	caaagagggc	300
cccagcatcc	tgagaatcca	gcaggttgtg	cggggagata	gcgccgccta	cttttgtgcc	360
agctctcccc	atgagagccg	ggactctaata	cagcctcagc	actttggcga	cggcaccagg	420
ctgtctattc	tgcaggacct	gcgcaatgtg	accccccta	agggtgtccct	gtttgagccc	480
tctaaggccg	agatcgccaa	caagcagaag	gccaccctgg	tgtgcctggc	cagaggcttc	540
ttccctgatc	acgtggagct	gagctgggtg	gtgaatggca	aggagggtgca	ctccggcgtg	600
tgcaccgacc	cacaggccta	caaggagtcc	aactactctt	attgtctgtc	ctctaggctg	660
cgcgtgagcg	ccacattctg	gcacaaccct	cggaatcact	tcagatgcca	ggtgcagttt	720
cacggcctga	gcgaggagga	taagtggcca	gagggtctcc	caaagcccgt	gaccagaaat	780
atctctgccg	aggcatgggg	cagggccgac	tgtggaatca	cctccgcctc	ttatcagcag	840
ggcgtgctgt	ccgccacaat	cctgtacgag	atcctgctgg	gcaaggccac	cctgtatgcc	900
gtgctgggtg	ccacactggg	ggatcatggc	atgggtgaagc	gcaagaacag	ctaaggctcc	960
ggagcaacca	atttcagcct	gctgaagcag	gccggcgatg	tggaggagaa	tcctggccca	1020
atggctcaag	agctgggcat	gcagtgtcag	gccagaggaa	tcctgcagca	gatgtgggga	1080
gtgttcctgc	tgtacgtgtc	catgaagatg	ggcggcacca	ccggccagaa	catcgatcag	1140
cctacagaga	tgaccgccac	cgagggcgcc	atcgtgcaga	tcaattgcac	ctaccagacc	1200
agcggcttca	acggcctgtt	ctggtatcag	cagcatgccg	gcgaggcccc	taccttcctg	1260
agctacaatg	tgctggacgg	cctggaagag	aagggcagat	tcagcagctt	cctgtccaga	1320
agcaagggct	acagctacct	gctgctgaaa	gaactgcaga	tgaaggacag	cgcttcctac	1380
ctgtgcgccg	ttagagattg	gggatacggc	ggagccacca	acaagctgat	ctttggcaca	1440
ggcacactgc	tggccgtgca	gcctaataatc	cagaatccgg	agcctgccgt	gtaccagctg	1500
aaggacccac	ggagccagga	tagcaccctg	tgctgttca	ccgactttga	ttctcagatc	1560
aacgtgcca	agaccatgga	gagcggcacc	ttcatcacag	acaagtgcgt	gctggatatg	1620
aaggccatgg	acagcaagtc	caacggcgcc	atcgcttgg	ccaatcagac	atctttcacc	1680
tgccaggata	tctttaagga	gacaaatgcc	acctatcctt	cctctgacgt	gcatgtgat	1740
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<210> 423
<211> 936
<212> DNA
<213> Artificial Sequence

<220>

<223> TCR 64 Native full sequence with human constant
(nt)

<400> 423

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<210> 424
<211> 939
<212> DNA
<213> Artificial Sequence

<220>

<223> TCR 65 Native full sequence with human constant
(nt)

<400> 424

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