

SEQUENCE LISTING

<110> Medigene Immunotherapies GmbH
<120> PRAME TCR RECEPTORS AND USES THEREOF
<130> MED16815PCT
<150> EP19209757.4
<151> 2019-11-18

<160> 33

<170> PatentIn version 3.5

<210> 1
<211> 9
<212> PRT
<213> artificial

<220>
<223> PRAME epitope, tumor associated antigene

<400> 1

Ser Leu Leu Gln His Leu Ile Gly Leu
1 5

<210> 2
<211> 5
<212> PRT
<213> artificial

<220>
<223> CDR1 alpha, human modified

<400> 2

Ser Ile Phe Asn Thr
1 5

<210> 3
<211> 5
<212> PRT
<213> artificial

<220>
<223> CDR1 beta, human modified

<400> 3

Ser Gly Asp Leu Ser
1 5

<210> 4

<211> 7

<212> PRT

<213> artificial

<220>

<223> CDR2 alpha, human modified

<400> 4

Leu Tyr Lys Ala Gly Glu Leu
1 5

<210> 5

<211> 6

<212> PRT

<213> artificial

<220>

<223> CDR2 beta, human modified

<400> 5

Tyr Tyr Asn Gly Glu Glu
1 5

<210> 6

<211> 16

<212> PRT

<213> artificial

<220>

<223> CDR3 alpha, human modified

<400> 6

Cys Ala Gly Leu Ala Asp Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe
1 5 10 15

<210> 7

<211> 15
<212> PRT
<213> artificial

<220>
<223> CDR3 beta, human modified

<400> 7

Cys	Ala	Ser	Ser	Val	Trp	Ala	Ser	Gly	Gly	Tyr	Glu	Gln	Tyr	Phe
1				5				10						15

<210> 8
<211> 108
<212> PRT
<213> artificial

<220>
<223> TCR alpha variable region, human modified

<400> 8

Met	Leu	Leu	Glu	His	Leu	Leu	Ile	Ile	Leu	Trp	Met	Gln	Leu	Thr	Trp
1				5					10					15	

Val	Ser	Gly	Gln	Gln	Leu	Asn	Gln	Ser	Pro	Gln	Ser	Met	Phe	Ile	Gln
			20					25					30		

Glu	Gly	Glu	Asp	Val	Ser	Met	Asn	Cys	Thr	Ser	Ser	Ser	Ile	Phe	Asn
		35					40					45			

Thr	Trp	Leu	Trp	Tyr	Lys	Gln	Asp	Pro	Gly	Glu	Gly	Pro	Val	Leu	Leu
	50					55					60				

Ile	Ala	Leu	Tyr	Lys	Ala	Gly	Glu	Leu	Thr	Ser	Asn	Gly	Arg	Leu	Thr
65					70					75				80	

Ala	Gln	Phe	Gly	Ile	Thr	Arg	Lys	Asp	Ser	Phe	Leu	Asn	Ile	Ser	Ala
				85					90					95	

Ser	Ile	Pro	Ser	Asp	Val	Gly	Ile	Tyr	Phe	Cys	Ala
					100			105			

<210> 9
<211> 114
<212> PRT
<213> artificial

<220>
<223> TCR beta variable region, human modified

<400> 9

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

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

Ala Thr Gly Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Val

<210> 10
<211> 273
<212> PRT
<213> artificial

<220>
<223> TCR alpha chain (mmC), human modified

<400> 10

Met Leu Leu Glu His Leu Leu Ile Ile Leu Trp Met Gln Leu Thr Trp
1 5 10 15

Val Ser Gly Gln Gln Leu Asn Gln Ser Pro Gln Ser Met Phe Ile Gln
20 25 30

Glu Gly Glu Asp Val Ser Met Asn Cys Thr Ser Ser Ser Ile Phe Asn
35 40 45

Thr Trp Leu Trp Tyr Lys Gln Asp Pro Gly Glu Gly Pro Val Leu Leu
50 55 60

Ile Ala Leu Tyr Lys Ala Gly Glu Leu Thr Ser Asn Gly Arg Leu Thr
65 70 75 80

Ala Gln Phe Gly Ile Thr Arg Lys Asp Ser Phe Leu Asn Ile Ser Ala
85 90 95

Ser Ile Pro Ser Asp Val Gly Ile Tyr Phe Cys Ala Gly Leu Ala Asp
100 105 110

Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe Gly Lys Gly Thr Lys Leu
115 120 125

Ser Val Lys Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
180 185 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
195 200 205

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 11
<211> 312
<212> PRT
<213> artificial

<220>
<223> TCR beta chain mmC, human modified

<400> 11

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

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

Ala Thr Gly Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Val Trp Ala Ser Gly Gly Tyr Glu Gln Tyr Phe Gly Pro Gly Thr
115 120 125

Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
130 135 140

Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala 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 Ser 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 Ile Thr Ser Arg Ser Tyr His

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> 12
<211> 27
<212> DNA
<213> artificial

<220>
<223> PRAME epitope, tumor associated antigen

<400> 12
agcctgctgc agcatctgat tggcctg 27

<210> 13
<211> 15
<212> DNA
<213> artificial

<220>
<223> CDR1 alpha, human modified

<400> 13
agcatattta acacc 15

<210> 14
<211> 15
<212> DNA
<213> artificial

<220>
<223> CDR1 beta, human modified

<400> 14
tctggagacc tctct 15

<210> 15
 <211> 21
 <212> DNA
 <213> artificial

 <220>
 <223> CDR2 alpha, human modified

 <400> 15
 ttatataagg ctggtgaatt g 21

<210> 16
 <211> 18
 <212> DNA
 <213> artificial

 <220>
 <223> CDR2 beta, human modified

 <400> 16
 tattataatg gagaagag 18

<210> 17
 <211> 48
 <212> DNA
 <213> artificial

 <220>
 <223> CDR3 alpha, human modified

 <400> 17
 tgtgctgggc ttgctgatta tggaggaagc caaggaaatc tcatcttt 48

<210> 18
 <211> 45
 <212> DNA
 <213> artificial

 <220>
 <223> CDR3 beta, human modified

 <400> 18
 tgtgccagca gcgtatgggc ctccggcggc tacgagcagt acttc 45

<210> 19

<211> 324
<212> DNA
<213> artificial

<220>
<223> TCR alpha variable region, human modified

<400> 19
atgctgctgg aacatctgct gatcatcctg tggatgcagc tgacctgggt ttccggccag 60
cagctgaatc agagccctca gagcatgttc atccaagaag gcgaggacgt ttccatgaat 120
tgcaccagca gcagcatctt caacacctgg ctgtggtaca agcaggaccc tggcgaagga 180
ccagtgtgc tgatcgctt gtacaaagcc ggcgagctga ccagcaacgg cagactgaca 240
gcccagttcg gcattacccg gaaggacagc ttcctgaaca tctccgccag cattccctcc 300
gacgtgggca tctatTTTTg tgcc 324

<210> 20
<211> 342
<212> DNA
<213> artificial

<220>
<223> TCR beta variable region, human modified

<400> 20
atgggcttca gactgctgtg ctgctggcc ttttgtctgc ttggagccgg acctgtggat 60
agcggcgcta cccagacacc taagcacctg atcacagcca caggccagcg cgtgaccctg 120
agatgttctc ctagaagcgg cgacctgagc gtgtactgggt atcagcagtc tctggaccag 180
ggcctgcagt tcctgatcca gtactacaac ggcgaggaaa gagccaaggg caacatcctg 240
gaacggttca gcgcccagca gttcccagat ctgcacagcg agctgaacct gagcagcctg 300
gaactgggag atagcgccct gtacttctgt gcctctagcg tg 342

<210> 21
<211> 819
<212> DNA
<213> artificial

<220>
<223> TCR alpha chain (mmC), human modified

<400> 21
atgctgctgg aacatctgct gatcatcctg tggatgcagc tgacctgggt ttccggccag 60
cagctgaatc agagccctca gagcatgttc atccaagaag gcgaggacgt ttccatgaat 120
tgcaccagca gcagcatctt caacacctgg ctgtggtaca agcaggaccc tggcgaagga 180
ccagtgtgc tgatgcctt gtacaaagcc ggcgagctga ccagcaacgg cagactgaca 240
gcccagttcg gcattaccg gaaggacagc ttcctgaaca tctccgccag cattccctcc 300
gacgtgggca tctatTTTTg tgccggcctg gccgattacg gcggctctca gggaaatctg 360
atcttcggca agggcaccaa gctgagcgtg aagcccaaca ttcagaaccc cgatcctgcc 420
gtgtaccagc tgagagacag caagagcagc gacaagagcg tgtgcctgtt caccgacttc 480
gacagccaga ccaacgtgtc ccagagcaag gacagcgacg tgtacatcac cgacaagacc 540
gtgctggaca tgcggagcat ggacttcaag agcaacagcg ccgtggcctg gtccaacaag 600
agcgatttcg cctgcgcaa cgccttcaac aacagcatta tccccgagga cacattcttc 660
cccagctccg atgtgccctg cgacgtgaag ctggtggaaa agagcttcga gacagacacc 720
aacctgaact tccagaacct gtccgtgatc ggcttcagaa tcctgctgct gaaggtggcc 780
ggcttcaacc tgctgatgac actgagactg tgggtccagc 819

<210> 22
<211> 936
<212> DNA
<213> artificial

<220>
<223> TCR beta chain (mmC), human modified

<400> 22
atgggcttca gactgctgtg ctgcgtggcc ttttgtctgc ttggagccgg acctgtggat 60
agcggcgтта cccagacacc taagcacctg atcacagcca caggccagcg cgtgacctg 120
agatgttctc ctagaagcgg cgacctgagc gtgtactggt atcagcagtc tctggaccag 180
ggcctgcagt tcctgatcca gtactacaac ggcgaggaaa gagccaaggg caacatcctg 240
gaacggttca gcgcccagca gttcccagat ctgcacagcg agctgaacct gagcagcctg 300

gaactgggag atagcgccct gtactttctgt gcctctagcg tgtgggcctc tggcggctac	360
gagcagtatt ttggccctgg caccagactg accgtgaccg aggatctgaa gaacgtgttc	420
ccacctgagg tggccgtgtt cgagccttct aaggccgaga ttgccacac acagaaagcc	480
acactcgtgt gtctggccac cggcttctat cccgatcacg tggaactgtc ttggtgggtc	540
aacggcaaag aggtgcacag cggcgtcagc acagatcccc agcctctgaa agaacagccc	600
gctctgaacg acagccggta ctgtctgagc agcagactga gagtgtccgc caccttctgg	660
cagaacccca gaaaccactt cagatgccag gtgcagttct acggcctgag cgagaacgat	720
gagtggaccc aggacagagc taagcccgtg acacagatcg tgtctgccga agcttggggc	780
agagccgatt gtggcatcac cagcagatct taccaccagg gcgtgctgag cgccaccatc	840
ctgtatgaga tcctgtctggg caaagccact ctgtacgccg tgctgggtgtc tgccctggtg	900
ctgatggcca tgggtcaagcg gaaggatagc agaggc	936

<210> 23
 <211> 13
 <212> PRT
 <213> artificial

<220>
 <223> 3825 CDR3 alpha, derived from mus musculus

<400> 23

Cys	Ala	Val	Glu	Pro	Gly	Gly	Ser	Tyr	Ile	Pro	Thr	Phe
1				5					10			

<210> 24
 <211> 13
 <212> PRT
 <213> artificial

<220>
 <223> 3825 CDR3 beta, derived from mus musculus

<400> 24

Cys	Ala	Ser	Ser	Pro	Gly	Leu	Ser	Tyr	Glu	Gln	Tyr	Phe
1				5					10			

<210> 25
<211> 8
<212> PRT
<213> artificial

<220>
<223> Irrelevant paptide, human

<400> 25

Gly Leu Ser Asn Thr His Val Leu
1 5

<210> 26
<211> 140
<212> PRT
<213> artificial

<220>
<223> TCR alpha constant, derived from human

<400> 26

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

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
20 25 30

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
35 40 45

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
50 55 60

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
65 70 75 80

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
85 90 95

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln

100

105

110

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
 115 120 125

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135 140

<210> 27
 <211> 177
 <212> PRT
 <213> artificial

<220>
 <223> TCR beta-01 constant, derived from human

<400> 27

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> 28
 <211> 179
 <212> PRT
 <213> artificial

<220>
 <223> TCR beta-02 constant, derived from human

<400> 28

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> 29

<211> 140

<212> PRT

<213> artificial

<220>

<223> TCR alpha constant, derived from mus musculus

<400> 29

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

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
 20 25 30

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
 35 40 45

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp

50

55

60

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 65 70 75 80

Ile Pro Glu Asp Thr Phe Phe Pro Ser Ser Asp Val Pro Cys Asp Val
 85 90 95

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
 100 105 110

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
 115 120 125

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135 140

<210> 30
 <211> 179
 <212> PRT
 <213> artificial

<220>
 <223> TCR beta constant, derived from mus musculus

<400> 30

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1 5 10 15

Ser Lys Ala Glu Ile Ala 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 Ile Thr Ser Arg Ser Tyr His 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> 31
 <211> 136
 <212> PRT
 <213> artificial

<220>
 <223> TCR alpha murC constant, murinized

<400> 31

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 Thr 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 Ser Val
 100 105 110

Met Gly 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> 32
 <211> 173
 <212> PRT
 <213> artificial

<220>
 <223> TCR beta murC constant, murinized

<400> 32

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Thr 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 His 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

Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
165 170

<210> 33

<211> 509

<212> PRT

<213> artificial

<220>

<223> PRAME full-length, derived from human

<400> 33

Met Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
1 5 10 15

Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
20 25 30

Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu

35

40

45

Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg
 50 55 60

His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys
 65 70 75 80

Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr
 85 90 95

Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val
 100 105 110

Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser
 115 120 125

His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr
 130 135 140

Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys
 145 150 155 160

Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu
 165 170 175

Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe
 180 185 190

Ser Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu
 195 200 205

Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys
 210 215 220

Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val
 225 230 235 240

Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu
245 250 255

Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala
260 265 270

Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe
275 280 285

Thr Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp
290 295 300

Ser Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val
305 310 315 320

Met Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu
325 330 335

Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser
340 345 350

Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro
355 360 365

Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val
370 375 380

Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro
385 390 395 400

Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn
405 410 415

Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly
420 425 430

Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr

435

440

445

Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His
450 455 460

Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val
465 470 475 480

Trp Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr
485 490 495

Asp Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
500 505