

SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania
Bear, Adham
Vonderheide, Bob
Linette, Gerald
Carreno, Beatriz

<120> Compositions and Methods for Targeting Mutant RAS

<130> 046483-6175-00W0

<150> 62/796,733

<151> 2019-01-25

<160> 203

<170> PatentIn version 3.5

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> KLV_C

<400> 1

Lys Leu Val Val Val Gly Ala Cys Gly Val
1 5 10

<210> 2

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> KLV_D

<400> 2

Lys Leu Val Val Val Gly Ala Asp Gly Val
1 5 10

<210> 3

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> KLV_R

<400> 3

Lys Leu Val Val Val Gly Ala Arg Gly Val
1 5 10

<210> 4

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> KLV_V

<400> 4

Lys Leu Val Val Val Gly Ala Val Gly Val
1 5 10

<210> 5

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VV_C

<400> 5

Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 6

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> VVV_C

<400> 6

Val Val Val Gly Ala Cys Gly Val Gly Lys

1 5 10

<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VV_D

<400> 7

Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VVV_D

<400> 8

Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VV_R

<400> 9

Val Val Gly Ala Arg Gly Val Gly Lys
1 5

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

<220>

<223> VVV_R

<400> 10

Val Val Val Gly Ala Arg Gly Val Gly Lys
1 5 10

<210> 11

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VV_V

<400> 11

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 12

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> VVV_V

<400> 12

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 13

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> GA_C

<400> 13

Gly Ala Cys Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GA_D

<400> 14

Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GA_R

<400> 15

Gly Ala Arg Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GA_V

<400> 16

Gly Ala Val Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV39 CDR1

<400> 17

Ser Thr Thr Ser Asp Arg Leu
1 5

<210> 18

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV39 CDR2

<400> 18

Val Leu Leu Ser Asn Gly Ala Val Lys
1 5

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV39 CDR3

<400> 19

Cys Ala Val Asp Lys Asp Gly Gly Tyr Gln Lys Val Thr Phe
1 5 10

<210> 20

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV39 VARIABLE DOMAIN

<400> 20

Glu Leu Lys Val Glu Gln Asn Pro Leu Phe Leu Ser Met Gln Glu Gly
1 5 10 15

Lys Asn Tyr Thr Ile Tyr Cys Asn Tyr Ser Thr Thr Ser Asp Arg Leu

20

25

30

Tyr Trp Tyr Arg Gln Asp Pro Gly Lys Ser Leu Glu Ser Leu Phe Val
 35 40 45

Leu Leu Ser Asn Gly Ala Val Lys Gln Glu Gly Arg Leu Met Ala Ser
 50 55 60

Leu Asp Thr Lys Ala Arg Leu Ser Thr Leu His Ile Thr Ala Ala Val
 65 70 75 80

His Asp Leu Ser Ala Thr Tyr Phe Cys Ala Val Asp Lys Asp Gly Gly
 85 90 95

Tyr Gln Lys Val Thr Phe Gly Thr Gly Thr Lys Leu Gln Val Ile Pro
 100 105 110

<210> 21

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR831 ALPHA CONSTANT DOMAIN

<400> 21

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> 22
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR831 ALPHA CHAIN

<400> 22

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

85

90

95

Ala Val His Asp Leu Ser Ala Thr Tyr Phe Cys Ala Val Asp Lys Asp
100 105 110

Gly Gly Tyr Gln Lys Val Thr Phe Gly Thr Gly Thr Lys Leu Gln Val
115 120 125

Ile Pro 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 Thr 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> 23

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV20-1 CDR1

<400> 23

Leu Asp Phe Gln Ala Thr Thr Met
1 5

<210> 24

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV20-1 CDR2

<400> 24

Thr Ser Asn Glu Gly Ser Lys Ala Thr
1 5

<210> 25

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV20-1CDR3

<400> 25

Cys Ser Ala Ser Pro Arg Ala Gly Gln Leu Ser Ser Tyr Asn Ser Pro
1 5 10 15

Leu His Phe

<210> 26

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV20-1 VARIABLE

<400> 26

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

Ser Pro Arg Ala Gly Gln Leu Ser Ser Tyr Asn Ser Pro Leu His Phe
100 105 110

Gly Asn Gly Thr Arg Leu Thr Val
115 120

<210> 27

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR831 BETA CONSTANT DOMAIN

<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> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR831 BETA CHAIN

<400> 28

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ile Ser Leu Leu Leu
1 5 10 15

Pro Gly Ser Leu Ala Gly Ser Gly Leu Gly Ala Val Val Ser Gln His
20 25 30

Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser Val Lys Ile Glu Cys
35 40 45

Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe Trp Tyr Arg Gln Phe
50 55 60

Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser Asn Glu Gly Ser Lys
65 70 75 80

Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys Phe Leu Ile Asn His
85 90 95

Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr Ser Ala His Pro Glu
100 105 110

Asp Ser Ser Phe Tyr Ile Cys Ser Ala Ser Pro Arg Ala Gly Gln Leu
115 120 125

Ser Ser Tyr Asn Ser Pro Leu His Phe Gly Asn Gly Thr Arg Leu Thr
130 135 140

Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe
145 150 155 160

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
165 170 175

Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
180 185 190

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro
195 200 205

Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
210 215 220

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
225 230 235 240

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
245 250 255

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
260 265 270

Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val
275 280 285

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
290 295 300

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg
305 310 315 320

Lys Asp Phe

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 29

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

Glu Asn Pro Gly Pro
20

<210> 30

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR831 fusion

<400> 30

Met Lys Lys Leu Leu Ala Met Ile Leu Trp Leu Gln Leu Asp Arg Leu
1 5 10 15

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

Glu Gly Lys Asn Tyr Thr Ile Tyr Cys Asn Tyr Ser Thr Thr Ser Asp
35 40 45

Arg Leu Tyr Trp Tyr Arg Gln Asp Pro Gly Lys Ser Leu Glu Ser Leu
50 55 60

Phe Val Leu Leu Ser Asn Gly Ala Val Lys Gln Glu Gly Arg Leu Met
65 70 75 80

Ala Ser Leu Asp Thr Lys Ala Arg Leu Ser Thr Leu His Ile Thr Ala
85 90 95

Ala Val His Asp Leu Ser Ala Thr Tyr Phe Cys Ala Val Asp Lys Asp
100 105 110

Gly Gly Tyr Gln Lys Val Thr Phe Gly Thr Gly Thr Lys Leu Gln Val
115 120 125

Ile Pro 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 Thr 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 Gly
260 265 270

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
275 280 285

Asn Pro Gly Pro Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ile
290 295 300

Ser Leu Leu Leu Pro Gly Ser Leu Ala Gly Ser Gly Leu Gly Ala Val
305 310 315 320

Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser Val
325 330 335

Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe Trp

340

345

350

Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser Asn
 355 360 365

Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys Phe
 370 375 380

Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr Ser
 385 390 395 400

Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Ser Pro Arg
 405 410 415

Ala Gly Gln Leu Ser Ser Tyr Asn Ser Pro Leu His Phe Gly Asn Gly
 420 425 430

Thr Arg Leu Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu
 435 440 445

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
 450 455 460

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
 465 470 475 480

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 485 490 495

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 500 505 510

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 515 520 525

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 530 535 540

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
545 550 555 560

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr
565 570 575

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
580 585 590

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
595 600 605

Met Val Lys Arg Lys Asp Phe
610 615

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV12-1 CDR1

<400> 31

Ser Asn Ser Ala Ser Gln Ser Phe
1 5

<210> 32
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV12-1 CDR2

<400> 32

Ser Val Tyr Ser Ser Gly Asn Glu
1 5

<210> 33

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV12-1 CDR3

<400> 33

Cys Ala Val Asn Pro Pro Asp Thr Gly Phe Gln Lys Leu Val Phe
1 5 10 15

<210> 34
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV12-1 VARIABLE DOMAIN

<400> 34

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 Ala Val Asn Pro Pro Asp Thr Gly
85 90 95

Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu Leu Val Ser Pro
100 105 110

<210> 35
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR833 ALPHA CONSTANT DOMAIN

<400> 35

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> 36
<211> 274
<212> PRT

<213> Artificial Sequence

<220>

<223> TCR833 ALPHA CHAIN

<400> 36

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

Trp Val Trp Ser Gln Arg Lys Glu Val Glu Gln Asp Pro Gly Pro Phe
20 25 30

Asn Val Pro Glu Gly Ala Thr Val Ala Phe Asn Cys Thr Tyr Ser Asn
35 40 45

Ser Ala Ser Gln Ser Phe Phe Trp Tyr Arg Gln Asp Cys Arg Lys Glu
50 55 60

Pro Lys Leu Leu Met Ser Val Tyr Ser Ser Gly Asn Glu Asp Gly Arg
65 70 75 80

Phe Thr Ala Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile
85 90 95

Arg Asp Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Asn
100 105 110

Pro Pro Asp Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg
115 120 125

Leu Leu Val Ser 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 Thr 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> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV28 CDR1

<400> 37

Asp Met Asp His Glu Asn Met
1 5

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV28 CDR2

<400> 38

Phe Ser Tyr Asp Val Lys Met Glu
1 5

<210> 39

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV28 CDR3

<400> 39

Cys Ala Ser Ser Leu Ser Phe Arg Gln Gly Leu Arg Glu Gln Tyr Phe
1 5 10 15

<210> 40

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV28 VARIABLE DOMAIN

<400> 40

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 Ser Phe Arg Gln Gly Leu Arg Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr
130

<210> 41

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR833 BETA CONSTANT DOMAIN

<400> 41

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> 42
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR833 BETA CHAIN

<400> 42

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 Ser Phe Arg Gln Gly Leu Arg Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn 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 Tyr Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser 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 Glu 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 Ser Arg Gly
305 310

<210> 43
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 43

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

Glu Asn Pro Gly Pro
20

<210> 44
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR833 FUSION

<400> 44

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

Trp Val Trp Ser Gln Arg Lys Glu Val Glu Gln Asp Pro Gly Pro Phe
20 25 30

Asn Val Pro Glu Gly Ala Thr Val Ala Phe Asn Cys Thr Tyr Ser Asn
35 40 45

Ser Ala Ser Gln Ser Phe Phe Trp Tyr Arg Gln Asp Cys Arg Lys Glu
50 55 60

Pro Lys Leu Leu Met Ser Val Tyr Ser Ser Gly Asn Glu Asp Gly Arg
65 70 75 80

Phe Thr Ala Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile
85 90 95

Arg Asp Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Asn
100 105 110

Pro Pro Asp Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg
115 120 125

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

Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala
435 440 445

Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly
450 455 460

Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu
465 470 475 480

Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro
485 490 495

Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
500 505 510

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
515 520 525

Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys
530 535 540

Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
545 550 555 560

Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile
565 570 575

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
580 585 590

Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600 605

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV17 CDR1

<400> 45

Lys Thr Ser Ile Asn Asn Leu

1 5

<210> 46

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV17 CDR2

<400> 46

Leu Ile Arg Ser Asn Glu Arg Glu Lys

1 5

<210> 47

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV17 CDR3

<400> 47

Cys Ala Thr Asp Pro Gly Gly Phe Lys Thr Ile Phe

1 5 10

<210> 48

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR897 ALPHA CONSTANT DOMAIN

<400> 48

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> 49
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR897 ALPHA CHAIN

<400> 49

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

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Pro Gly Gly Phe Lys Thr Ile Phe Gly Ala Gly Thr Arg Leu Phe Val
115 120 125

Lys 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 Thr 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

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

<220>
<223> TRBV11-2 CDR1

Ile Ser Gly His Ala Thr Leu
1 5

<220>
<223> TRBV11-2 CDR2

Gln Phe Gln Asn Asn Gly Val Val
1 5

<220>
<223> TRBV11-2 CDR3

Cys Ala Ser Ser Leu Tyr Gly Gly Ser Ile Ser Tyr Glu Gln Tyr Phe

1 5 10 15

<210> 53
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR897 BETA CONSTANT DOMAIN

<400> 53

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> 54
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR897 BETA CHAIN

<400> 54

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 Tyr Gly Gly Ser Ile Ser Tyr Glu Gln Tyr Phe Gly Pro

115

120

125

Gly Thr Arg Leu Thr Val Thr 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 Ser
 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> 55
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> LINKER

<400> 55

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

Glu Asn Pro Gly Pro
20

<210> 56
<211> 606
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR897 FUSION

<400> 56

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

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile

85

90

95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
 100 105 110

Pro Gly Gly Phe Lys Thr Ile Phe Gly Ala Gly Thr Arg Leu Phe Val
 115 120 125

Lys 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 Thr 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 Gly
 260 265 270

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
 275 280 285

Asn Pro Gly Pro Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys
290 295 300

Leu Leu Gly Ala Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg
305 310 315 320

Tyr Lys Ile Ile Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro
325 330 335

Ile Ser Gly His Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln
340 345 350

Gly Pro Lys Leu Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp
355 360 365

Ser Gln Leu Pro Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val
370 375 380

Asp Ser Thr Leu Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val
385 390 395 400

Tyr Leu Cys Ala Ser Ser Leu Tyr Gly Gly Ser Ile Ser Tyr Glu Gln
405 410 415

Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn
420 425 430

Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile
435 440 445

Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr
450 455 460

Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His
465 470 475 480

Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu

485

490

495

Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
 500 505 510

Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr
 515 520 525

Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val
 530 535 540

Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe
 545 550 555 560

Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr
 565 570 575

Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala
 580 585 590

Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
 595 600 605

<210> 57
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRAV19 CDR1

<400> 57

Glu Thr Arg Asp Thr Thr Tyr Tyr Leu
 1 5

<210> 58
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TRAV19 CDR2

<400> 58

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu
1 5 10

<210> 59

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV19 CDR3

<400> 59

Cys Ala Leu Ser Glu Ala Gly Thr Tyr Lys Tyr Ile Phe
1 5 10

<210> 60

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR896 ALPHA CONSTANT DOMAIN

<400> 60

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> 61
 <211> 275
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR896 ALPHA CHAIN

<400> 61

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

85

90

95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
 100 105 110

Ala Leu Ser Glu Ala Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr
 115 120 125

Arg Leu Lys Val Leu Ala 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 Thr 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> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV9 CDR1

<400> 62

Arg Ser Gly Asp Leu Ser Val
1 5

<210> 63
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV9 CDR2

<400> 63

Gln Tyr Tyr Asn Gly Glu Glu Arg
1 5

<210> 64
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV9 CDR3

<400> 64

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

<210> 65
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR896 BETA CONSTANT DOMAIN

<400> 65

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> 66
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR896 BETA CHAIN

<400> 66

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 Ala Gly Gly Gly Gln Glu Thr Gln Tyr Phe Gly Pro Gly Thr
115 120 125

Arg Leu Leu 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 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 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> 67

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> LINKER

<400> 67

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

Glu Asn Pro Gly Pro
20

<210> 68
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR896 FUSION

<400> 68

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

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
35 40 45

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

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Ser Glu Ala Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr
115 120 125

Arg Leu Lys Val Leu Ala 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 Thr 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 Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
275 280 285

Asp Val Glu Glu Asn Pro Gly Pro Met Gly Phe Arg Leu Leu Cys Cys
290 295 300

Val Ala Phe Cys Leu Leu Gly Ala Gly Pro Val Asp Ser Gly Val Thr
305 310 315 320

Gln Thr Pro Lys His Leu Ile Thr Ala Thr Gly Gln Arg Val Thr Leu

325

330

335

Arg Cys Ser Pro Arg Ser Gly Asp Leu Ser Val Tyr Trp Tyr Gln Gln
 340 345 350

Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile Gln Tyr Tyr Asn Gly Glu
 355 360 365

Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe Ser Ala Gln Gln Phe
 370 375 380

Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser Leu Glu Leu Gly Asp
 385 390 395 400

Ser Ala Leu Tyr Phe Cys Ala Ser Ser Val Ala Gly Gly Gly Gln Glu
 405 410 415

Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu Leu Val Leu Glu Asp Leu
 420 425 430

Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala
 435 440 445

Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly
 450 455 460

Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu
 465 470 475 480

Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro
 485 490 495

Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
 500 505 510

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
 515 520 525

Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys
530 535 540

Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
545 550 555 560

Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile
565 570 575

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
580 585 590

Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600 605

<210> 69
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV17 CDR1

<400> 69

Lys Thr Ser Ile Asn Asn Leu
1 5

<210> 70
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV17 CDR2

<400> 70

Leu Ile Arg Ser Asn Glu Arg Glu Lys
1 5

<210> 71

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

<220>
<223> TRAV17 CDR3

<400> 71

Cys Ala Thr Phe Pro Asn Phe Gly Asn Glu Lys Leu Thr Phe
1 5 10

<210> 72
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR847 ALPHA CONSTANT DOMAIN

<400> 72

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> 73
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR847 ALPHA CHAIN

<400> 73

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

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Phe
100 105 110

Pro Asn Phe Gly Asn Glu Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Thr Ile Ile 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 Pro Glu
210 215 220

Ser Ser 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> 74

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV10-3 CDR1

<400> 74

Thr Glu Asn His Arg Tyr Met
1 5

<210> 75
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV10-3 CDR2

<400> 75

Tyr Ser Tyr Gly Val Lys Asp Thr
1 5

<210> 76
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV10-3 CDR3

<400> 76

Cys Ala Ile Ser Glu Ser Glu Arg Tyr Tyr Glu Gln Tyr Phe
1 5 10

<210> 77
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR847 BETA CONSTANT DOMAIN

<400> 77

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> 78
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR847 BETA CHAIN

<400> 78

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

Gly His Met Asp Ala Gly Ile Thr Gln Ser Pro Arg His Lys Val Thr
20 25 30

Glu Thr Gly Thr Pro Val Thr Leu Arg Cys His Gln Thr Glu Asn His
35 40 45

Arg Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly His Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Tyr Gly Val Lys Asp Thr Asp Lys Gly Glu Val Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Ser Lys Thr Glu Asp Phe Leu Leu Thr
85 90 95

Leu Glu Ser Ala Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Ile
100 105 110

Ser Glu Ser Glu Arg Tyr 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 Ser 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> 79

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> LINKER

<400> 79

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

Glu Asn Pro Gly Pro
20

<210> 80

<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR847 FUSION

<400> 80

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

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Phe
100 105 110

Pro Asn Phe Gly Asn Glu Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Thr Ile Ile 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 Pro Glu
 210 215 220

Ser Ser 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 Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 275 280 285

Glu Glu Asn Pro Gly Pro Met Gly Thr Arg Leu Phe Phe Tyr Val Ala
 290 295 300

Leu Cys Leu Leu Trp Thr Gly His Met Asp Ala Gly Ile Thr Gln Ser
 305 310 315 320

Pro Arg His Lys Val Thr Glu Thr Gly Thr Pro Val Thr Leu Arg Cys
 325 330 335

His Gln Thr Glu Asn His Arg Tyr Met Tyr Trp Tyr Arg Gln Asp Pro
 340 345 350

Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Gly Val Lys Asp Thr
 355 360 365

Asp Lys Gly Glu Val Ser Asp Gly Tyr Ser Val Ser Arg Ser Lys Thr
370 375 380

Glu Asp Phe Leu Leu Thr Leu Glu Ser Ala Thr Ser Ser Gln Thr Ser
385 390 395 400

Val Tyr Phe Cys Ala Ile Ser Glu Ser Glu Arg Tyr Tyr Glu Gln Tyr
405 410 415

Phe Gly Pro Gly Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val
420 425 430

Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser
435 440 445

His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro
450 455 460

Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser
465 470 475 480

Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn
485 490 495

Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe
500 505 510

Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly
515 520 525

Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr
530 535 540

Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr
545 550 555 560

Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu

565

570

575

Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu
580 585 590

Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600 605

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV4 CDR1

<400> 81

Asn Asn Ile Ala Thr Asn Asp Tyr Ile
1 5

<210> 82
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV4 CDR2

<400> 82

Gln Gly Tyr Lys Thr Lys Val
1 5

<210> 83
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV4 CDR3

<400> 83

Cys Leu Val Gly Asp Phe Asn Ser Asn Ser Gly Tyr Ala Leu Asn Phe

1 5 10 15

<210> 84
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR864 ALPHA CONSTANT DOMAIN

<400> 84

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> 85

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

<220>
<223> TCR864 ALPHA CHAIN

<400> 85

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
65 70 75 80

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Phe Asn Ser
100 105 110

Asn Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val
115 120 125

Thr Pro His 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 Thr 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> 86
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRBV7-2 CDR1

<400> 86

Ile Ser Gly His Thr Ala Leu
 1 5

<210> 87
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRBV7-2 CDR2

<400> 87

Tyr Phe Gln Gly Asn Ser Ala Pro
1 5

<210> 88
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV7-2 CDR3

<400> 88

Cys Ala Ser Lys Val Tyr Gly Tyr Thr Phe
1 5 10

<210> 89
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR864 BETA CONSTANT DOMAIN

<400> 89

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> 90

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR864 BETA CHAIN

<400> 90

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

Tyr His Thr Gly Ala Gly Val Ser Gln Ser Pro Ser Asn Lys Val Thr
 20 25 30

Glu Lys Gly Lys Asp Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His
 35 40 45

Thr Ala Leu Tyr Trp Tyr Arg Gln Arg Leu Gly Gln Gly Leu Glu Phe

50

55

60

Leu Ile Tyr Phe Gln Gly Asn Ser Ala Pro Asp Lys Ser Gly Leu Pro
 65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Thr Gly Glu Ser Val Ser Thr Leu
 85 90 95

Thr Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala
 100 105 110

Ser Lys Val Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg Leu Thr Val
 115 120 125

Val Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu
 130 135 140

Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
 145 150 155 160

Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val
 165 170 175

Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu
 180 185 190

Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg
 210 215 220

Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
 225 230 235 240

Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
 245 250 255

Arg Ala Asp Cys Gly Phe Thr Ser Val 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 Ala Leu Val Leu Met Ala Met Val Lys Arg Lys
290 295 300

Asp Phe
305

<210> 91
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> LINKER

<400> 91

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

Glu Asn Pro Gly Pro
20

<210> 92
<211> 598
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR864 FUSION

<400> 92

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly

20

25

30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
 35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
 50 55 60

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
 65 70 75 80

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
 85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Phe Asn Ser
 100 105 110

Asn Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val
 115 120 125

Thr Pro His 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 Thr 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 Gly
260 265 270

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
275 280 285

Asn Pro Gly Pro Met Gly Thr Arg Leu Leu Phe Trp Val Ala Phe Cys
290 295 300

Leu Leu Gly Ala Tyr His Thr Gly Ala Gly Val Ser Gln Ser Pro Ser
305 310 315 320

Asn Lys Val Thr Glu Lys Gly Lys Asp Val Glu Leu Arg Cys Asp Pro
325 330 335

Ile Ser Gly His Thr Ala Leu Tyr Trp Tyr Arg Gln Arg Leu Gly Gln
340 345 350

Gly Leu Glu Phe Leu Ile Tyr Phe Gln Gly Asn Ser Ala Pro Asp Lys
355 360 365

Ser Gly Leu Pro Ser Asp Arg Phe Ser Ala Glu Arg Thr Gly Glu Ser
370 375 380

Val Ser Thr Leu Thr Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val
385 390 395 400

Tyr Leu Cys Ala Ser Lys Val Tyr Gly Tyr Thr Phe Gly Ser Gly Thr
405 410 415

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

420

425

430

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
 435 440 445

Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu
 450 455 460

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
 465 470 475 480

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
 485 490 495

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
 500 505 510

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
 515 520 525

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
 530 535 540

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln
 545 550 555 560

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
 565 570 575

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
 580 585 590

Val Lys Arg Lys Asp Phe
 595

<210> 93

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAV39 CDR1

<400> 93

accacttcag a

11

<210> 94

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAV39 CDR2

<400> 94

ttgctatcaa atggagcagt g

21

<210> 95

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAV39 CDR3

<400> 95

gccgtggaca aggatggggg ttacc

25

<210> 96

<211> 391

<212> DNA

<213> Artificial Sequence

<220>

<223> TRAV39 VARIABLE DOMAIN

<400> 96

atgaagaagc tactagcaat gattctgtgg cttcaactag accggttaag tggagagctg

60

aaagtgaac aaaaccctct gttcctgagc atgcaggagg gaaaaaacta taccatctac

120

tgcaattatt caaccacttc agacagactg tattggtaca ggcaggatcc tgggaaaagt

180

ctggaatctc tgtttgtgtt gctatcaaat ggagcagtga agcaggaggg acgattaatg

240

gcctcacttg ataccaaagc ccgtctcagc accctccaca tcacagctgc cgtgcatgac	300
ctctctgcca cctacttctg tgccgtggac aaggatgggg gttaccagaa agttaccttt	360
ggaactggaa caaagctcca agtcatccca a	391

<210> 97
 <211> 422
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR831 ALPHA CONSTANT DOMAIN

<400> 97	
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt	60
ctgtctgcct attcaccgat ttgtattctc aaacaaatgt gtcacaaagt aaggattctg	120
atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca	180
gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca	240
ttattccaga agacaccttc ttccccagcc cagaaagtgc ctgtgatgtc aagctggctg	300
agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc	360
gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg ctgtggtcca	420
gc	422

<210> 98
 <211> 813
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR831 ALPHA CHAIN

<400> 98	
atgaagaagc tactagcaat gattctgtgg cttcaactag accggttaag tggagagctg	60
aaagtgaac aaaaccctct gttcctgagc atgcaggagg gaaaaaacta taccatctac	120
tgcaattatt caaccacttc agacagactg tattggtaca ggcaggatcc tgggaaaagt	180
ctggaatctc tgtttgtgtt gctatcaa at ggagcagtga agcaggaggg acgattaatg	240

gcctcacttg ataccaaagc ccgtctcagc accctccaca tcacagctgc cgtgcatgac	300
ctctctgcca cctacttctg tgccgtggac aaggatgggg gttaccagaa agttaccttt	360
ggaactggaa caaagctcca agtcatccca aatatccaga accctgaccc tgccgtgtac	420
cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct	480
caaacaaatg tgtcacaag taaggattct gatgtgtata tcacagacaa aactgtgttg	540
gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac	600
tttgcattgt caaacgcctt caacaacagc attattccag aagacacctt cttccccagc	660
ccagaaagtt cctgtgatgt caagctggtc gagaaaagct ttgaaacaga tacgaacct	720
aactttcaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt	780
aatctgctca tgacgctgcg gctgtggtcc agc	813

<210> 99
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV20-1 CDR1

<400> 99	
gactttcagg ccacaact	18

<210> 100
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV20-1 CDR2

<400> 100	
tcctaatgagg gctccaaggc c	21

<210> 101
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>

<223> TRBV20-1CDR3

<400> 101

agtgctagcc cacgggcggg acagttgagc tcctataatt caccctcca c 51

<210> 102

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> TRBV20-1 VARIABLE

<400> 102

atgctgctgc ttctgctgct tctggggcca ggtataagcc tccttctacc tgggagcttg 60

gcaggctccg ggcttggtgc tgcgtctct caacatccga gctgggttat ctgtaagagt 120

ggaacctctg tgaagatcga gtgccgttcc ctggactttc aggccacaac tatgttttgg 180

tatcgtcagt tcccgaaca gagtctcatg ctgatggcaa cttccaatga gggctccaag 240

gccacatacg agcaaggcgt cgagaaggac aagtttctca tcaaccatgc aagcctgacc 300

ttgtccactc tgacagtgc cagtggccat cctgaagaca gcagcttcta catctgcagt 360

gctagcccac gggcgggaca gttgagctcc tataattcac ccctccactt tgggaatggg 420

accaggctca ctgtgac 437

<210> 103

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR831 BETA CONSTANT DOMAIN

<400> 103

gaggacctga acaagggtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60

atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttctt ccccgaccac 120

gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacggacccg 180

cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240

agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc	300
tacgggctct cggagaatga tgagtggaca caagataggg ccaaaccgt caccagatc	360
gtcagcgccg aggcctgggg tagagcagac tgtggcttta cctcgggtgtc ctaccagcaa	420
ggggctctgt ctgccacat cctctatgag atcctgctag ggaaggccac cctgtatgct	480
gtgctggta gcgcccttgt gttgatggcc atggtcaaga gaaaggattt c	531

<210> 104
 <211> 972
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR831 BETA CHAIN

<400> 104	
atgctgctgc ttctgctgct tctggggcca ggtataagcc tccttctacc tgggagcttg	60
gcaggctccg ggcttgggtg tgctgtctct caacatccga gctgggttat ctgtaagagt	120
ggaacctctg tgaagatcga gtgccgttcc ctggactttc aggccacaac tatgttttgg	180
tatcgtcagt tcccgaacaa gagtctcatg ctgatggcaa cttccaatga gggctccaag	240
gccacatacg agcaaggcgt cgagaaggac aagtttctca tcaacatgc aagcctgacc	300
ttgtccactc tgacagtgac cagtgcccac cctgaagaca gcagcttcta catctgcagt	360
gctagcccac gggcgggaca gttgagctcc tataattcac ccctccactt tgggaatggg	420
accaggctca ctgtgacaga ggacctgaac aaggtgttcc caccgaggt cgctgtgttt	480
gagccatcag aagcagagat ctccacacc caaaaggcca cactggtgtg cctggccaca	540
ggcttcttcc ccgaccacgt ggagctgagc tgggtgggtga atgggaagga ggtgcacagt	600
ggggtcagca cggacccgca gcccctcaag gagcagcccg ccctcaatga ctccagatac	660
tgctgagca gccgcctgag ggtctcggcc accttctggc agaacccccg caaccattc	720
cgctgtcaag tccagttcta cgggctctcg gagaatgatg agtggacaca agatagggcc	780
aaacccgtca cccagatcgt cagcgccgag gcctggggta gagcagactg tggctttacc	840
tcggtgtcct accagcaagg ggtcctgtct gccaccatcc tctatgagat cctgctaggg	900

aaggccaccc tgtatgctgt gctggtcagc gcccttgtgt tgatggccat ggtcaagaga	960
aaggatttct ga	972

<210> 105
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> linker

<400> 105	
ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatcccggc	60
cct	63

<210> 106
 <211> 1848
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR831 fusion

<400> 106	
atgaagaagc tactagcaat gattctgtgg cttcaactag accggttaag tggagagctg	60
aaagtggaac aaaaccctct gttcctgagc atgcaggagg gaaaaaacta taccatctac	120
tgcaattatt caaccacttc agacagactg tattggtaca ggcaggatcc tgggaaaagt	180
ctggaatctc tgtttgtgtt gctatcaa at ggagcagtga agcaggaggg acgattaatg	240
gcctcacttg ataccaaagc ccgtctcagc accctccaca tcacagctgc cgtgcatgac	300
ctctctgcca cctacttctg tgccgtggac aaggatgggg gttaccagaa agttaccttt	360
ggaactggaa caaagctcca agtcatccca aatatccaga accctgaccc tgccgtgtac	420
cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct	480
caaacaaatg tgtcacaaag taaggattct gatgtgtata tcacagacaa aactgtgttg	540
gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac	600
tttgcattgtg caaacgcctt caacaacagc attattccag aagacacctt cttccccagc	660

ccagaaagtt cctgtgatgt caagctgggtc gagaaaagct ttgaaacaga tacgaaccta	720
aactttcaaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt	780
aatctgctca tgacgtgctg gctgtgggtcc agcggcagcg gagagggcag aggaagtctt	840
ctaakatgctg gtgacgtgga ggagaatccc ggccctatgc tgctgcttct gctgcttctg	900
gggccaggta taagcctcct tctacctggg agcttggcag gctccgggct tgggtgctgtc	960
gtctctcaac atccgagctg gggttatctgt aagagtggaa cctctgtgaa gatcgagtgc	1020
cgttccctgg actttcaggc cacaactatg ttttgggtatc gtcagttccc gaaacagagt	1080
ctcatgctga tggcaacttc caatgagggc tccaaggcca catacgagca aggcgtcgag	1140
aaggacaagt ttctcatcaa ccatgcaagc ctgaccttgt cactctgac agtgaccagt	1200
gcccaccttg aagacagcag cttctacatc tgcagtgcta gcccacgggc gggacagttg	1260
agctcctata attcaccctt ccactttggg aatgggacca ggctcactgt gacagaggac	1320
ctgaacaagg tgttcccacc cgaggctgct gtgtttgagc catcagaagc agagatctcc	1380
cacacccaaa aggccacact ggtgtgcctg gccacaggct tcttccccga ccacgtggag	1440
ctgagctggg ggggtgaatgg gaaggagggtg cacagtgggg tcagcacgga cccgcagccc	1500
ctcaaggagc agcccgccct caatgactcc agatactgcc tgagcagccg cctgaggggtc	1560
tcggccacct tctggcagaa cccccgcaac cacttccgct gtcaagtcca gttctacggg	1620
ctctcggaga atgatgagtg gacacaagat agggccaaac ccgtcaccca gatcgtcagc	1680
gccgaggcct ggggtagagc agactgtggc ttacctcgg tgcctacca gcaaggggtc	1740
ctgtctgcca ccatcctcta tgagatcctg ctagggaagg ccaccctgta tgctgtgctg	1800
gtcagcgccc ttgtgttgat ggccatgggtc aagagaaaagg atttctga	1848

<210> 107
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TRAV12-1 CDR1

 <400> 107

aacagtgctt ctcagtct 18

<210> 108
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAV12-1 CDR2

<400> 108
gtatactcca gtggtaac 18

<210> 109
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAV12-1 CDR3

<400> 109
gcggtgaacc ccccgacac aggctttcag aaacttgta 39

<210> 110
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAV12-1 VARIABLE DOMAIN

<400> 110
atgatatcct tgagagtttt actggtgatc ctgtggcttc agttaagctg ggtttggagc 60
caacggaagg aggtggagca ggatcctgga cccttcaatg ttccagaggg agccactgtc 120
gctttcaact gtacttacag caacagtgtc tctcagtcct tcttctggta cagacaggat 180
tgcaggaaag aacctaaagt gctgatgtcc gtatactcca gtggtaacga agatggaagg 240
tttacagcac agctcaatag agccagccag tatattttccc tgctcatcag agactccaag 300
ctcagtgtatt cagccaccta cctctgtgcg gtgaaccccc cggacacagg ctttcagaaa 360
cttgatatttg gaactggcac ccgacttctg gtcagtccaa 400

<210> 111
<211> 422
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR833 ALPHA CONSTANT DOMAIN

<400> 111
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 60
ctgtctgcct attcaccgat tttgattctc aaacaaatgt gtcacaaagt aaggattctg 120
atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca 180
gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca 240
ttattccaga agacaccttc ttccccagcc cagaaagttc ctgtgatgtc aagctgggtcg 300
agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc 360
gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg ctgtggtcca 420
gc 422

<210> 112
<211> 822
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR833 ALPHA CHAIN

<400> 112
atgatatcct tgagagtttt actgggtgatc ctgtggcttc agttaagctg ggtttggagc 60
caacggaagg aggtggagca ggatcctgga cccttcaatg ttccagaggg agccactgtc 120
gctttcaact gtacttacag caacagtgtc tctcagtcct tcttctggta cagacaggat 180
tgcaggaaag aacctaaagt gctgatgtcc gtatactcca gtggtaacga agatggaagg 240
tttacagcac agctcaatag agccagccag tatatttccc tgctcatcag agactccaag 300
ctcagtgatt cagccaccta cctctgtgcg gtgaaccccc cggacacagg ctttcagaaa 360
cttgatatttg gaactggcac ccgacttctg gtcagtccaa atatccagaa ccctgaccct 420

gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat	480
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa	540
actgtgttgg acatgcgag catggacttc aagagcaaca gtgctgtggc ctggagcaac	600
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc	660
ttccccagcc cagaaagttc ctgtgatgtc aagctggctg agaaaagctt tgaaacagat	720
acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg	780
gccgggttta atctgctcat gacgctgcgg ctgtggtcca gc	822

<210> 113
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV28 CDR1

<400> 113	
atggaccatg aaaat	15

<210> 114
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV28 CDR2

<400> 114	
tcatatgatg ttaaaatg	18

<210> 115
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV28 CDR3

<400> 115	
gccagcagtt tatccttccg gcagggcctt cgcgagcagt ac	42

<210> 116
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBV28 VARIABLE DOMAIN

<400> 116
atggggaatca ggctcctgtg tcgtgtggcc ttttgtttcc tggctgtagg cctcgtagat 60
gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg 120
gaatgtgtcc aggatatgga ccatgaaaat atgttctggt atcgacaaga cccaggtctg 180
gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct 240
gaggggtaca gtgtctccag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgt gccagcagtt tacccttccg gcagggcctt 360
cgcgagcagt acttcgggcc gggcaccagg ctacaggtca ca 402

<210> 117
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR833 BETA CONSTANT DOMAIN

<400> 117
gaggacctga aaaacgtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60
atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttcta ccccgaccac 120
gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacagacccg 180
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240
agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc 300
tacgggctct cggagaatga tgagtggaca caagataggg ccaaacctgt caccagatc 360
gtcagcgccg aggcctgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa 420
ggggctcctgt ctgccaccat cctctatgag atcttgctag ggaaggccac cttgtatgcc 480

gtgctgggtca gtgccctcgt gctgatggcc atgggtcaaga gaaaggattc cagaggc 537

<210> 118

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR833 BETA CHAIN

<400> 118

atgggaatca ggctcctgtg tcgtgtggcc ttttgtttcc tggctgtagg cctcgtagat 60
gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg 120
gaatgtgtcc aggatatgga ccatgaaaat atgttcttgt atcgacaaga cccaggctctg 180
gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct 240
gaggggtaca gtgtctccag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgt gccagcagtt tatccttccg gcagggcctt 360
cgcgagcagt acttcgggcc gggcaccagg ctacaggtca cagaggacct gaaaaacgtg 420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca cacccaaaag 480
gccacactgg tgtgcctggc cacaggcttc taccgacc acgtggagct gagctggtgg 540
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgagcccct caaggagcag 600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat 720
gatgagtgga cacaagatag ggccaaacct gtcaccaga tcgtcagcgc cgaggcctgg 780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840
atcctctatg agatcttgct aggggaaggcc accttgatg ccgtgctggc cagtgccctc 900
gtgctgatgg ccatggtcaa gagaaaggat tccagaggct ga 942

<210> 119

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> LINKER

<400> 119

ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatcccggc 60

cct 63

<210> 120

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR833 FUSION

<400> 120

atgatatcct tgagagtttt actggtgatc ctgtggcttc agttaagctg ggtttggagc 60

caacggaagg aggtggagca ggatcctgga ccttcaatg ttccagaggg agccactgtc 120

gctttcaact gtacttacag caacagtgtc tctcagctt tcttctggta cagacaggat 180

tgcaggaaaag aacctaaagt gctgatgtcc gtatactcca gtggtaacga agatggaagg 240

tttacagcac agctcaatag agccagccag tatattttccc tgctcatcag agactccaag 300

ctcagtgtt cagccaccta cctctgtgcg gtgaaccccc cggacacagg ctttcagaaa 360

cttgatattt gaactggcac ccgacttctg gtcagtcaa atatccagaa ccctgaccct 420

gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 480

tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 540

actgtgttgg acatgcgcag catggacttc aagagcaaca gtgctgtggc ctggagcaac 600

aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 660

ttccccagcc cagaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat 720

acgaacctaa actttcaaaa cctgtcagtgt attgggttcc gaatcctcct cctgaaagtgt 780

gccgggttta atctgtcat gacgtgcgg ctgtggtcca gcggcagcgg agagggcaga 840

ggaagtcttc taacatgcgg tgacgtggag gagaatccc gccctatggg aatcaggctc 900

ctgtgtcgtg tggccttttg tttcctggct gtaggcctcg tagatgtgaa agtaaccag 960

agctcgagat atctagtcaa aaggacggga gagaaagttt ttctggaatg tgtccaggat	1020
atggaccatg aaaatatgtt ctggtatcga caagaccag gtctggggct acggctgac	1080
tattttctcat atgatgttaa aatgaaagaa aaaggagata ttcctgaggg gtacagtgtc	1140
tccagagaga agaaggagcg cttctccctg attctggagt ccgccagcac caaccagaca	1200
tctatgtacc tctgtgccag cagtttatcc ttccggcagg gccttcgcga gcagtacttc	1260
gggccgggca ccaggctcac ggtcacagag gacctgaaaa acgtgttccc acccgaggtc	1320
gctgtgtttg agccatcaga agcagagatc tcccacaccc aaaaggccac actggtgtgc	1380
ctggccacag gcttctaccc cgaccacgtg gagctgagct ggtgggtgaa tgggaaggag	1440
gtgcacagtg gggtcagcac agacccgcag cccctcaagg agcagccgc cctcaatgac	1500
tccagatact gcctgagcag ccgcctgagg gtctcggcca ctttctggca gaacccccgc	1560
aaccacttcc gctgtcaagt ccagttctac gggctctcgg agaatgatga gtggacacaa	1620
gatagggccca aacctgtcac ccagatcgtc agcgccgagg cctggggtag agcagactgt	1680
ggcttcacct ccgagtctta ccagcaaggg gtcctgtctg ccaccatcct ctatgagatc	1740
ttgctaggga aggccacctt gtatgccgtg ctggtcagtg ccctcgtgct gatggccatg	1800
gtcaagagaa aggattccag aggctga	1827

<210> 121
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV17 CDR1

<400> 121	
actagtataa acaat	15

<210> 122
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV17 CDR2

<400> 122
atacgttcaa atgaaagaga g 21

<210> 123
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAV17 CDR3

<400> 123
tgtgctacgg accctggagg cttcaaaact atcttt 36

<210> 124
<211> 422
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR897 ALPHA CONSTANT DOMAIN

<400> 124
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 60
ctgtctgcct attcaccgat ttgtattctc aaacaaatgt gtcacaaagt aaggattctg 120
atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca 180
gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca 240
ttattccaga agacaccttc ttccccagcc cagaaagttc ctgtgatgtc aagctgggtcg 300
agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc 360
gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg ctgtggtcca 420
gc 422

<210> 125
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR897 ALPHA CHAIN

<400> 125
 atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc tagggatgaac 60
 agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc 120
 atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt 180
 agaggccttg tccacctaatt ttttaatacgt tcaaatgaaa gagagaaaca cagtgaaga 240
 ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg 300
 gcagcagaca ctgcttctta cttctgtgct acggaccctg gaggcttcaa aactatcttt 360
 ggagcaggaa caagactatt tgtaaagca aatatccaga accctgaccc tgccgtgtac 420
 cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct 480
 caaacaatg tgtcacaag taaggattct gatgtgtata tcacagacaa aactgtgttg 540
 gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac 600
 tttgcatgtg caaacgcctt caacaacagc attattccag aagacacctt cttccccagc 660
 ccagaaaagt cctgtgatgt caagctggtc gagaaaagct ttgaaacaga tacgaaccta 720
 aactttcaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt 780
 aatctgctca tgacgtgctg gctgtggtcc agc 813

<210> 126
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV11-2 CDR1

<400> 126
 tctggccatg ctacc 15

<210> 127
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV11-2 CDR2

<400> 127
tttcagaata acggtgta 18

<210> 128
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBV11-2 CDR3

<400> 128
tgtgccagca gcttatatgg ggggtcgatc tcctacgagc agtacttc 48

<210> 129
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR897 BETA CONSTANT DOMAIN

<400> 129
gaggacctga aaaacgtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60
atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttcta ccccgaccac 120
gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacagacccg 180
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240
agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc 300
tacgggctct cggagaatga tgagtggaca caagataggg ccaaacctgt caccagatc 360
gtcagcgccg aggcctgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa 420
ggggtcctgt ctgccacat cctctatgag atcttgctag ggaaggccac cttgtatgcc 480
gtgctgggtca gtgccctcgt gctgatggcc atggtcaaga gaaaggattc cagaggc 537

<210> 130
<211> 945
<212> DNA
<213> Artificial Sequence

<220>

<223> TCR897 BETA CHAIN

<400> 130

atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa	60
gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt	120
tgggtcaatc ctatatctgg ccatgctacc ctttactggt accagcagat cctgggacag	180
ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct	240
aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct	300
gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttatatgg ggggtcgate	360
tcctacgagc agtacttcgg gccgggcacc aggtcacgg tcacagagga cctgaaaaac	420
gtgttccac ccgaggtcgc tgtgtttgag ccatcagaag cagagatctc ccacacccaa	480
aaggccacac tgggtgtgcct ggccacaggc ttctacccc accacgtgga gctgagctgg	540
tgggtgaatg ggaaggaggt gcacagtggg gtcagcacag acccgagcc cctcaaggag	600
cagcccgccc tcaatgactc cagatactgc ctgagcagcc gcctgagggt ctcggccacc	660
ttctggcaga acccccgcaa ccacttccgc tgtcaagtcc agttctacgg gctctcggag	720
aatgatgagt ggacacaaga tagggccaaa cctgtcacc agatcgtcag cgccgaggcc	780
tggggtagag cagactgtgg cttcacctcc gagtcttacc agcaaggggt cctgtctgcc	840
accatcctct atgagatctt gctaggggaag gccaccttgt atgccgtgct ggtcagtgcc	900
ctcgtgctga tggccatggt caagagaaag gattccagag gctga	945

<210> 131

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> LINKER

<400> 131

ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatcccggc	60
cct	63

<210> 132
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR897 FUSION

<400> 132
atggaaaactc tcctgggagt gtcttttggtg attctatggc ttcaactggc taggggtgaac 60
agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc 120
atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt 180
agaggccttg tccacctaatt tttaatacgt tcaaatgaaa gagagaaaca cagtggaaga 240
ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg 300
gcagcagaca ctgcttctta cttctgtgct acggaccctg gaggcttcaa aactatcttt 360
ggagcaggaa caagactatt tgtaaagca aatatccaga accctgaccc tgccgtgtac 420
cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct 480
caaacaaatg tgtcacaaag taaggattct gatgtgtata tcacagacaa aactgtgttg 540
gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac 600
tttgcattgt caaacgcctt caacaacagc attattccag aagacacctt cttccccagc 660
ccagaaaagt cctgtgatgt caagctggtc gagaaaagct ttgaaacaga tacgaaccta 720
aactttcaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt 780
aatctgctca tgacgtgcg gctgtggtcc agcggcagcg gagagggcag aggaagtctt 840
ctaactgctg gtgacgtgga ggagaatccc ggccctatgg gcaccaggct cctctgctgg 900
gcggccctct gtctcctggg agcagaactc acagaagctg gagttgcca gtctcccaga 960
tataagatta tagagaaaag gcagagtgtg gctttttggt gcaatcctat atctggccat 1020
gctacccttt actggtacca gcagatcctg ggacagggcc caaagcttct gattcagttt 1080
cagaataacg gtgtagtgga tgattcacag ttgcctaagg atcgattttc tgcagagagg 1140
ctcaaaggag tagactccac tctcaagatc cagcctgcaa agcttgagga ctcggccgtg 1200

tatctctgtg ccagcagctt atatgggggg tcgatctcct acgagcagta cttcgggccg	1260
ggcaccaggc tcacggtcac agaggacctg aaaaacgtgt tcccaccga ggtcgtgtg	1320
tttgagccat cagaagcaga gatctccac acccaaaagg ccacactggt gtgcctggcc	1380
acaggcttct accccgacca cgtggagctg agctggtggg tgaatgggaa ggaggtgcac	1440
agtggggtca gcacagaccc gcagcccctc aaggagcagc ccgccctcaa tgactccaga	1500
tactgcctga gcagccgcct gagggctctg gccaccttct ggcagaaccc ccgcaaccac	1560
ttccgctgtc aagtccagtt ctacgggctc tcggagaatg atgagtggac acaagatagg	1620
gccaaacctg tcaccagat cgtcagcgcc gaggcctggg gtagagcaga ctgtggcttc	1680
acctccgagt cttaccagca aggggtcctg tctgccacca tcctctatga gatcttgcta	1740
gggaaggcca ccttgatatgc cgtgctggtc agtgccctcg tgctgatggc catggtcaag	1800
agaaaggatt ccagaggctg a	1821

<210> 133
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV19 CDR1

<400> 133	
acccgtgata ctacttatta c	21

<210> 134
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV19 CDR2

<400> 134	
cggaactctt ttgatgagca aaat	24

<210> 135
 <211> 39
 <212> DNA

<213> Artificial Sequence

<220>

<223> TRAV19 CDR3

<400> 135

tgtgctctga gtgaggcagg aacctacaaa tacatcttt 39

<210> 136

<211> 422

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR896 ALPHA CONSTANT DOMAIN

<400> 136

atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 60

ctgtctgcct attcaccgat ttgtattctc aaacaaatgt gtcacaaagt aaggattctg 120

atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca 180

gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca 240

ttattccaga agacaccttc ttccccagcc cagaaagttc ctgtgatgtc aagctggctg 300

agaaaagctt tgaacacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc 360

gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgtgcgg ctgtggtcca 420

gc 422

<210> 137

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR896 ALPHA CHAIN

<400> 137

atgctgactg ccagcctgtt gagggcagtc atagcctcca tctgtgttgt atccagcatg 60

gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc 120

ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca 180

ccaagtggag aattggtttt ctttattcgt cggaactctt ttgatgagca aaatgaaata	240
agtggtcggt attcttggaa cttccagaaa tccaccagtt ctttcaactt caccatcaca	300
gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgagtgaggc aggaacctac	360
aaatacatct ttggaacagg caccaggctg aaggtattag caaatatcca gaacctgac	420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc	480
gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac	540
aaaactgtgt tggacatgcg cagcatggac ttcaagagca acagtgtctg ggcctggagc	600
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc	660
ttcttcccca gcccagaaaag ttctgtgat gtcaagctgg tcgagaaaag ctttgaaaca	720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa	780
gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagc	825

<210> 138
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV9 CDR1

<400> 138	
tctggagacc tctct	15

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV9 CDR2

<400> 139	
cggaactctt ttgatgagca aaat	24

<210> 140
 <211> 39
 <212> DNA

<213> Artificial Sequence

<220>

<223> TRBV9 CDR3

<400> 140

tgtgctctga gtgaggcagg aacctacaaa tacatcttt 39

<210> 141

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR896 BETA CONSTANT DOMAIN

<400> 141

gaggacctga aaaacgtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60

atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttcta ccccgaccac 120

gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacagacccg 180

cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240

agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc 300

tacgggctct cggagaatga tgagtggaca caagataggg ccaaacctgt caccagatc 360

gtcagcgccg aggcctgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa 420

ggggctcctgt ctgccaccat cctctatgag atcttgctag ggaaggccac cttgtatgcc 480

gtgctgggtca gtgccctcgt gctgatggcc atggtaaga gaaaggattc cagaggc 537

<210> 142

<211> 939

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR896 BETA CHAIN

<400> 142

atgggcttca ggctcctctg ctgtgtggcc ttttgtctcc tgggagcagg cccagtggat 60

tctggagtca cacaaccccc aaagcacctg atcacagcaa ctggacagcg agtgacgctg 120

agatgctccc ctaggtctgg agacctctct gtgtactggg accaacagag cctggaccag	180
ggcctccagt tcctcattca gtattataat ggagaagaga gagcaaaagg aaacattctt	240
gaacgattct ccgcacaaca gttccctgac ttgcactctg aactaaacct gagctctctg	300
gagctggggg actcagcttt gtatttctgt gccagcagcg tagctggggg gggacaagag	360
accagtgact tcgggccagg cacgcggctc ctggtgctcg aggacctgaa aaacgtgttc	420
ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctccacac ccaaaaggcc	480
acactgggtg gcctggccac aggcttctac cccgaccacg tggagctgag ctggtgggtg	540
aatgggaagg aggtgcacag tggggtcagc acagaccgc agcccctcaa ggagcagccc	600
gccctcaatg actccagata ctgcctgagc agccgcctga gggctctggc caccttctgg	660
cagaaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgat	720
gagtggacac aagatagggc caaacctgtc acccagatcg tcagcgccga ggcctggggg	780
agagcagact gtggcttcac ctccgagtct taccagcaag gggtcctgtc tgccaccatc	840
ctctatgaga tcttgctagg gaaggccacc ttgtatgccg tgctgggtcag tgccctcgtg	900
ctgatggcca tgggtcaagag aaaggattcc agaggctga	939

<210> 143
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LINKER

<400> 143	
ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatcccggc	60
cct	63

<210> 144
 <211> 1827
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR896 FUSION

<400> 144

atgctgactg ccagcctgtt gagggcagtc atagcctcca tctgtgttgt atccagcatg	60
gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc	120
ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca	180
ccaagtggag aattggtttt ctttattcgt cggaactctt ttgatgagca aaatgaaata	240
agtggtcggt attcttggaa cttccagaaa tccaccagtt ctttcaactt caccatcaca	300
gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgagtgaggc aggaacctac	360
aaatacatct ttggaacagg caccaggctg aaggatttag caaatatcca gaaccctgac	420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc	480
gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac	540
aaaactgtgt tggacatgcg cagcatggac ttcaagagca acagtgtctg ggccctggagc	600
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc	660
ttcttcccca gcccagaaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca	720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa	780
gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagcggcag cggagagggc	840
agaggaaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctat gggcttcagg	900
ctcctctgct gtgtggcctt ttgtctcctg ggagcaggcc cagtggattc tggagtcaca	960
caaaccccaa agcacctgat cacagcaact ggacagcgag tgacgctgag atgctcccct	1020
aggtctggag acctctctgt gtactggtac caacagagcc tggaccaggg cctccagttc	1080
ctcattcagt attataatgg agaagagaga gcaaaaaggaa acattcttga acgattctcc	1140
gcacaacagt tccctgactt gcactctgaa ctaaacctga gctctctgga gctggggggac	1200
tcagctttgt atttctgtgc cagcagcgta gctggggggg gacaagagac ccagtacttc	1260
gggccaggca cgcggctcct ggtgctcgag gacctgaaaa acgtgttccc acccgaggtc	1320
gctgtgtttg agccatcaga agcagagatc tcccacaccc aaaaggccac actggtgtgc	1380
ctggccacag gcttctaccc cgaccacgtg gagctgagct ggtgggtgaa tgggaaggag	1440

gtgcacagtg gggtcagcac agacccgcag cccctcaagg agcagcccg cctcaatgac	1500
tccagatact gcctgagcag ccgcctgagg gtctcggcca ctttctggca gaacccccgc	1560
aaccacttcc gctgtcaagt ccagttctac gggctctcgg agaatgatga gtggacacaa	1620
gatagggcca aacctgtcac ccagatcgtc agcgccgagg cctggggtag agcagactgt	1680
ggcttcacct ccgagtctta ccagcaaggg gtcctgtctg ccaccatcct ctatgagatc	1740
ttgctaggga aggccacctt gtatgccgtg ctggtcagtg ccctcgtgct gatggccatg	1800
gtcaagagaa aggattccag aggctga	1827

<210> 145
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV17 CDR1

<400> 145	
actagtataa acaat	15

<210> 146
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV17 CDR2

<400> 146	
atacgttcaa atgaaagaga g	21

<210> 147
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV17 CDR3

<400> 147	
gctacttttc ctaactttgg aaatgagaaa ttaacc	36

<210> 148
<211> 422
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR847 ALPHA CONSTANT DOMAIN

<400> 148
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 60
ctgtctgcct attcaccgat ttgtattctc aaacaaatgt gtcacaaagt aaggattctg 120
atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca 180
gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca 240
ttattccaga agacaccttc ttccccagcc cagaaagtgc ctgtgatgtc aagctgggtcg 300
agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc 360
gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg ctgtggtcca 420
gc 422

<210> 149
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR847 ALPHA CHAIN

<400> 149
atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc tagggtgaac 60
agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc 120
atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt 180
agaggccttg tccacctaat tttaatacgt tcaaatgaaa gagagaaaca cagtggaaga 240
ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg 300
gcagcagaca ctgcttctta cttctgtgct acttttccta actttggaaa tgagaaatta 360
acctttggga ctggaacaag actcaccatc atacccaata tccagaaccc tgaccctgcc 420

gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt	480
gatttctcaaa caaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact	540
gtgttggaca tgcgcagcat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa	600
tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc	660
cccagcccag aaagttcctg tgatgtcaag ctggtcgaga aaagctttga aacagatacg	720
aacctaaact ttcaaaacct gtcagtgatt gggttccgaa tcctcctcct gaaagtggcc	780
gggtttaatc tgctcatgac gctgcggtg tggtccagc	819

<210> 150
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV10-3 CDR1

<400> 150	
gagaaccacc gcta	14

<210> 151
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV10-3 CDR2

<400> 151	
tcatatggtg ttaaagat	18

<210> 152
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV10-3 CDR3

<400> 152	
gccatcagtg agtcggagcg gtactacgag cagtac	36

<210> 153
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR847 BETA CONSTANT DOMAIN

<400> 153
gaggacctga aaaacgtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60
atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttcta ccccgaccac 120
gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacagacccg 180
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240
agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc 300
tacgggctct cggagaatga tgagtggaca caagataggg ccaaacctgt caccagatc 360
gtcagcgccg aggcttgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa 420
ggggctcctgt ctgccaccat cctctatgag atcttgctag ggaaggccac cttgtatgcc 480
gtgctgggtca gtgccctcgt gctgatggcc atggtcaaga gaaaggattc cagaggc 537

<210> 154
<211> 936
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR847 BETA CHAIN

<400> 154
atgggacaaa ggttgttctt ctatgtggcc ctttgtctcc tgtggacagg acacatggat 60
gctggaatca cccagagccc aagacacaag gtcacagaga caggaacacc agtgactctg 120
agatgtcacc agactgagaa ccaccgctat atgtactgggt atcgacaaga cccggggcat 180
gggctgaggc tgatccatta ctcatatgggt gttaaagata ctgacaaagg agaagtctca 240
gatggctata gtgtctccag atcaaagaca gaggatttcc tcctcactct ggagtccgct 300
accagctccc agacatctgt gtacttctgt gccatcagtg agtcggagcg gtactacgag 360

cagtacttcg ggccgggcac caggctcacg gtcacagagg acctgaaaaa cgtgttccca	420
cccgaggtcg ctgtgtttga gccatcagaa gcagagatct cccacaccca aaaggccaca	480
ctgggtgtgcc tggccacagg cttctacccc gaccacgtgg agctgagctg gtgggtgaat	540
gggaaggagg tgcacagtgg ggtcagcaca gacccgcagc ccctcaagga gcagcccgcc	600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcgccac cttctggcag	660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgatgag	720
tggacacaag atagggccaa acctgtcacc cagatcgtca gcgccgaggc ctggggtaga	780
gcagactgtg gcttcacctc cgagtcttac cagcaagggg tcctgtctgc caccatcctc	840
tatgagatct tgctagggaa ggccaccttg tatgccgtgc tggtcagtgc cctcgtctg	900
atggccatgg tcaagagaaa ggattccaga ggctga	936

<210> 155
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LINKER

<400> 155	
ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatcccggc	60
cct	63

<210> 156
 <211> 1818
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR847 FUSION

<400> 156	
atggaaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc tagggtgaac	60
agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc	120
atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt	180

agaggccttg tccacctaat ttttaatacgt tcaaatagaaa gagagaaaca cagtgggaaga	240
ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg	300
gcagcagaca ctgcttctta cttctgtgct acttttccta actttggaaa tgagaaatta	360
acctttggga ctggaacaag actcaccatc atacccaata tccagaaccc tgaccctgcc	420
gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt	480
gattctcaaa caaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact	540
gtgttggaca tgcgcagcat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa	600
tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc	660
cccagcccag aaagttcctg tgatgtcaag ctggtcgaga aaagctttga aacagatacg	720
aacctaaact ttcaaaacct gtcagtgatt gggttccgaa tcctcctcct gaaagtggcc	780
gggtttaatc tgctcatgac gctgcggctg tgggtccagcg gcagcggaga gggcagagga	840
agtcttctaa catgcggtga cgtggaggag aatcccggcc ctatgggcac aaggttgttc	900
ttctatgtgg ccctttgtct cctgtggaca ggacacatgg atgctggaat caccagagc	960
ccaagacaca aggtcacaga gacaggaaca ccagtgactc tgagatgtca ccagactgag	1020
aaccaccgct atatgtactg gtatcgacaa gaccgggggc atgggctgag gctgatccat	1080
tactcatatg gtgttaaaga tactgacaaa ggagaagtct cagatggcta tagtgtctcc	1140
agatcaaaga cagaggattt cctcctcact ctggagtccg ctaccagctc ccagacatct	1200
gtgtacttct gtgccatcag tgagtcggag cgggtactacg agcagtactt cgggccgggc	1260
accaggctca cggtcacaga ggacctgaaa aacgtgttcc caccgaggt cgctgtgttt	1320
gagccatcag aagcagagat ctcccacacc caaaaggcca cactgggtgtg cctggccaca	1380
ggcttctacc ccgaccacgt ggagctgagc tgggtgggtga atgggaagga ggtgcacagt	1440
ggggtcagca cagaccgca gccctcaag gagcagcccg ccctcaatga ctccagatac	1500
tgcttgagca gccgcctgag ggtctcggcc accttctggc agaacccccg caaccattc	1560
cgctgtcaag tccagttcta cgggctctcg gagaatgatg agtggacaca agatagggcc	1620
aaacctgtca ccagatcgt cagcgccgag gcctggggta gagcagactg tggcttcacc	1680

tccgagtctt accagcaagg ggtcctgtct gccaccatcc tctatgagat cttgctaggg	1740
aaggccacct tgtatgccgt gctggtcagt gccctcgtgc tgatggccat ggtcaagaga	1800
aaggattcca gaggctga	1818

<210> 157
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV4 CDR1

<400> 157	
aacattgcta caaatgatta t	21

<210> 158
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV4 CDR2

<400> 158	
ggatacaaga caaaa	15

<210> 159
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRAV4 CDR3

<400> 159	
ctcgtgggtg acttcaactc aaattccggg tatgcactca ac	42

<210> 160
 <211> 422
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR864 ALPHA CONSTANT DOMAIN

<400> 160
 atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 60
 ctgtctgcct attcaccgat tttgattctc aaacaaatgt gtcacaaagt aaggattctg 120
 atgtgtatat cacagacaaa actgtgttgg acatgcgcag catggacttc aagagcaaca 180
 gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc aacaacagca 240
 ttattccaga agacaccttc ttccccagcc cagaaaagttc ctgtgatgtc aagctggctg 300
 agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg attgggttcc 360
 gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg ctgtggtcca 420
 gc 422

<210> 161
 <211> 813
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR864 ALPHA CHAIN

<400> 161
 atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ccttgctaag 60
 accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc 120
 cacaacaaca ttgtacaaa tgattatatac acgtgggtacc aacagtttcc cagccaagga 180
 ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt 240
 atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttcctt gagcgacact 300
 gctgtgtact actgcctcgt gggtgacttc aactcaaatt ccgggtatgc actcaacttc 360
 ggcaaaggca cctcgctgtt gggtcacacc catatccaga accctgacct tgccgtgtac 420
 cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct 480
 caaacaatg tgtcacaag taaggattct gatgtgtata tcacagacaa aactgtgttg 540
 gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac 600
 tttgcatgtg caaacgcctt caacaacagc attattccag aagacacctt cttccccagc 660

ccagaaagtt cctgtgatgt caagctggtc gagaaaagct ttgaaacaga tacgaaccta	720
aactttcaaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccggggtt	780
aatctgctca tgacgctgcg gctgtgggtcc agc	813

<210> 162
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV7-2 CDR1

<400> 162	
tcaggtcata ctgcc	15

<210> 163
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV7-2 CDR2

<400> 163	
ttccaaggca acagtgc	18

<210> 164
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBV7-2 CDR3

<400> 164	
gccagcaagg tctatggcta cacc	24

<210> 165
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR864 BETA CONSTANT DOMAIN

<400> 165
gaggacctga acaagggtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag 60
atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttctt ccccgaccac 120
gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtcag cacggacccg 180
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg 240
agggtctcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc 300
tacgggctct cggagaatga tgagtggaca caagataggg ccaaaccctg caccagatc 360
gtcagcgccg aggcttgggg tagagcagac tgtggcttta cctcgggtgtc ctaccagcaa 420
ggggctcctgt ctgccaccat cctctatgag atcctgctag ggaaggccac cctgtatgct 480
gtgctgggtca gcgcccctgt gttgatggcc atggtcaaga gaaaggattt c 531

<210> 166
<211> 921
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR864 BETA CHAIN

<400> 166
atgggcacca ggctcctctt ctgggtggcc ttctgtctcc tgggggcata tcacacagga 60
gctggagtct cccagtcccc cagtaacaag gtcacagaga agggaaaagga tgtagagctc 120
agggtgtgatc caatttcagg tcatactgcc ctttactgggt accgacagag gctggggcag 180
ggcctggagt ttttaattta cttccaaggc aacagtgcac cagacaaatc agggctgccc 240
agtgatcgct tctctgcaga gaggactggg gaatccgtct ccaactctgac gatccagcgc 300
acacagcagg aggactcggc cgtgtatctc tgtgccagca aggtctatgg ctacaccttc 360
ggttcgggga ccaggttaac cgttgtagag gacctgaaca aggtgttccc acccgaggtc 420
gctgtgtttg agccatcaga agcagagatc tcccacaccc aaaaggccac actggtgtgc 480
ctggccacag gcttcttccc cgaccacgtg gagctgagct ggtgggtgaa tgggaaggag 540
gtgcacagtg gggtcagcac ggacccgcag cccctcaagg agcagcccg cctcaatgac 600

tccagatact gcctgagcag ccgcctgagg gtctcggcca ctttctggca gaacccccgc	660
aaccacttcc gctgtcaagt ccagttctac gggctctcgg agaatgatga gtggacacaa	720
gatagggcca aaccggtcac ccagatcgtc agcgccgagg cctggggtag agcagactgt	780
ggctttacct cgggtgtccta ccagcaaggg gtctgtctg ccaccatcct ctatgagatc	840
ctgctaggga aggccaccct gtatgctgtg ctggtcagcg cccttggtt gatggccatg	900
gtcaagagaa aggatttctg a	921

<210> 167
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LINKER

<400> 167	
ggcagcggag agggcagagg aagtcttcta acatgcggtg acgtggagga gaatccccgc	60
cct	63

<210> 168
 <211> 1797
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR864 FUSION

<400> 168	
atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ctttgctaag	60
accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc	120
cacaacaaca ttgctacaaa tgattatatc acgtggtacc aacagtttcc cagccaagga	180
ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt	240
atccctgccg acagaaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact	300
gctgtgtact actgcctcgt gggtgacttc aactcaaatt ccgggtatgc actcaacttc	360
ggcaaaggca cctcgtgtgt ggtcacaccc catatccaga accctgaccc tgccgtgtac	420

cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct	480
caaacaaatg tgtcacaaag taaggattct gatgtgtata tcacagacaa aactgtgttg	540
gacatgcgca gcatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac	600
tttgcattgtg caaacgcctt caacaacagc attattccag aagacacctt cttccccagc	660
ccagaaaagt cctgtgatgt caagctggtc gagaaaagct ttgaaacaga tacgaaccta	720
aactttcaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt	780
aatctgctca tgacgctgcg gctgtgggtcc agcggcagcg gagagggcag aggaagtctt	840
ctaacatgcg gtgacgtgga ggagaatccc ggccctatgg gcaccaggct cctcttctgg	900
gtggccttct gtctcctggg ggcatatcac acaggagctg gagtctccca gtccccagt	960
aacaaggtca cagagaaggg aaaggatgta gagctcaggt gtgatccaat ttcaggatcat	1020
actgcccttt actggtaccg acagaggctg gggcagggcc tggagttttt aatttacttc	1080
caaggcaaca gtgcaccaga caaatcaggg ctgcccagtg atcgcttctc tgcagagagg	1140
actggggaat cagtctccac tctgacgac cagcgcacac agcaggagga ctcggccgtg	1200
tatctctgtg ccagcaaggt ctatggctac accttcggtt cggggaccag gttaaccgtt	1260
gtagaggacc tgaacaaggt gttcccaccc gaggtcgctg tgtttgagcc atcagaagca	1320
gagatctccc acacccaaaa ggccacactg gtgtgcctgg ccacaggctt cttccccgac	1380
cacgtggagc tgagctgggt ggtgaatggg aaggagggtgc acagtgggggt cagcacggac	1440
ccgcagcccc tcaaggagca gcccgcctc aatgactcca gatactgcct gagcagccgc	1500
ctgagggtct cggccacctt ctggcagaac ccccgcaacc acttccgctg tcaagtccag	1560
ttctacgggc tctcggagaa tgatgagtgg acacaagata gggccaaacc cgtcaccag	1620
atcgctcagcg ccgaggcctg gggtagagca gactgtggct ttacctcggt gtcctaccag	1680
caaggggtcc tgtctgccac catcctctat gagatcctgc tagggaaggc caccctgtat	1740
gctgtgctgg tcagcgccct tgtgttgatg gccatgggtca agagaaagga tttctga	1797

<210> 169

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV17 VARIABLE DOMAIN

<400> 169

Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly
1 5 10 15

Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu
20 25 30

Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu
35 40 45

Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr
50 55 60

Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg
65 70 75 80

Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
85 90

<210> 170

<211> 96

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV11-2 VARIABLE DOMAIN

<400> 170

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

<210> 171

<211> 96

<212> PRT

<213> Artificial Sequence

<220>

<223> TRAV19 VARIABLE DOMAIN

<400> 171

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 Glu
 85 90 95

<210> 172

<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV9 VARIABLE DOMAIN

<400> 172

Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr Ala Thr Gly
1 5 10 15

Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp Leu Ser Val
20 25 30

Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile Gln
35 40 45

Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe
50 55 60

Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser
65 70 75 80

Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser Ser Val
85 90 95

<210> 173
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV17 VARIABLE

<400> 173

Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly
1 5 10 15

Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu
20 25 30

Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu
35 40 45

Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr
50 55 60

Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg
65 70 75 80

Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Phe
85 90

<210> 174

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> TRBV10-3 VARIABLE

<400> 174

Asp Ala Gly Ile Thr Gln Ser Pro Arg His Lys Val Thr Glu Thr Gly
1 5 10 15

Thr Pro Val Thr Leu Arg Cys His Gln Thr Glu Asn His Arg Tyr Met
20 25 30

Tyr Trp Tyr Arg Gln Asp Pro Gly His Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Tyr Gly Val Lys Asp Thr Asp Lys Gly Glu Val Ser Asp Gly Tyr
50 55 60

Ser Val Ser Arg Ser Lys Thr Glu Asp Phe Leu Leu Thr Leu Glu Ser
65 70 75 80

Ala Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Ile Ser Glu
85 90 95

<210> 175
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> TRAV4 VARIABLE

<400> 175

Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly Gln
1 5 10 15

Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp Tyr
20 25 30

Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile Ile
35 40 45

Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe Ile
50 55 60

Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser Leu
65 70 75 80

Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp
85 90

<210> 176
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBV7-2 VARIABLE

<400> 176

Gly Ala Gly Val Ser Gln Ser Pro Ser Asn Lys Val Thr Glu Lys Gly
1 5 10 15

Lys Asp Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His Thr Ala Leu

20

25

30

Tyr Trp Tyr Arg Gln Arg Leu Gly Gln Gly Leu Glu Phe Leu Ile Tyr
35 40 45

Phe Gln Gly Asn Ser Ala Pro Asp Lys Ser Gly Leu Pro Ser Asp Arg
50 55 60

Phe Ser Ala Glu Arg Thr Gly Glu Ser Val Ser Thr Leu Thr Ile Gln
65 70 75 80

Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Lys
85 90 95

<210> 177
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS

<400> 177

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

Ser Ala Leu Thr Ile Gln Leu Ile
20

<210> 178
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<400> 178

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

Ala Leu Thr Ile Gln Leu Ile
20

<210> 179
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 179

Xaa Gly Val Gly Lys Ser Ala Leu Thr Ile
1 5 10

<210> 180
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<400> 180

Ala Xaa Gly Val Gly Lys Ser Ala Leu Thr
1 5 10

<210> 181
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 181

Gly Ala Xaa Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 182
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 182

Val Gly Ala Xaa Gly Val Gly Lys Ser Ala
1 5 10

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 183

Val Val Gly Ala Xaa Gly Val Gly Lys Ser
1 5 10

<210> 184
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 184

Val Val Val Gly Ala Xaa Gly Val Gly Lys
1 5 10

<210> 185
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 185

Leu Val Val Val Gly Ala Xaa Gly Val Gly
1 5 10

<210> 186
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<400> 186

Lys Leu Val Val Val Gly Ala Xaa Gly Val
1 5 10

<210> 187
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 187

Tyr Lys Leu Val Val Val Gly Ala Xaa Gly
1 5 10

<210> 188
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> RAS G12 Mutated Fragment

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 188

Glu Tyr Lys Leu Val Val Val Gly Ala Xaa
1 5 10

<210> 189
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> KLV_G

<400> 189

Lys Leu Val Val Val Gly Ala Gly Gly Val
1 5 10

<210> 190
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VV_G

<400> 190

Val Val Gly Ala Gly Gly Val Gly Lys
1 5

<210> 191
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VVV_G

<400> 191

Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10

<210> 192
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> GA_G

<400> 192

Gly Ala Gly Gly Val Gly Lys Ser Ala Leu
1 5 10

<210> 193

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> WT

<400> 193

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 194

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> G12A

<400> 194

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 195

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> G12C

<400> 195

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Cys	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile	Gln
			20					25

<210> 196

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> G12D

<400> 196

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Asp	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile	Gln
			20					25

<210> 197

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> G12R

<400> 197

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Arg	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile	Gln
			20					25

<210> 198
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> G12S

<400> 198

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 199
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> G12V

<400> 199

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 200
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> CMV pp65- NLV (A*02:01)

<400> 200

Gly Ile Leu Ala Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly
1 5 10 15

Gln Asn Leu Lys
20

<210> 201
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Influenza A NP - ILR (A*03:01)

<400> 201

Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His Lys Ser Cys
1 5 10 15

Leu Pro Ala Cys
20

<210> 202
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> EBV EBNA4 - IVT (A*11:01)

<400> 202

Lys Lys Cys Arg Ala Ile Val Thr Asp Phe Ser Val Ile Lys Ala Ile
1 5 10 15

Glu Glu Glu His
20

<210> 203
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> CMV pp65 - TPR (B*07:02)

<400> 203

Thr	Thr	Glu	Arg	Lys	Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala
1				5					10					15	

Gly	Ala	Ser	Thr
			20