

SEQUENCE LISTING

<110> Fred Hutchinson Cancer Research Center
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<120> HIGH AFFINITY MAGE-A1 SPECIFIC TCRS AND USES THEREOF

<130> 360056.446W0

<140> PCT

<141> 2018-03-15

<150> US 62/471,956

<151> 2017-03-15

<160> 148

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$ 1

<211> 133

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic sequence beta chain variable domain
(amino acid)

$\langle 400 \rangle$ 1

[illegible]

130

<210> 2

<211> 177

<212> PRT

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<220>

<223> Synthetic sequence beta chain constant domain
(amino acid)

<400> 2

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Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1              5              10              15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
 20              25              30
Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35              40              45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
 50              55              60
Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
 65              70              75              80
Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
 85              90              95
Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100              105              110
Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115              120              125
Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
130              135              140
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145              150              155              160
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165              170              175
Phe
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<210> 3

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence alpha chain variable domain
(amino acid)

<400> 3

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

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

<210> 4

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence alpha chain constant domain
(amino acid)

<400> 4

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

<210> 5

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence beta chain variable domain

(amino acid)

<400> 5

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	Gln	Gly	Asp	Glu	Lys	Leu	Phe	Phe	Gly	Ser	Gly	Thr	Gln	Leu	Ser
		115					120						125		
Val	Leu														
	130														

<210> 6

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence beta chain constant domain
(amino acid)

<400> 6

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

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
 145 150 155 160
 Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
 165 170 175
 Phe

<210> 7
 <211> 130
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 <213> Artificial Sequence

<220>
 <223> Synthetic sequence alpha chain variable domain
 (amino acid)

<400> 7
 Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
 1 5 10 15
 Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
 20 25 30
 Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
 35 40 45
 Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
 50 55 60
 Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
 65 70 75 80
 Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
 85 90 95
 Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
 100 105 110
 Ser Ile Asp Ala Arg Leu Met Phe Gly Asp Gly Thr Gln Leu Val Val
 115 120 125
 Lys Pro
 130

<210> 8
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence alpha chain constant domain
 (amino acid)

<400> 8
 Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1 5 10 15
 Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
 20 25 30

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

<210> 9

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence beta chain variable domain
(amino acid)

<400> 9

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

<210> 10

<211> 178

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence beta chain constant domain
(amino acid)

<400> 10

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Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
 1           5           10           15
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
      20           25           30
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
      35           40           45
Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu
      50           55           60
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
      65           70           75           80
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
      85           90           95
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
      100          105          110
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
      115          120          125
Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
      130          135          140
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
      145          150          155          160
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
      165          170          175
Arg Gly
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<210> 11

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence slpha chain variable domain
(amino acid)

<400> 11

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

		100						105					110				
Ala	Phe	Met	Lys	Ser	His	Ser	Gly	Tyr	Ile	Phe	Gly	Thr	Gly	Thr	Arg		
		115					120						125				
Leu	Lys	Val	Leu	Ala													
		130															

<210> 12
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence alpha chain constant domain
 (amino acid)

<400> 12																	
Asp	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys		
1				5					10					15			
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr		
			20					25					30				
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys		
			35				40					45					
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala		
	50					55					60						
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser		
65					70					75				80			
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp		
				85					90					95			
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe		
			100					105					110				
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala		
		115					120						125				
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser					
	130					135					140						

<210> 13
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence beta chain variable domain
 (amino acid)

<400> 13																	
Met	Leu	Cys	Ser	Leu	Leu	Ala	Leu	Leu	Leu	Gly	Thr	Phe	Phe	Gly	Val		
1				5					10					15			
Arg	Ser	Gln	Thr	Ile	His	Gln	Trp	Pro	Ala	Thr	Leu	Val	Gln	Pro	Val		
			20					25					30				
Gly	Ser	Pro	Leu	Ser	Leu	Glu	Cys	Thr	Val	Glu	Gly	Thr	Ser	Asn	Pro		

<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence alpha chain variable domain
(amino acid)

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

<210> 16
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence alpha chain constant domain
(amino acid)

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

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

<210> 17
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence beta chain variable domain
 (amino acid)

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

Leu

<210> 18
 <211> 178
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence beta chain constant domain
 (amino acid)

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

<210> 20
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence alpha chain constant domain
(amino acid)

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

<210> 21
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 beta chain CDR1 domain
(amino acid)

<400> 21
Met Asp His Glu Asn
1 5

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain CDR2 domain
(amino acid)

<400> 22

Ser Tyr Asp Val Lys Met

1 5

<210> 23

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain CDR3 domain
(amino acid)

<400> 23

Cys Ala Ser Asn Asn Arg Asp Ser Tyr Asn Ser Pro Leu His Phe

1 5 10 15

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 alpha chain CDR1 domain
(amino acid)

<400> 24

Tyr Ser Gly Ser Pro Glu

1 5

<210> 25

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 alpha chain CDR2 domain
(amino acid)

<400> 25

His Ile Ser Arg

1

<210> 26
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 alpha chain CDR3 domain
(amino acid)

<400> 26
Cys Ala Leu Arg Ser Gly Gly Tyr Gln Lys Val Thr Phe
1 5 10

<210> 27
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b beta chain CDR1 domain
(amino acid)

<400> 27
Ser Gly Asp Leu Ser
1 5

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b beta chain CDR2 domain
(amino acid)

<400> 28
Tyr Tyr Asn Gly Glu Glu
1 5

<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b beta chain CDR3 domain

(amino acid)

<400> 29

Cys Ala Ser Ser Gln Gly Asp Glu Lys Leu Phe Phe
1 5 10

<210> 30

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain CDR1 domain
(amino acid)

<400> 30

Asp Ser Ser Ser Thr Tyr
1 5

<210> 31

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain CDR2 domain
(amino acid)

<400> 31

Ile Phe Ser Asn Met Asp Met
1 5

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain CDR3 domain
(amino acid)

<400> 32

Cys Ala Glu Ser Ile Asp Ala Arg Leu Met Phe
1 5 10

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain CDR1 domain
(amino acid)

<400> 33

Gly Thr Ser Asn Pro Asn
1 5

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain CDR2 domain
(amino acid)

<400> 34

Ser Val Gly Ile Gly
1 5

<210> 35

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain CDR3 domain
(amino acid)

<400> 35

Cys Ala Leu Ser Thr Ser Tyr Glu Gln Tyr Phe
1 5 10

<210> 36

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR1 domain
(amino acid)

<400> 36

Thr Ser Glu Asn Asn Tyr Tyr

1 5

<210> 37

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR2 domain
(amino acid)

<400> 37

Gln Glu Ala Tyr Lys Gln Gln Asn

1 5

<210> 38

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR3 domain
(amino acid)

<400> 38

Cys Ala Phe Met Lys Ser His Ser Gly Tyr Ile Phe

1 5 10

<210> 39

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain CDR1 domain
(amino acid)

<400> 39

Gly Thr Ser Asn Pro Asn

1 5

<210> 40

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain CDR2 domain
(amino acid)

<400> 40

Ser Val Gly Ile Gly

1 5

<210> 41

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain CDR3
domain (amino acid)

<400> 41

Cys Ala Trp Ser Val Ala Val Asn Thr Glu Ala Phe Phe

1 5 10

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b alpha chain CDR1
domain (amino acid)

<400> 42

Thr Ser Glu Asn Asn Tyr Tyr

1 5

<210> 43

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b alpha chain CDR2
domain (amino acid)

<400> 43

Gln Glu Ala Tyr Lys Gln Gln Asn

1 5

<210> 44

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

<220>
<223> Synthetic sequence 17804.1b alpha chain CDR3
domain (amino acid)

<400> 44
Cys Ala Phe Gly Glu Gly Ala Arg Leu Met Phe
1 5 10

<210> 45
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 beta chain CDR1 domain
(amino acid)

<400> 45
Gly Thr Ser Asn Pro Asn
1 5

<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 beta chain CDR2 domain
(amino acid)

<400> 46
Ser Ile Gly Ile Asp
1 5

<210> 47
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 beta chain CDR3 domain
(amino acid)

<400> 47

Cys Ala Trp Ser Val Thr Arg His Asn Glu Gln Phe Phe
1 5 10

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 alpha chain CDR1 domain
(amino acid)

<400> 48

Lys Thr Leu Tyr Gly
1 5

<210> 49

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 alpha chain CDR2 domain
(amino acid)

<400> 49

Leu Gln Lys Gly Gly Glu Glu
1 5

<210> 50

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 alpha chain CDR3 domain
(amino acid)

<400> 50

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

<210> 51

<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence 18648.2 alpha chain CDR3 domain
(amino acid)

<400> 51
Cys Ala Leu Arg Gly Leu Asn Tyr Gly Gln Asn Phe Val Phe
1 5 10

<210> 52
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 beta chain variable
domain

<400> 52
atgggaatca ggctcctctg tcgtgtggcc ttttgtttcc tggctgtagg cctcgtagat 60
gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg 120
gaatgtgtcc aggatatgga ccatgaaaat atgttctggt atcgacaaga cccagggtctg 180
gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct 240
gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtccgcc 300
agcaccaacc agacatctat gtacctctgc gccagcaaca acagagacag ctacaacagc 360
cccctccact ttgggaacgg gaccaggctc actgtgacg 399

<210> 53
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 beta chain constant
domain (Native NA)

<400> 53
gaggacctga acaaagtgtt cccccagag gtggccgtgt tcgagccttc tgaggccgag 60
atcagccaca cccagaaagc caccctcgtg tgcctggcca ccggcttttt ccccgaccac 120
gtggaactgt cttggtgggt caacggcaaa gaggtgcact ccggcgtgtg caccgatccc 180
cagcctctga aagaacagcc cgccctgaac gacagccggt actgcctgtc cagcagactg 240
agagtgtccg ccaccttctg gcagaacccc cggaaccact tcagatgcca ggtgcagttc 300
tacggcctga gcgagaacga cgagtggacc caggacagag ccaagcccgt gacacagatc 360
gtgtctgccg aagcctgggg cagagccgat tgcggcttta cctccgtgtc ctatcagcag 420
ggcgtgtctga gcgccaccat cctgtacgag atcctgctgg gcaaggccac actgtacgcc 480
gtgctggtgt ctgccctggt gctgatggcc atggtcaagc ggaaggactt c 531

<210> 54

<211> 384
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 alpha chain variable
domain (Native NA)

<400> 54
atgaagccca ccctcatctc agtgcttgtg ataatatatta tactcagagg aacaagagcc 60
cagagagtga ctcagcccga gaagctcctc tctgtcttta aaggggcccc agtggagctg 120
aagtgcaact attcctattc tgggagtcct gaactcttct ggtatgtcca gtactccaga 180
caacgcctcc agttactctt gagacacatc tctagagaga gcatcaaagg cttcactgct 240
gaccttaaca aaggcgagac atctttccac ctgaagaaac catttgctca agaggaagac 300
tcagccatgt attactgcgc cctgagaagc ggccggctacc agaagggtgac ctttggaact 360
ggaacaaagc tccaagtcac ccca 384

<210> 55
<211> 426
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 alpha chain constant
domain (Native NA)

<400> 55
gatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 60
tctgtctgcc tattcaccga ttttgattct caaacaatg tgtcacaaag taaggattct 120
gatgtgtata tcacagacaa atgtgtgcta gacatgaggt ctatggactt caagagcaac 180
agtgtgtgg cctggagcaa caaatctgac tttgcatgtg caaacgcctt caacaacagc 240
attattccag aagacacctt cttccccagc ccagaaaagt cctgtgatgt caagctggtc 300
gagaaaaagct ttgaaacaga tacgaaccta aactttcaaa acctgtcagt gattgggttc 360
cgaatcctcc tcctgaaagt ggccgggttt aatctgctca tgacgctgcg gctgtgggtcc 420
agctga 426

<210> 56
<211> 399
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain variable
domain (Codon-optimized NA)

<400> 56
atgggaatta gactgctgtg ccgggtggcc ttctgcttcc tggctgtggg actggtggac 60
gtgaaagtga cccagagcag cagatacctc gtgaagcgga ccggcgagaa ggtgttcctg 120
gaatgcgtgc aggacatgga ccacgagaat atgttctggt acagacagga ccccggcctg 180
ggcctgcggc tgatctactt cagctacgac gtgaagatga aggaaaaggg cgacatcccc 240

gagggctaca	gcgtgtccag	agagaagaaa	gagcggttca	gcctgaccc	ggaaagcgcc	300
agcaccaacc	agaccagcat	gtacctgtgc	gcctccaaca	accgggacag	ctacaacagc	360
cccctgcact	tcggcaacgg	caccagactg	accgtgacc			399

<210> 57

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain constant domain (Codon-optimized NA)

<400> 57

gaggacctga	acaaagtgtt	ccccccagag	gtggccgtgt	tcgagccttc	tgaggccgag	60
atcagccaca	cccagaaaagc	caccctcgtg	tgcttgccca	ccggcttttt	ccccgaccac	120
gtggaactgt	cttggtgggt	caacggcaaaa	gaggtgcact	ccggcgtgtg	caccgatccc	180
cagcctctga	aagaacagcc	cgccctgaac	gacagccggt	actgcctgtc	cagcagactg	240
agagtgtccg	ccaccttctg	gcagaacccc	cggaaccact	tcagatgcca	ggtgcagtgc	300
tacggcctga	gcgagaacga	cgagtggacc	caggacagag	ccaagcccgt	gacacagatc	360
gtgtctgccg	aagcctgggg	cagagccgat	tgccgcttta	cctccgtgtc	ctatcagcag	420
ggcgtgctga	gcgccaccat	cctgtacgag	atcctgctgg	gcaaggccac	actgtacgcc	480
gtgctggtgt	ctgccctggt	gctgatggcc	atggtcaagc	ggaaggactt	c	531

<210> 58

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain variable domain (Native NA)

<400> 58

atgaagacat	ttgctggatt	ttcgttcctg	tttttgtggc	tgacgtgga	ctgtatgagt	60
agaggagagg	atgtggagca	gagtcctttc	ctgagtgtcc	gagagggaga	cagctccgtt	120
ataaaactgca	cttacacaga	cagctcctcc	acctacttat	actggtataa	gcaagaacct	180
ggagcagggtc	tccagttgct	gacgtatatt	ttttcaaata	tgacatgaa	acaagaccaa	240
agactcactg	ttctattgaa	taaaaaggat	aaacatctgt	ctctgcgcac	tgacagacac	300
cagactggggg	actcagctat	ctacttctgt	gcagagagta	tcgatgccag	actcatgttt	360
ggagatggaa	ctcagctggt	ggtgaagccc				390

<210> 59

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 alpha chain constant

domain (Codon-optimized NA)

<400> 59

gacatccaga	accccgaccc	tgcaagtgtac	cagctgcggg	acagcaagag	cagcgacaag	60
agcgtgtgcc	tggtcaccga	cttcgacagc	cagaccaacg	tgtcccagag	caaggacagc	120
gacgtgtaca	tcaccgataa	gtgcgtgctg	gacatgcgga	gcatggactt	caagagcaac	180
agcgccgtgg	cctgggtccaa	caagagcgac	ttcgcctgcg	ccaacgcctt	caacaacagc	240
attatccccg	aggacacatt	cttcccaagc	cccagagagca	gctgcgacgt	gaagctgggtg	300
gaaaagagct	tcgagacaga	caccaacctg	aacttccaga	acctcagcgt	gatcggcttc	360
cggatcctgc	tgctgaaggt	ggccggcttc	aacctgctga	tgaccctgcg	gctgtgggtcc	420
agctga						426

<210> 60

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b beta chain variable
domain (Native NA)

<400> 60

atgggcttca	ggctcctctg	ctgtgtggcc	ttttgtctcc	tgggagcagg	cccagtggat	60
tctggagtca	cacaaacccc	aaagcacctg	atcacagcaa	ctggacagcg	agtgcgctg	120
agatgctccc	ctaggtctgg	agacctctct	gtgtactggg	accaacagag	cctggaccag	180
ggcctccagt	tcctcattca	gtattataat	ggagaagaga	gagcaaaaagg	aaacattctt	240
gaacgattct	ccgcacaaca	gttccctgac	ttgcactctg	aactaaacct	gagctctctg	300
gagctggggg	actcagcttt	gtatttctgt	gccagcagcc	aggggggatga	aaaactgttt	360
tttggcagtg	gaaccagct	ctctgtcttg				390

<210> 61

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b beta chain constant
domain (Native NA)

<400> 61

gaggacctga	acaaagtgtt	ccccccagag	gtggccgtgt	tcgagccttc	tgaggccgag	60
atcagccaca	cccagaaagc	caccctcgtg	tgcttgccca	ccggcttttt	ccccgaccac	120
gtggaactgt	cttgggtggg	caacggcaaa	gagggtgact	ccggcgtgtg	caccgatccc	180
cagcctctga	aagaacagcc	cgccctgaac	gacagccggg	actgcctgtc	cagcagactg	240
agagtgtccg	ccaccttctg	gcagaacccc	cgggaaccact	tcagatgcca	ggtgcagttc	300
tacggcctga	gcgagaacga	cgagtggacc	caggacagag	ccaagcccgt	gacacagatc	360
gtgtctgccg	aagcctgggg	cagagccgat	tgcggtctta	cctccgtgtc	ctatcagcag	420
ggcgtgtctga	gcgccaccat	cctgtacgag	atcctgctgg	gcaaggccac	actgtacgcc	480
gtgctggtgt	ctgccctggg	gctgatggcc	atggtcaagc	ggaaggactt	c	531

<210> 62
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b alpha chain variable
domain (Native NA)

<400> 62
atgaagacat ttgctggatt ttcgttcctg tttttgtggc tgcagctgga ctgtatgagt 60
agaggagagg atgtggagca gagtcttttc ctgagtgtcc gagagggaga cagctccggt 120
ataaactgca cttacacaga cagctcctcc acctacttat actggtataa gcaagaacct 180
ggagcaggtc tccagttgct gacgtatatt ttttcaaata tggacatgaa acaagaccaa 240
agactcactg ttctattgaa taaaaaggat aaacatctgt ctctgcgcac tgcagacacc 300
cagactgggg actcagctat ctacttctgt gcagagagta tcgatgccag actcatgttt 360
ggagatggaa ctcagctggg ggtgaagccc 390

<210> 63
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b alpha chain constant
domain (Native NA)

<400> 63
gatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 60
tctgtctgcc tattcaccga ttttgattct caaacaaatg tgtcacaaag taaggattct 120
gatgtgtata tcacagacaa atgtgtgcta gacatgaggt ctatggactt caagagcaac 180
agtgtgtgg cctggagcaa caaatctgac tttgcatgtg caaacgcctt caacaacagc 240
attattccag aagacacctt cttccccagc ccagaaaagt cctgtgatgt caagctggtc 300
gagaaaagct ttgaaacaga tacgaacctt aactttcaaa acctgtcagt gattgggttc 360
cgaatcctcc tcctgaaagt ggccgggttt aatctgctca tgacgctgcg gctgtgggtcc 420
agctga 426

<210> 64
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b beta chain variable
domain(Codon-optimized NA)

<400> 64
atgggcttca gactgctgtg ctgcgtggcc ttctgtctgc tgggagccgg ccctgtggat 60
agcggcgtga cacagacacc caagcacctg atcaccgcca ccggccagcg cgtgacactg 120
agatgtagcc ctagaagcgg cgacctgagc gtgtactggg atcagcagag cctggaccag 180

ggcctgcagt	tcctgatcca	gtactacaac	ggcgaggaac	gggccaaggg	caacatcctg	240
gaacggttca	gcgcccagca	gttccccgat	ctgcacagcg	agctgaacct	gagcagcctg	300
gaactgggcg	acagcgccct	gtactttctgt	gccagttctc	agggcgacga	gaagctgttc	360
ttcggcagcg	gcacacagct	gagcgtgctg				390

<210> 65

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b beta chain constant domain (Codon-optimized NA)

<400> 65

gaagatctga	acaagggtgtt	ccccccagag	gtggccgtgt	tcgagccttc	tgaggccgag	60
atcagccaca	cccagaaaagc	caccctcgtg	tgcctggcca	ccggcttttt	ccccgaccac	120
gtggaactgt	cttggtgggt	caacggcaaa	gagggtgact	ccggcgtgtg	caccgatccc	180
cagcctctga	aagaacagcc	cgccctgaac	gacagccggt	actgcctgtc	cagcagactg	240
agagtgtccg	ccaccttctg	gcagaacccc	cgggaaccact	tcagatgcca	ggtgcagttc	300
tacggcctga	gcgagaacga	cgagtggacc	caggacagag	ccaagcccgt	gacccagatc	360
gtgtctgccg	aagcctgggg	cagagccgat	tgcggcttta	ccagcgtgtc	ctatcagcag	420
ggcgtgctga	gcgccaccat	cctgtacgag	atcctgctgg	gcaaggccac	cctgtacgcc	480
gtgctggtgt	ctgccctggt	gctgatggcc	atggtcaagc	ggaaggactt	c	531

<210> 66

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain variable domain (Codon-optimized NA)

<400> 66

atgaagacct	tcgccggctt	cagcttcctg	ttcctgtggc	tgcagctgga	ctgcatgagc	60
agaggcgagg	acgtggaaca	gagcctgttt	ctgtccgtgc	gcgagggcga	ctccagcgtg	120
atcaattgca	cctacaccga	cagcagcagc	acctacctgt	attggtacaa	gcaggaaccc	180
ggcgctggcc	tgcagctgct	gacctacatc	ttcagcaaca	tggacatgaa	gcaggaccag	240
cggctgaccg	tgctgctgaa	caagaaggat	aagcacctgt	ccctgcggat	cgccgatacc	300
cagacaggcg	actccgccat	ctacttttgc	gccgagagca	tcgacgcccg	gctgatgttt	360
ggagatggca	cccagctggt	cgtgaagccc				390

<210> 67

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.2b alpha chain constant

domain (Codon-optimized NA)

<400> 67

gacatccaga	accccgaccc	tgcagtgtac	cagctgcggg	acagcaagag	cagcgacaag	60
agcgtgtgcc	tggtcaccga	cttcgacagc	cagaccaacg	tgtcccagag	caaggacagc	120
gacgtgtaca	tcaccgataa	gtgcgtgctg	gacatgcgga	gcatggactt	caagagcaac	180
agcgccgtgg	cctgggtccaa	caagagcgac	ttcgcctgcg	ccaacgcctt	caacaacagc	240
attatccccg	aggacacatt	cttcccaagc	cccagagagca	gctgcgacgt	gaagctgggtg	300
gaaaagagct	tcgagacaga	caccaacctg	aacttccaga	acctcagcgt	gatcggcttc	360
cggatcctgc	tgctgaaggt	ggccggcttc	aacctgctga	tgaccctgcg	gctgtgggtcc	420
agctga						426

<210> 68

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain variable
domain (Native NA)

<400> 68

atgctctgct	ctctccttgc	ccttctcctg	ggcactttct	ttggggtcag	atctcagact	60
attcatcaat	ggccagcgac	cctgggtgcag	cctgtgggca	gcccgccttc	tctggagtgc	120
actgtggagg	gaacatcaaa	ccccaaccta	tactggtacc	gacaggctgc	aggcaggggc	180
ctccagctgc	tcttctactc	cgttgggtatt	ggccagatca	gctctgaggt	gccccagaat	240
ctctcagcct	ccagacccca	ggaccggcag	ttcatcctga	gttctaagaa	gctccttctc	300
agtgactctg	gcttctatct	ctgcgccctg	agcaccagct	acgagcagta	cttcggggccg	360
ggcaccaggc	tcacggtcac	a				381

<210> 69

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain constant
domain (Native NA)

<400> 69

gacctgaaaa	acgtgttccc	acccgaggtc	gctgtgtttg	agccatcaga	agcagagatc	60
tcccacaccc	aaaaggccac	actggtgtgc	ctggccacag	gcttctaccc	cgaccacgtg	120
gagctgagct	ggtgggtgaa	tgggaaggag	gtgcacagtg	gggtctgcac	agacccgcag	180
cccctcaagg	agcagcccg	cctcaatgac	tccagatact	gcctgagcag	ccgcctgagg	240
gtctcggcca	ccttctggca	gaacccccgc	aaccacttcc	gctgtcaagt	ccagttctac	300
gggctctcgg	agaatgacga	gtggacccag	gatagggccca	aacctgtcac	ccagatcgtc	360
agcgccgagg	cctggggtag	agcagactgt	ggcttcacct	ccgagtctta	ccagcaaggg	420
gtcctgtctg	ccaccatcct	ctatgagatc	ttgctaggga	aggccacctt	gtatgccgtg	480
ctggctcagt	ccctcgtgct	gatggccatg	gtcaagagaa	aggattccag	aggctag	537

<210> 70
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 1388.3 alpha chain variable
 domain (Native NA)

<400> 70
 atgacacgag ttagcttgct gtgggcagtc gtggctctcca cctgtcttga atccggcatg 60
 gccagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gactgtgacc 120
 ctgagttgca catatgacac cagtgagaat aattattatt tggtctggta caagcagcct 180
 cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaacg 240
 gagaatcgtt tctctgtgaa cttccagaaa gcagccaaat ctttcagtct caagatctca 300
 gactcacagc tgggggacac tgcgatgtat ttctgtgctt tcatgaagtc ccactccgga 360
 tacatctttg gaacaggcac caggctgaag gttttagca 399

<210> 71
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 1388.3 alpha chain constant
 domain (Native NA)

<400> 71
 gatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 60
 tctgtctgcc tattcaccga ttttgattct caaacaatg tgtcacaaag taaggattct 120
 gatgtgtata tcacagacaa atgtgtgcta gacatgaggt ctatggactt caagagcaac 180
 agtgcgtgtg cctggagcaa caaatctgac tttgcatgtg caaacgcctt caacaacagc 240
 attattccag aagacacctt cttccccagc ccagaaaagt cctgtgatgt caagctggtc 300
 gagaaaagct ttgaaacaga tacgaaccta aactttcaaa acctgtcagt gattgggttc 360
 cgaatcctcc tcctgaaagt ggccgggttt aatctgtctca tgacgctgcg gctgtgggtcc 420
 agctga 426

<210> 72
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 1388.3 beta chain variable
 domain(Codon-optimized NA)

<400> 72
 atgctgtgtt ctctgctggc cctgctgctg ggcaccttct ttggagtgcg gagccagacc 60
 atccaccagt ggccctgtac actggtgcag cctgtgggca gccctctgag cctggaatgt 120
 accgtggaag gcaccagcaa cccaacctg tactggtaca gacaggccgc tggcagaggc 180

ctgcagctgc	tgttttacag	cgtgggcatc	ggccagatca	gcagcgaggt	gccccagaat	240
ctgagcgcca	gcagacccca	ggaccggcag	tttatcctga	gcagcaagaa	gctgtgtgtg	300
agcgacagcg	gcttctacct	gtgtgccctg	agcaccagct	acgagcagta	cttcggccca	360
ggcaccagac	tgaccgtgac	c				381

<210> 73

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 beta chain constant domain (Codon-optimized NA)

<400> 73

gacctgaaga	acgtgttccc	cccagagggtg	gccgtgttcg	agccttctga	ggccgagatc	60
agccacaccc	agaaagccac	cctcgtgtgt	ctggccaccg	gcttttaccc	cgaccacgtg	120
gaactgtctt	ggtgggtcaa	cggcaaagag	gtgcactccg	gcgtgtgcac	cgatccccag	180
cctctgaaag	aacagcccgc	cctgaacgac	agccggtact	gcctgtccag	cagactgaga	240
gtgtccgcca	ccttctggca	gaacccccgg	aaccacttca	gatgccagggt	gcagttctac	300
ggcctgagcg	agaacgacga	gtggacccag	gacagagcca	agcccgtgac	ccagatcgtg	360
tctgccgaag	cctggggcag	agccgattgc	ggctttacca	gcgagagcta	ccagcagggc	420
gtgctgtctg	ccaccatcct	gtacgagatc	ctgctgggaa	aggccaccct	gtacgccgtg	480
ctgggtgtctg	ccctggtgct	gatggccatg	gtcaagcgga	aggacagcag	aggc	534

<210> 74

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain variable domain (Codon-optimized NA)

<400> 74

atgacccggg	tgtcactgct	gtgggctgtg	gtgggtgtcca	cctgtctgga	aagcggcatg	60
gccagaccg	tgacacagtc	ccagcctgag	atgagcgtgc	aggaagccga	gacagtgacc	120
ctgagctgca	cctacgacac	ctccgagaac	aactactacc	tgttttggtg	caagcagccc	180
cccagccggc	agatgatcct	cgtgatcaga	caggaagcct	ataagcagca	gaacgccacc	240
gagaacagat	tcagcgtgaa	cttcagaaag	gccgccaaga	gcttttagcct	gaagatcagc	300
gacagccagc	tgggcgacac	cgccatgtac	ttttgcgctt	ttatgaagtc	ccacagcggc	360
tacatcttcg	gcaccggcac	acggctgaaa	gtgctggct			399

<210> 75

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain constant

domain (Codon-optimized NA)

<400> 75

gacatccaga	accccgaccc	tgcagtgtac	cagctgcggg	acagcaagag	cagcgacaag	60
agcgtgtgcc	tggtcaccga	cttcgacagc	cagaccaacg	tgtcccagag	caaggacagc	120
gacgtgtaca	tcaccgataa	gtgcgtgctg	gacatgcgga	gcatggactt	caagagcaac	180
agcggcgtgg	cctgggtccaa	caagagcgac	ttcgcctgcg	ccaacgcctt	caacaacagc	240
attatccccg	aggacacatt	cttcccaagc	cccagagagca	gctgcgacgt	gaagctgggtg	300
gaaaagagct	tcgagacaga	caccaacctg	aacttccaga	acctcagcgt	gatcggcttc	360
cggatcctgc	tgctgaaggt	ggccggcttc	aacctgctga	tgaccctgcg	gctgtgggtcc	420
agctga						426

<210> 76

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain variable domain (Native NA)

<400> 76

atgctctgct	ctctccttgc	ccttctcctg	ggcactttct	ttggggtcag	atctcagact	60
attcatcaat	ggccagcgac	cctgggtgcag	cctgtgggca	gcccgccttc	tctggagtgc	120
actgtggagg	gaacatcaaa	ccccaaccta	tactggtacc	gacaggctgc	aggcaggggc	180
ctccagctgc	tcttctactc	cgttgggtatt	ggccagatca	gctctgaggt	gccccagaat	240
ctctcagcct	ccagacccca	ggaccggcag	ttcatcctga	gttctaagaa	gctccttctc	300
agtgactctg	gcttctatct	ctgtgcctgg	agtgttgcgg	tgaacactga	agctttcttt	360
ggacaaggca	ccagactcac	agttgta				387

<210> 77

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain constant domain (Native NA)

<400> 77

gaggacctga	acaaagtgtt	ccccccagag	gtggccgtgt	tcgagccttc	tgaggccgag	60
atcagccaca	cccagaaagc	caccctcgtg	tgcttgccca	ccggcttttt	ccccgaccac	120
gtggaactgt	cttgggtgggt	caacggcaaa	gagggtgact	ccggcgtgtg	caccgatccc	180
cagcctctga	aagaacagcc	cgccctgaac	gacagccggt	actgcctgtc	cagcagactg	240
agagtgtccg	ccaccttctg	gcagaacccc	cggaaaccact	tcagatgcca	ggtgcagttc	300
tacggcctga	gcgagaacga	cgagtggacc	caggacagag	ccaagcccgt	gacacagatc	360
gtgtctgccg	aagcctgggg	cagagccgat	tgccggcttta	cctccgtgtc	ctatcagcag	420
ggcgtgtctga	gcgccaccat	cctgtacgag	atcctgctgg	gcaaggccac	actgtacgcc	480
gtgctgggtg	ctgccctgggt	gctgatggcc	atggtcaagc	ggaaggactt	c	531

<210> 78
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.1b alpha chain variable
domain (Native NA)

<400> 78
atgacacgag ttagcttgct gtgggcagtc gtggctctcca cctgtcttga atccggcatg 60
gccagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gactgtgacc 120
ctgagttgca catatgacac cagtgagaat aattattatt tggtctggta caagcagcct 180
cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaacg 240
gagaatcgtt tctctgtgaa cttccagaaa gcagccaaat ctttcagtct caagatctca 300
gactcacagc tgggggacac tgcgatgtat ttctgcgcct tcggcgaggg cgccagactc 360
atgtttggag atggaactca gctggtggtg aagccc 396

<210> 79
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.1b alpha chain constant
domain (Native NA)

<400> 79
gatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 60
tctgtctgcc tattcaccga ttttgattct caaacaaatg tgtcacaaag taaggattct 120
gatgtgtata tcacagacaa atgtgtgcta gacatgaggt ctatggactt caagagcaac 180
agtgtgtgg cctggagcaa caaatctgac tttgcatgtg caaacgcctt caacaacagc 240
attattccag aagacacctt cttccccagc ccagaaaagt cctgtgatgt caagctggtc 300
gagaaaagct ttgaaacaga tacgaaccta aactttcaaa acctgtcagt gattgggttc 360
cgaatcctcc tcctgaaagt ggccgggttt aatctgtctca tgacgctgcg gctgtgggtc 420
agctga 426

<210> 80
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.1b beta chain variable
domain (Codon-optimized NA)

<400> 80
atgctgtgtt ctctgctggc cctgctgctg ggcaccttct ttggagtgcg gagccagacc 60
atccaccagt ggctgtctac actggtgcag cctgtgggca gccctctgag cctggaatgt 120
accgtggaag gcaccagcaa cccaacctg tactggtaca gacaggccgc tggcagaggc 180

ctgcagctgc	tgttttacag	cgtgggcatc	ggccagatca	gcagcgaggt	gccccagaat	240
ctgagcgcca	gcagacccca	ggaccggcag	tttatcctga	gcagcaagaa	gctgctgctg	300
agcgacagcg	gcttctacct	gtgcgcttgg	agcgtggccg	tgaacaccga	ggcattcttt	360
gggcagggca	cccggctgac	cgtggtg				387

<210> 81

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b beta chain constant domain (Codon-optimized NA)

<400> 81

gaagatctga	acaagggtgtt	ccccccagag	gtggccgtgt	tcgagccttc	tgaggccgag	60
atcagccaca	cccagaaaagc	caccctcgtg	tgcctggcca	ccggcttttt	ccccgaccac	120
gtggaactgt	cttggtgggt	caacggcaaaa	gagggtgact	ccggcgtgtg	caccgatccc	180
cagcctctga	aagaacagcc	cgccctgaac	gacagccggt	actgcctgtc	cagcagactg	240
agagtgtccg	ccaccttctg	gcagaacccc	cgggaaccact	tcagatgcca	ggtgcagttc	300
tacggcctga	gcgagaacga	cgagtggacc	caggacagag	ccaagcccgt	gacccagatc	360
gtgtctgccg	aagcctgggg	cagagccgat	tgcggcttta	ccagcgtgtc	ctatcagcag	420
ggcgtgctgt	ctgccaccat	cctgtacgag	atcctgctgg	gaaaggccac	cctgtacgcc	480
gtgctggtgt	ctgccctggt	gctgatggcc	atggtcaagc	ggaaggactt	c	531

<210> 82

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b alpha chain variable domain (Codon-optimized NA)

<400> 82

atgaccagag	tgtctctgct	gtgggctgtg	gtggtgtcca	cctgtctgga	aagcggcatg	60
gccagaccg	tgacacagtc	ccagcctgag	atgagcgtgc	aggaagccga	gacagtgacc	120
ctgagctgca	cctacgacac	cagcgagaac	aactactacc	tgttttggtg	caagcagccc	180
cccagccggc	agatgatcct	cgtgatcaga	caggaagcct	ataagcagca	gaacgccacc	240
gagaacagat	tcagcgtgaa	cttcacagaag	gccgccaaga	gcttcagcct	gaagatcagc	300
gacagccagc	tgggcgacac	cgccatgtac	ttttgcgccct	ttggcgaggg	cgccagactg	360
atgtttggcg	acggaaccca	gctggtcgtg	aagccc			396

<210> 83

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.1b alpha chain constant

domain (Codon-optimized NA)

<400> 83

gacatccaga	accccgaccc	tgcagtgtac	cagctgcggg	acagcaagag	cagcgacaag	60
agcgtgtgcc	tgttcaccga	cttcgacagc	cagaccaacg	tgtcccagag	caaggacagc	120
gacgtgtaca	tcaccgataa	gtgcgtgctg	gacatgcgga	gcatggactt	caagagcaac	180
agcggcgtgg	cctgggtccaa	caagagcgac	ttcgcctgcg	ccaacgcctt	caacaacagc	240
attatccccg	aggacacatt	cttcccaagc	cccgagagca	gctgcgacgt	gaagctgggtg	300
gaaaagagct	tcgagacaga	caccaacctg	aacttccaga	acctcagcgt	gatcggcttc	360
cggatcctgc	tgctgaaggt	ggccggcttc	aacctgctga	tgaccctgcg	gctgtgggtcc	420
agctga						426

<210> 84

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 beta chain variable
domain (Native NA)

<400> 84

atgctctgct	ctctccttgc	ccttctcctg	ggcactttct	ttggggtcag	atctcagact	60
attcatcaat	ggccagcgac	cctgggtgcag	cctgtgggca	gcccgccttc	tctggagtgc	120
actgtggagg	gaacatcaaa	ccccaaccta	tactggtacc	gacaggctgc	aggcaggggc	180
ctccagctgc	tcttctactc	catttggtatt	gaccagatca	gctctgaggt	gccccagaat	240
ctctcagcct	ccagacccca	ggaccggcag	ttcattctga	gttctaagaa	gctcctcctc	300
agtgactctg	gcttctatct	ctgtgcctgg	agtgtaacca	ggcacaaatga	gcagttcttc	360
gggccaggga	cacggctcac	cgtgcta				387

<210> 85

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 beta chain constant
domain (Native NA)

<400> 85

gacctgaaaa	acgtgttccc	acccgaggtc	gctgtgtttg	agccatcaga	agcagagatc	60
tcccacaccc	aaaaggccac	actggtgtgc	ctggccacag	gcttctaccc	cgaccacgtg	120
gagctgagct	ggtgggtgaa	tgggaaggag	gtgcacagtg	gggtctgcac	agacccgcag	180
cccctcaagg	agcagcccg	cctcaatgac	tccagatact	gcctgagcag	ccgcctgagg	240
gtctcggcca	ccttctggca	gaacccccgc	aaccacttcc	gctgtcaagt	ccagttctac	300
gggctctcgg	agaatgacga	gtggacccag	gatagggccca	aacctgtcac	ccagatcgtc	360
agcggcgagg	cctggggtag	agcagactgt	ggcttcacct	ccgagtctta	ccagcaaggg	420
gtcctgtctg	ccaccatcct	ctatgagatc	ttgctaggga	aggccacctt	gtatgccgtg	480
ctggctcagt	ccctcgtgct	gatggccatg	gtcaagagaa	aggattccag	aggctag	537

<210> 86
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 alpha chain variable
domain (Native NA)

<400> 86
atgctgtgca gcctgctggc cctgctgctg ggcaccttct tcgagcccag aaccagccaa 60
gaactggagc agagtcctca gtccttgatc gtccaagagg gaaagaatct caccataaac 120
tgcacgtcat caaagacggt atatggctta tactgggtata agcaaaaagta tgggtgaagg 180
cttatcttct tgatgatgct acagaaagggt ggggaagaga aaagtcatga aaagataact 240
gccaaagttgg atgagaaaaa gcagcaaagt tccctgcata tcacagcctc ccagcccagc 300
catgcaggca tctacctctg tggagcagcc cctacatact cgaattatgg aggaagccaa 360
ggaaatctca tctttggaaa aggactaaa ctctctgtta aacca 405

<210> 87
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 alpha chain constant
domain (Native NA)

<400> 87
gatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 60
tctgtctgcc tattcaccga ttttgattct caaacaatg tgtcacaag taaggattct 120
gatgtgtata tcacagacaa atgtgtgcta gacatgagggt ctatggactt caagagcaac 180
agtgtgtgg cctggagcaa caaatctgac tttgcatgtg caaacgcctt caacaacagc 240
attattccag aagacacctt cttccccagc ccagaaaagtt cctgtgatgt caagctgggtc 300
gagaaaagct ttgaaacaga tacgaaccta aactttcaaa acctgtcagt gattgggttc 360
cgaatcctcc tcctgaaagt ggccgggttt aatctgtctca tgacgctgcg gctgtgggtcc 420
agctga 426

<210> 88
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17804.2 beta chain variable
domain(Codon-optimized NA)

<400> 88
atgctgtgtt ctctgctggc tctgctgctg ggcaccttct ttggagtgcg gagccagacc 60
atccaccagt ggctgtctac actggtgcag cctgtgggca gccctctgag cctggaatgt 120
accgtggaag gcaccagcaa cccaacctg tactggtaca gacaggccgc tggcagaggc 180

ctgcagctgc	tgttttacag	catcggcatc	gaccagatca	gcagcgaggt	gccccagaac	240
ctgagcgcca	gcagacccca	ggaccggcag	tttatcctga	gcagcaagaa	gctgctgctg	300
agcgacagcg	gcttctacct	gtgcgcttgg	agcgtgaccc	ggcacaacga	gcagttcttt	360
ggccctggca	cccggctgac	cgctgctg				387

<210> 89

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 beta chain constant domain (Codon-optimized NA)

<400> 89

gacctgaaga	acgtgttccc	cccagaggtg	gccgtgttcg	agccttctga	ggccgagatc	60
agccacaccc	agaaagccac	cctcgtgtgt	ctggccaccg	gcttttaccc	cgaccacgtg	120
gaactgtctt	ggtgggtcaa	cggcaaagag	gtgcactccg	gcgtgtgcac	cgatccccag	180
cctctgaaaag	aacagcccgc	cctgaacgac	agccggtact	gcctgtccag	cagactgaga	240
gtgtccgcca	ccttctggca	gaacccccgg	aaccacttca	gatgccaggt	gcagttctac	300
ggcctgagcg	agaacgacga	gtggacccag	gacagagcca	agcccgtgac	ccagatcgtg	360
tctgccgaag	cctggggcag	agccgattgc	ggctttacca	gcgagagcta	ccagcagggc	420
gtgctgtctg	ccaccatcct	gtacgagatc	ctgctgggaa	aggccaccct	gtacgccgtg	480
ctggtgtctg	ccctggtgct	gatggccatg	gtcaagcgga	aggacagcag	aggc	534

<210> 90

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 alpha chain variable domain (Codon-optimized NA)

<400> 90

atgctgtgca	gcctgctggc	cctgctgctg	ggaacatfff	tcgagccccg	gaccagccag	60
gaactggaac	agagcccaca	gagcctgatc	gtgcaggaag	gcaagaacct	gaccatcaac	120
tgcaccagct	ccaagacact	gtacggcctg	tattggtata	agcagaagta	cggcgagggc	180
ctgatcttcc	tgatgatgct	gcagaagggc	ggcgaggaaa	agagccacga	gaagatcacc	240
gccaagctgg	acgagaagaa	gcagcagtc	agcctgcaca	tcaccgcctc	ccagccttct	300
cacgccggca	tctatctgtg	tggcgccgct	cccacctaca	gcaactatgg	cggcagccag	360
ggcaatctga	tcttcggcaa	gggcaccaag	ctgagcgtga	agccc		405

<210> 91

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17804.2 alpha chain constant

domain (Codon-optimized NA)

<400> 91
gacatccaga accccgaccc tgcagtgtac cagctgcggg acagcaagag cagcgacaag 60
agcgtgtgcc tgttcaccga cttcgacagc cagaccaacg tgtcccagag caaggacagc 120
gacgtgtaca tcaccgataa gtgcgtgctg gacatgcgga gcatggactt caagagcaac 180
agcgccgtgg cctgggtccaa caagagcgac ttcgcctgcg ccaacgcctt caacaacagc 240
attatccccg aggacacatt cttcccaagc cccgagagca gctgcgacgt gaagctgggtg 300
gaaaagagct tcgagacaga caccaacctg aacttccaga acctcagcgt gatcggcttc 360
cggatcctgc tgctgaaggt ggccggcttc aacctgctga tgaccctgcg gctgtggtcc 420
agctga 426

<210> 92

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain CDR1 domain
(Codon-optimized NA)

<400> 92

atggaccacg agaat 15

<210> 93

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain CDR2 domain
(Codon-optimized NA)

<400> 93

agctacgacg tgaagatg 18

<210> 94

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.1 beta chain CDR3 domain
(Codon-optimized NA)

<400> 94

tgcgccctcca acaaccggga cagctacaac agccccctgc acttc 45

<210> 95

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

<220>
<223> Synthetic sequence 1388.1 alpha chain CDR1 domain
(Codon-optimized NA)

<400> 95
tacagcggca gccccgag 18

<210> 96
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 alpha chain CDR2 domain
(Codon-optimized NA)

<400> 96
cacatcagca ga 12

<210> 97
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.1 alpha chain CDR3 domain
(Codon-optimized NA)

<400> 97
tgcgccctga gatccggcgg ctaccagaaa gtgacattt 39

<210> 98
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 1388.2b beta chain CDR1 domain
(Codon-optimized NA)

<400> 98
agcggcgacc tgagc 15

<210> 99
<211> 18

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic sequence 1388.2b beta chain CDR2 domain
 (Codon-optimized NA)

 <400> 99
 tactacaacg gcgaggaa 18

 <210> 100
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.2b beta chain CDR3 domain
 (Codon-optimized NA)

 <400> 100
 tactacaacg gcgaggaa 18

 <210> 101
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.2b alpha chain CDR1
 domain (Codon-optimized NA)

 <400> 101
 gacagcagca gcacctac 18

 <210> 102
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.2b alpha chain CDR2
 domain (Codon-optimized NA)

 <400> 102
 atcttcagca acatggacat g 21

 <210> 103
 <211> 33

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.2b alpha chain CDR3 domain (Codon-optimized NA)

 <400> 103
 tgcgccgaga gcatcgacgc ccggctgatg ttt 33

 <210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.3 beta chain CDR1 domain (Codon-optimized NA)

 <400> 104
 ggcaccagca accccaac 18

 <210> 105
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.3 beta chain CDR2 domain (Codon-optimized NA)

 <400> 105
 agcgtgggca tcggc 15

 <210> 106
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence 1388.3 beta chain CDR3 domain (Codon-optimized NA)

 <400> 106
 tgtgccctga gcaccagcta cgagcagtac ttc 33

 <210> 107
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR1 domain
(Codon-optimized NA)

<400> 107

acctccgaga acaactacta c

21

<210> 108

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR2 domain
(Codon-optimized NA)

<400> 108

caggaagcct ataagcagca gaac

24

<210> 109

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 1388.3 alpha chain CDR3 domain
(Codon-optimized NA)

<400> 109

tgcgcccttta tgaagtccca cagcggctac atcttcggc

39

<210> 110

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence 17084.1b beta chain CDR1 domain
(Codon-optimized NA)

<400> 110

ggcaccagca accccaac

18

<210> 111

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic sequence 17084.1b beta chain CDR2 domain
 (Codon-optimized NA)

<400> 111
 agcgtgggca tcggc 15

<210> 112
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 17084.1b beta chain CDR3 domain
 (Codon-optimized NA)

<400> 112
 tgcgcttgga gcgtggccgt gaacaccgag gcattcttt 39

<210> 113
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 17084.1b alpha chain CDR1
 domain (Codon-optimized NA)

<400> 113
 accagcgaga acaactacta c 21

<210> 114
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 17084.1b alpha chain CDR2
 domain (Codon-optimized NA)

<400> 114
 caggaagcct ataagcagca gaac 24

<210> 115
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence 17084.1b alpha chain CDR3

domain (Codon-optimized NA)

<400> 115
tgcgcctttg gcgagggcgc cagactgatg ttt 33

<210> 116
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 beta chain CDR1 domain
(Codon-optimized NA)

<400> 116
ggcaccagca accccaac 18

<210> 117
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 beta chain CDR2 domain
(Codon-optimized NA)

<400> 117
agcatcggca tcgac 15

<210> 118
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 beta chain CDR3 domain
(Codon-optimized NA)

<400> 118
tgcgcttgga gcgtgacccg gcacaacgag cagttcttt 39

<210> 119
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 alpha chain CDR1
domain (Codon-optimized NA)

<400> 119
aagacactgt acggc 15

<210> 120
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 alpha chain CDR2
domain (Codon-optimized NA)

<400> 120
ctgcagaagg gcggcgagga a 21

<210> 121
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence 17084.2 alpha chain CDR3
domain (Codon-optimized NA)

<400> 121
tgtggcgccg ctcccaccta cagcaactat ggcggcagcc agggcaatct gatcttc 57

<210> 122
<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence Human MAGE-A1 (amino acid)

<400> 122
Met Ser Leu Glu Gln Arg Ser Leu His Cys Lys Pro Glu Glu Ala Leu
1 5 10 15
Glu Ala Gln Gln Glu Ala Leu Gly Leu Val Cys Val Gln Ala Ala Thr
20 25 30
Ser Ser Ser Ser Pro Leu Val Leu Gly Thr Leu Glu Glu Val Pro Thr
35 40 45
Ala Gly Ser Thr Asp Pro Pro Gln Ser Pro Gln Gly Ala Ser Ala Phe
50 55 60
Pro Thr Thr Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser
65 70 75 80
Ser Ser Arg Glu Glu Glu Gly Pro Ser Thr Ser Cys Ile Leu Glu Ser
85 90 95
Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp Leu Val Gly Phe

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

<210> 123
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence Human MAGE-A1 278-286

<400> 123
 Lys Val Leu Glu Tyr Val Ile Lys Val
 1 5

<210> 124
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence Porcine teschovirus-1 2A (P2A)
 peptide

<400> 124

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

<210> 125

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence Foot-and-Mouth disease virus 2A
(F2A) peptide

<400> 125

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15
Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 126

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence Equine rhinitis A virus (ERAV)
2A (E2A) peptide

<400> 126

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

<210> 127

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence Thosaasigna virus 2A (T2A)
peptide

<400> 127

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

<210> 128
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence Porcine teschovirus-1 2A (P2A)
 peptide (NA)

 <400> 128
 ggaagcggag ctactaactt cagcctgctg aagcaggctg gagacgtgga ggagaaccct 60
 ggacct 66

 <210> 129
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence Porcine teschovirus-1 2A (P2A)
 peptide (CO-NA)

 <400> 129
 ggttccggag ccacgaactt ctctctgtta aagcaagcag gagacgtgga agaaaacccc 60
 ggtccc 66

 <210> 130
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence Foot-and-Mouth disease virus 2A
 (F2A) peptide (NA)

 <400> 130
 ggaagcggag tgaaacagac tttgaatttt gaccttctca agttggcggg agacgtggag 60
 tccaaccctg gacct 75

 <210> 131
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence Equine rhinitis A virus (ERAV)
 2A (E2A) peptide (NA)

<400> 131
ggaagcggac agtgactaa ttatgctctc ttgaaattgg ctggagatgt tgagagcaac 60
cctggacct 69

<210> 132
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence Thoseaasigna virus 2A (T2A)
peptide (NA)

<400> 132
ggaagcggag agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctgga 60
cct 63

<210> 133
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence Glycine-serine linker

<400> 133
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 134
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence Glycine-serine linker

<400> 134
Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15
Ser Ser

<210> 135
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence sgRNA Forward Oligo:
TRAC_sgRNA_pLenti_F1

<400> 135

caccggagaa tcaaaatcgg tgaat

25

<210> 136

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence sgRNA Reverse Oligo:
TRAC_sgRNA_pLenti_R1

<400> 136

aaacattcac cgattttgat tctcc

25

<210> 137

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence sgRNA Forward Oligo:
PD1_sgRNA_F1

<400> 137

caccgcagtt gtgtgacacg gaag

24

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence sgRNA Reverse Oligo:
PD1_sgRNA_R1

<400> 138

aaaccttccg tgtcacacaa ctgc

24

<210> 139

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence sgRNA Forward Oligo:
CTLA4_sgRNA_F1

<400> 139	
caccggcaaaa ggtgagtgag acttt	25
<210> 140	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic sequence sgRNA Reverse Oligo: CTLA4_sgRNA_R1	
<400> 140	
aaacaaagtc tcactcacct ttgcc	25
<210> 141	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic sequence sgRNA Forward Oligo: LAG3_sgRNA_F1	
<400> 141	
caccggtttc tgcagccgct ttggg	25
<210> 142	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic sequence sgRNA Reverse Oligo: LAG3_sgRNA_R2	
<400> 142	
aaacccccaaa gcggctgcag aaacc	25
<210> 143	
<211> 214	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Synthetic sequence CD8 co-receptor alpha chain	
<400> 143	

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

<210> 144

<211> 189

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence "CD8 co-receptor beta chain
isoform 1

<400> 144

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

Ile	Val	Gly	Ser	Pro	Glu	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Gln	Leu	Ser
			100					105					110		
Val	Val	Asp	Phe	Leu	Pro	Thr	Thr	Ala	Gln	Pro	Thr	Lys	Lys	Ser	Thr
		115					120					125			
Leu	Lys	Lys	Arg	Val	Cys	Arg	Leu	Pro	Arg	Pro	Glu	Thr	Gln	Lys	Gly
	130					135					140				
Pro	Leu	Cys	Ser	Pro	Ile	Thr	Leu	Gly	Leu	Leu	Val	Ala	Gly	Val	Leu
145					150					155					160
Val	Leu	Leu	Val	Ser	Leu	Gly	Val	Ala	Ile	His	Leu	Cys	Cys	Arg	Arg
			165					170						175	
Arg	Arg	Ala	Arg	Leu	Arg	Phe	Met	Lys	Gln	Phe	Tyr	Lys			
			180					185							

<210> 145

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence CD8 co-receptor beta chain
isoform 2

<400> 145

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

<210> 146
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 3

<400> 146
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
1 5 10 15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
20 25 30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
35 40 45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
50 55 60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65 70 75 80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
85 90 95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
100 105 110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
115 120 125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
130 135 140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145 150 155 160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
165 170 175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Lys Phe Asn Ile Val Cys
180 185 190
Leu Lys Ile Ser Gly Phe Thr Thr Cys Cys Cys Phe Gln Ile Leu Gln
195 200 205
Ile Ser Arg Glu Tyr Gly Phe Gly Val Leu Leu Gln Lys Asp Ile Gly
210 215 220
Gln
225

<210> 147
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 4

<400> 147

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

Gln
225

<210> 148

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence CD8 co-receptor beta chain
isoform 5

<400> 148

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

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