

726288_ST25 (3)
SEQUENCE LISTING

<110> THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

<120> T CELL RECEPTORS RECOGNIZING HLA-CW8 RESTRICTED MUTATED KRAS

<130> 726288

<150> US 62/218,688

<151> 2015-09-15

<160> 33

<170> PatentIn version 3.5

<210> 1

<211> 189

<212> PRT

<213> Homo sapiens

<400> 1

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 Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val

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100

105

110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
 115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
 130 135 140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
 145 150 155 160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
 165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
 180 185

<210> 2
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 2

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 Asn His Phe Val Asp Glu Tyr
 20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
 35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
 50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
 65 70 75 80

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Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

<210> 3
<211> 7
<212> PRT
<213> Homo sapiens

<400> 3

Asn Ile Ala Thr Asn Asp Tyr
1 5

<210> 4
<211> 5
<212> PRT
<213> Homo sapiens

<400> 4

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Gly Tyr Lys Thr Lys
1 5

<210> 5
<211> 13
<212> PRT
<213> Homo sapiens

<400> 5

Leu Val Gly Asp Met Asp Gln Ala Gly Thr Ala Leu Ile
1 5 10

<210> 6
<211> 5
<212> PRT
<213> Homo sapiens

<400> 6

Ser Gly His Asp Thr
1 5

<210> 7
<211> 6
<212> PRT
<213> Homo sapiens

<400> 7

Tyr Tyr Glu Glu Glu Glu
1 5

<210> 8
<211> 12
<212> PRT
<213> Homo sapiens

<400> 8

Ala Ser Ser Leu Gly Gln Thr Asn Tyr Gly Tyr Thr
1 5 10

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<210> 9
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 9

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 Met Asp Gln
 100 105 110

Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly Thr Thr Leu Ser Val Ser
 115 120 125

Ser

<210> 10
 <211> 132
 <212> PRT
 <213> Homo sapiens

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<400> 10

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

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

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

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

Ile Phe Gln Tyr Tyr Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

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

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

Ser Leu Gly Gln Thr Asn Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg
115 120 125

Leu Thr Val Val
130

<210> 11

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

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<221> MISC_FEATURE
 <222> (48)..(48)
 <223> X at position 48 is Thr or Cys

<220>
 <221> MISC_FEATURE
 <222> (112)..(112)
 <223> X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<220>
 <221> MISC_FEATURE
 <222> (114)..(114)
 <223> X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp

<220>
 <221> MISC_FEATURE
 <222> (115)..(115)
 <223> X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<400> 11

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

Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile
			20					25					30		

Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Xaa
		35					40					45			

Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala
	50					55					60				

Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr
65					70					75				80	

Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr
				85					90					95	

Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Xaa
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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100

105

110

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

Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135

<210> 12
 <211> 173
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (57)..(57)
 <223> X at position 57 is Ser or Cys

<400> 12

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1 5 10 15

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45

Gly Lys Glu Val His Ser Gly Val Xaa Thr Asp Pro Gln Ala Tyr Lys
 50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
 65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe

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85

90

95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
 100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
 115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
 130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
 145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
 165 170

<210> 13
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (177)..(177)
 <223> X at position 177 is Thr or Cys

<220>
 <221> MISC_FEATURE
 <222> (241)..(241)
 <223> X at position 241 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<220>
 <221> MISC_FEATURE
 <222> (243)..(243)
 <223> X at position 243 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp

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<220>

<221> MISC_FEATURE

<222> (244)..(244)

<223> X at position 244 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<400> 13

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	Met	Asp	Gln
			100					105					110		

Ala	Gly	Thr	Ala	Leu	Ile	Phe	Gly	Lys	Gly	Thr	Thr	Leu	Ser	Val	Ser
		115					120					125			

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

Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln
145					150					155					160

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Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Xaa Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Xaa Val Xaa Xaa Leu Arg Ile Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 14
<211> 305
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (189)..(189)
<223> X at position 189 is Ser or Cys

<400> 14

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

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

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
 35 40 45

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

Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
 65 70 75 80

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

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

Ser Leu Gly Gln Thr Asn Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg
 115 120 125

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

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
 145 150 155 160

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
 165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Xaa Thr Asp Pro
 180 185 190

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

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

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

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

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser
260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
275 280 285

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

Ser
305

<210> 15
<211> 189
<212> PRT
<213> Homo sapiens

<400> 15

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 Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr

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50

55

60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
 65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
 85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
 100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
 115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
 130 135 140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
 145 150 155 160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
 165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
 180 185

<210> 16
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 16

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 Asn His Phe Val Asp Glu Tyr
 20 25 30

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Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

<210> 17

<211> 9

<212> PRT

<213> Homo sapiens

<400> 17

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Gly Ala Gly Gly Val Gly Lys Ser Ala
1 5

<210> 18
<211> 9
<212> PRT
<213> Homo sapiens

<400> 18

Gly Ala Asp Gly Val Gly Lys Ser Ala
1 5

<210> 19
<211> 24
<212> PRT
<213> Homo sapiens

<400> 19

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> 20
<211> 24
<212> PRT
<213> Homo sapiens

<400> 20

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
20

<210> 21
<211> 26

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 21
gccacagcac tgtgctcttg aagtcc 26

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 22
caggcagtat ctggagtcac tgag 24

<210> 23
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 23

Arg	Ala	Lys	Arg	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
1				5				10					15		

Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
			20				25			

<210> 24
<211> 137
<212> PRT
<213> Mus musculus

<400> 24

Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg

726288_ST25 (3)

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

<210> 25
 <211> 173
 <212> PRT
 <213> Mus musculus

<400> 25

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1 5 10 15

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30

726288_ST25 (3)

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
85 90 95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
165 170

<210> 26
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 26

726288_ST25 (3)

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 Met Asp Gln
 100 105 110

Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly Thr Thr Leu Ser Val Ser
 115 120 125

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

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
 145 150 155 160

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
 165 170 175

Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
 180 185 190

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Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 27
<211> 305
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 27

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

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

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

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

Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

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

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

Ser Leu Gly Gln Thr Asn Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg
115 120 125

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

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175

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

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

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

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

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

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser
260 265 270

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Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
 275 280 285

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

Ser
 305

<210> 28
 <211> 387
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 28
 atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ccttgctaag 60
 accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc 120
 cacaacaaca ttgctacaaa tgattatatc acgtggtacc aacagtttcc cagccaagga 180
 ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt 240
 atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact 300
 gctgtgtact actgcctcgt gggtgacatg gaccaggcag gaactgctct gatctttggg 360
 aagggaacca ccttatcagt gagttcc 387

<210> 29
 <211> 396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

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<221> misc_feature
<222> (385)..(385)
<223> n is a, c, g, or t

<400> 29
atgggccccg ggctcctctg ctgggcactg ctttgtctcc tgggagcagg cttagtggac 60
gctggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg 120
agatgctctc ctaagtctgg gcatgacact gtgtcctggg accaacaggc cctggggtcag 180
gggccccagt ttatctttca gtattatgag gaggaagaga gacagagagg caacttcctt 240
gatcgattct caggtcacca gttccctaac tatagctctg agctgaatgt gaacgccttg 300
ttgctggggg actcggccct ctatctctgt gccagcagct tgggacagac caactatggc 360
tacaccttcg gttcggggac caggntaacc gttgta 396

<210> 30
<211> 10
<212> PRT
<213> Homo sapiens

<400> 30

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