

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Murphy, Andrew J.

<120> GENETICALLY MODIFIED NON-HUMAN ANIMALS FOR GENERATING THERAPEUTIC
ANTIBODIES AGAINST PEPTIDE-MHC COMPLEXES, METHODS OF MAKING AND
USES THEREOF

<130> 009108.116W01/10116W001

<150> 62/647,720

<151> 2018-03-24

<150> 62/647,724

<151> 2018-03-24

<160> 29

<170> PatentIn version 3.5

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Gly Gly Gly Ser
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Gly Gly Ser Gly Gly
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Gly Ser Gly Ser Gly
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Gly Ser Gly Gly Gly
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Gly Gly Gly Ser Gly
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Gly Cys Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Gly Gly Gly Ala Ser Gly Gly Gly Gly Ser
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tatgtgagcg gatttcaccc ttcagacata gaggtagacc ttctgaaaaa cggagagaga 180
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gggggcggaa gcggcggagg aggctccggt gggggtggtt cagggtccca ttctatgaga 420
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<400> 18

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Gly Cys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile
1           5           10          15

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Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn
          20          25          30

```

```

Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser
          35          40          45

```

```

Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val
50          55          60

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```

Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu
65          70          75          80

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Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg
85 90 95

Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg
100 105 110

Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr
130 135 140

Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly
145 150 155 160

Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser
165 170 175

Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu
180 185 190

Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His
195 200 205

Arg Val Asp Leu Gly Thr Leu Arg Gly Cys Tyr Asn Gln Ser Glu Ala
210 215 220

Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp
225 230 235 240

Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp
245 250 255

Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met
260 265 270

Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu
275 280 285

Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg
290 295 300

Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys
 305 310 315 320

Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg
 325 330 335

Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln
 340 345 350

Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
 355 360 365

Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro
 370 375 380

Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu
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Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro
 405 410

<210> 19
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ggggagcccc ggtttatcgc tgtggggtac gtggatgata ctcaattcgt gcggttcgac 540
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 gaatactggg acggcgaaac ccgcaaggta aaagcgcaca gccagacgca tagggtggat 660
 ctgggcaccc tgcggggctg ttataaccag tcagaggctg gctcacacac tgtacagcgg 720
 atgtatggtt gtgacgtcgg ttccgattgg agatttcttc gcggctacca ccaatacgcc 780
 tacgatggca aggactacat cgcactgaag gaagatttga gatcttggac cgcggcggat 840
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 gcctatctgg agggcacttg cgtcgagtgg ttgcggagat acctggagaa tggaaaagaa 960
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 cagcgcgacg gcgaagatca gacgcaggac acagagcttg ttgaaactcg ccctgctggc 1140
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 20 25 30

Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser
35 40 45

Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val
50 55 60

Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu
65 70 75 80

Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg
85 90 95

Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg
100 105 110

Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr
130 135 140

Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly
145 150 155 160

Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser
165 170 175

Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu
180 185 190

Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His
195 200 205

Arg Val Asp Leu Gly Thr Leu Arg Gly Cys Tyr Asn Gln Ser Glu Ala
210 215 220

Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp
225 230 235 240

Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp
245 250 255

Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met
260 265 270

Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu
275 280 285

Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg
290 295 300

Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys
305 310 315 320

Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg
325 330 335

Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln
340 345 350

Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
355 360 365

Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro
370 375 380

Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu
385 390 395 400

Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile
405 410 415

Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile
420 425 430

Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser Ser Asp
435 440 445

Arg Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln
450 455 460

Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490

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cgccaccccg cagagaatgg aaagtccaac ttccttaact gttatgtgag cggatttcac 180
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gaacaggagg gcccggaata ctgggacggc gaaaccgcga aggtaaaagc gcacagccag 660
acgcataggg tggatctggg caccctgcgg ggctattata accagtcaga ggctggctca 720
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gctgtgtccg accacgaggc aacactccgg tgttgggcac tcagcttcta ccctgctgaa	1080
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caggaacagc ggtatacttg ccacgtgcag catgaaggtc tccccaagcc cctcactttg	1260
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tctgatagga agggcggatc ttattcccag gctgcgtcca gtgacagcgc ccaggggtca	1440
gatgtcagcc tgaccgcatg caaggtgtaa	1470

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<400> 23

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Leu	Ala	Ala	Leu	Leu	Leu	Ala	Ala	Arg	Gly	Ala	Asp	Ala	Ile	Gln	Arg
			20					25					30		

Thr	Pro	Lys	Ile	Gln	Val	Tyr	Ser	Arg	His	Pro	Ala	Glu	Asn	Gly	Lys
		35					40					45			

Ser	Asn	Phe	Leu	Asn	Cys	Tyr	Val	Ser	Gly	Phe	His	Pro	Ser	Asp	Ile
	50					55					60				

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

Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr
85 90 95

Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn
100 105 110

His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val
145 150 155 160

Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val
165 170 175

Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg
180 185 190

Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp
195 200 205

Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val
210 215 220

Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser
225 230 235 240

His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg
245 250 255

Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile
260 265 270

Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala
275 280 285

Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu
290 295 300

Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu
305 310 315 320

Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His
325 330 335

Met Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp
340 345 350

Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp
355 360 365

Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala
370 375 380

Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly
385 390 395 400

Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys
405 410 415

Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile Pro Ile
420 425 430

Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile Thr Gly
435 440 445

Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser Ser Asp Arg Lys
450 455 460

Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser
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Asp Val Ser Leu Thr Ala Cys Lys Val
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<210> 24

<211> 372

<212> PRT

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<223> Chimeric Human HLA-A2/Mouse H2-K

<220>

<221> SIGNAL

<222> (1)..(24)

<400> 24

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20 25 30

Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
35 40 45

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
50 55 60

Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
65 70 75 80

Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln
85 90 95

Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
100 105 110

Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly
115 120 125

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

Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala
145 150 155 160

Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val
165 170 175

Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu
180 185 190

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala
 195 200 205

Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr
 210 215 220

Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr
 225 230 235 240

Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
 245 250 255

Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
 260 265 270

Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
 275 280 285

Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Pro Pro Ser Thr
 290 295 300

Val Ser Asn Met Ala Thr Val Ala Val Leu Val Val Leu Gly Ala Ala
 305 310 315 320

Ile Val Thr Gly Ala Val Val Ala Phe Val Met Lys Met Arg Arg Arg
 325 330 335

Asn Thr Gly Gly Lys Gly Gly Asp Tyr Ala Leu Ala Pro Gly Ser Gln
 340 345 350

Thr Ser Asp Leu Ser Leu Pro Asp Cys Lys Val Met Val His Asp Pro
 355 360 365

His Ser Leu Ala
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<223> GCGGS-G4Sx2-hB2m-G4Sx4-HLA-A*02:01 ecto
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20 25 30

Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser
35 40 45

Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val
50 55 60

Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu
65 70 75 80

Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg
85 90 95

Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg
100 105 110

Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr
130 135 140

Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly
145 150 155 160

Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser
165 170 175

Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu
180 185 190

Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His
Page 18

195					200					205					
Arg	Val	Asp	Leu	Gly	Thr	Leu	Arg	Gly	Cys	Tyr	Asn	Gln	Ser	Glu	Ala
	210					215					220				
Gly	Ser	His	Thr	Val	Gln	Arg	Met	Tyr	Gly	Cys	Asp	Val	Gly	Ser	Asp
225					230					235					240
Trp	Arg	Phe	Leu	Arg	Gly	Tyr	His	Gln	Tyr	Ala	Tyr	Asp	Gly	Lys	Asp
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Tyr	Ile	Ala	Leu	Lys	Glu	Asp	Leu	Arg	Ser	Trp	Thr	Ala	Ala	Asp	Met
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Ala	Ala	Gln	Thr	Thr	Lys	His	Lys	Trp	Glu	Ala	Ala	His	Val	Ala	Glu
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Gln	Leu	Arg	Ala	Tyr	Leu	Glu	Gly	Thr	Cys	Val	Glu	Trp	Leu	Arg	Arg
	290					295					300				
Tyr	Leu	Glu	Asn	Gly	Lys	Glu	Thr	Leu	Gln	Arg	Thr	Asp	Ala	Pro	Lys
305					310					315					320
Thr	His	Met	Thr	His	His	Ala	Val	Ser	Asp	His	Glu	Ala	Thr	Leu	Arg
				325					330					335	
Cys	Trp	Ala	Leu	Ser	Phe	Tyr	Pro	Ala	Glu	Ile	Thr	Leu	Thr	Trp	Gln
			340					345					350		
Arg	Asp	Gly	Glu	Asp	Gln	Thr	Gln	Asp	Thr	Glu	Leu	Val	Glu	Thr	Arg
		355					360					365			
Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala	Ala	Val	Val	Val	Pro
	370					375					380				
Ser	Gly	Gln	Glu	Gln	Arg	Tyr	Thr	Cys	His	Val	Gln	His	Glu	Gly	Leu
385					390					395					400
Pro	Lys	Pro	Leu	Thr	Leu	Arg	Trp	Glu	Pro	Ala	Lys	Phe	Val	Ala	Ala
				405					410					415	

Trp Thr Leu Lys Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
420 425 430

Leu Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu His His His
435 440 445

His His His
450

<210> 26
<211> 438
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<213> Artificial Sequence

<220>
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<400> 26

Gly Cys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile
1 5 10 15

Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn
20 25 30

Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser
35 40 45

Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val
50 55 60

Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu
65 70 75 80

Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg
85 90 95

Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg
100 105 110

Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr
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130

135

140

Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly
 145 150 155 160

Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser
 165 170 175

Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu
 180 185 190

Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His
 195 200 205

Arg Val Asp Leu Gly Thr Leu Arg Gly Cys Tyr Asn Gln Ser Glu Ala
 210 215 220

Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp
 225 230 235 240

Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp
 245 250 255

Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met
 260 265 270

Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu
 275 280 285

Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg
 290 295 300

Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys
 305 310 315 320

Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg
 325 330 335

Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln
 340 345 350

Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
355 360 365

Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro
370 375 380

Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu
385 390 395 400

Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Glu Gln Lys Leu Ile Ser
405 410 415

Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
420 425 430

His His His His His
435

<210> 27

<211> 733

<212> PRT

<213> Artificial Sequence

<220>

<223> GCGGS-G4Sx2-hB2m-G4Sx4-HLA-A*02:01 full length (Y108C)-G4Sx4-eGFP

<400> 27

Gly Cys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile
1 5 10 15

Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn
20 25 30

Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser
35 40 45

Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val
50 55 60

Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu
65 70 75 80

Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg
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85

90

95

Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg
 100 105 110

Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr
 130 135 140

Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly
 145 150 155 160

Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser
 165 170 175

Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu
 180 185 190

Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His
 195 200 205

Arg Val Asp Leu Gly Thr Leu Arg Gly Cys Tyr Asn Gln Ser Glu Ala
 210 215 220

Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp
 225 230 235 240

Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp
 245 250 255

Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met
 260 265 270

Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu
 275 280 285

Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg
 290 295 300

Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys
 305 310 315 320

Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg
 325 330 335

Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln
 340 345 350

Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
 355 360 365

Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro
 370 375 380

Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu
 385 390 395 400

Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile
 405 410 415

Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile
 420 425 430

Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser Ser Asp
 435 440 445

Arg Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln
 450 455 460

Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val
 485 490 495

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 500 505 510

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 515 520 525

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
530 535 540

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr
545 550 555 560

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
565 570 575

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
580 585 590

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
595 600 605

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
610 615 620

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
625 630 635 640

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
645 650 655

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
660 665 670

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
675 680 685

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
690 695 700

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
705 710 715 720

Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
725 730

<210> 28

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<213> Artificial Sequence

<220>
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<400> 28

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

<210> 29
<211> 8
<212> PRT
<213> Homo sapiens

<400> 29

Pro Cys Pro Ala Pro Pro Val Ala
1 5