

SEQUENCE LISTING

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<110>  Amsterdam Molecular Therapeutics B.V.

<120>  Parvoviral capsid with incorporated Gly-Ala repeat region

<130>  P6019299EP

<150>  EP 08158418.7
<151>  2008-06-17

<150>  US 61/073,295
<151>  2008-06-17

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<170>  PatentIn version 3.3

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ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg      192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
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gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac      240
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
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Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
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Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
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Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
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Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
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Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
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Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
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Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
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 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
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 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
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 aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct 384

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Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly	
450 455 460	
aga tac gcc aac acc tac aaa aac tgg ttc ccg ggg ccc atg ggc cga	1440
Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg	
465 470 475 480	
acc cag ggc tgg aac ctg ggc tcc ggg gtc aac cgc gcc agt gtc agc	1488
Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser	
485 490 495	
gcc ttc gcc acg acc aat agg atg gag ctc gag ggc gcg agt tac cag	1536
Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln	
500 505 510	
gtg ccc ccg cag ccg aac ggc atg acc aac aac ctc cag ggc agc aac	1584
Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn	
515 520 525	
acc tat gcc ctg gag aac act atg atc ttc aac agc cag ccg gcg aac	1632
Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn	
530 535 540	
ccg ggc acc acc gcc acg tac ctc gag ggc aac atg ctc atc acc agc	1680
Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser	
545 550 555 560	
gag agc gag acg cag ccg gtg aac cgc gtg gcg tac aac gtc ggc ggg	1728
Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly	
565 570 575	
cag atg gcc acc aac aac cag agc tcc acc act gcc ccc gcg acc ggc	1776

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly	
580 585 590	
acg tac aac ctc cag gaa atc gtg ccc ggc agc gtg tgg atg gag agg	1824
Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg	
595 600 605	
gac gtg tac ctc caa gga ccc atc tgg gcc aag atc cca gag acg ggg	1872
Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly	
610 615 620	
gcg cac ttt cac ccc tct ccg gcc atg ggc gga ttc gga ctc aaa cac	1920
Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His	
625 630 635 640	
cca ccg ccc atg atg ctc atc aag aac acg cct gtg ccc gga aat atc	1968
Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile	
645 650 655	
acc agc ttc tcg gac gtg ccc gtc agc agc ttc atc acc cag tac agc	2016
Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser	
660 665 670	
acc ggg cag gtc acc gtg gag atg gag tgg gag ctc aag aag gaa aac	2064
Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn	
675 680 685	
tcc aag agg tgg aac cca gag atc cag tac aca aac aac tac aac gac	2112
Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp	
690 695 700	
ccc cag ttt gtg gac ttt gcc ccg gac agc acc ggg gaa tac aga acc	2160
Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr	
705 710 715 720	
acc aga cct atc gga acc cga tac ctt acc cga ccc ctt taa	2202
Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu	
725 730	

<210> 4
 <211> 733
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 4

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Gly
245 250 255

Gly Ala Gly Ala Gly Ala Gly Val Asp Gly Ser Asn Ala Asn Ala Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Ser His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp
290 295 300

Gly Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr
340 345 350

Val Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln
355 360 365

Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn
370 375 380

Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu
420 425 430

Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val
435 440 445

Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 5
 <211> 2202
 <212> DNA
 <213> Artificial

<220>
 <223> Cap2/5 - g382

<220>
 <221> CDS
 <222> (1)..(2202)

<220>
 <221> misc_feature
 <222> (1132)..(1155)
 <223> immune evasion repeat sequence

<400> 5
 acg gct gcc gac ggt tat cta ccc gat tgg ttg gag gac act ctc tct 48
 Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca 96
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct 144
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg 192
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac 240
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc 288
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc 336
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct 384
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag cgg 432
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
 130 135 140
 ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac 480

Ile 145	Asp	Asp	His	Phe	Pro 150	Lys	Arg	Lys	Lys	Ala 155	Arg	Thr	Glu	Glu	Asp 160	
tcc Ser	aag Lys	cct Pro	tcc Ser	acc Thr 165	tcg Ser	tca Ser	gac Asp	gcc Ala	gaa Glu 170	gct Ala	gga Gly	ccc Pro	agc Ser	gga Gly 175	tcc Ser	528
cag Gln	cag Gln	ctg Leu	caa Gln 180	atc Ile	cca Pro	gcc Ala	caa Gln 185	cca Pro	gcc Ala	tca Ser	agt Ser	ttg Leu	gga Gly 190	gct Ala	gat Asp	576
aca Thr	atg Met	tct Ser 195	gcg Ala	gga Gly	ggt Gly	ggc Gly	ggc Gly 200	cca Pro	ttg Leu	ggc Gly	gac Asp 205	aat Asn	aac Asn	caa Gln	ggt Gly	624
gcc Ala 210	gat Asp	gga Gly	gtg Val	ggc Gly	aat Asn 215	gcc Ala	tcg Ser 215	gga Gly	gat Asp	tgg Trp	cat His 220	tgc Cys	gat Asp	tcc Ser	acg Thr	672
tgg Trp 225	atg Met	ggg Gly	gac Asp	aga Arg	gtc Val 230	gtc Val	acc Thr	aag Lys	tcc Ser	acc Thr 235	cga Arg	acc Thr	tgg Trp	gtg Val	ctg Leu 240	720
ccc Pro	agc Ser	tac Tyr	aac Asn 245	aac Asn	cac His	cag Gln	tac Tyr	cga Arg	gag Glu 250	atc Ile	aaa Lys	agc Ser	ggc Gly 255	tcc Ser	gtc Val	768
gac Asp	gga Gly	agc Ser	aac Asn 260	gcc Ala	aac Asn	gcc Ala	tac Tyr 265	ttt Phe	gga Gly	tac Tyr	agc Ser	acc Thr	ccc Pro 270	tgg Trp	ggg Gly	816
tac Tyr	ttt Phe 275	gac Asp	ttt Phe	aac Asn	cgc Arg	ttc Phe	cac His 280	agc Ser	cac His	tgg Trp	agc Ser	ccc Pro 285	cga Arg	gac Asp	tgg Trp	864
caa Gln 290	aga Arg	ctc Leu	atc Ile	aac Asn	aac Asn	tac Tyr 295	tgg Trp	ggc Gly	ttc Phe	aga Arg 300	ccc Pro	cgg Arg	tcc Ser	ctc Leu	aga Arg	912
gtc Val 305	aaa Lys	atc Ile	ttc Phe	aac Asn	att Ile 310	caa Gln	gtc Val	aaa Lys	gag Glu 315	gtc Val	acg Thr	gtg Val	cag Gln	gac Asp 320	tcc Ser	960
acc Thr	acc Thr	acc Thr	atc Ile	gcc Ala 325	aac Asn	aac Asn	ctc Leu	acc Thr	tcc Ser 330	acc Thr	gtc Val	caa Gln	gtg Val	ttt Phe 335	acg Thr	1008
gac Asp	gac Asp	gac Asp	tac Tyr 340	cag Gln	ctg Leu	ccc Pro	tac Tyr 345	gtc Val	gtc Val	ggc Gly	aac Asn	ggg Gly 350	acc Thr	gag Glu	gga Gly	1056
tgc Cys	ctg Leu	ccg Pro 355	gcc Ala	ttc Phe	cct Pro	ccg Pro	cag Gln 360	gtc Val	ttt Phe	acg Thr	ctg Leu	ccg Pro 365	cag Gln	tac Tyr	ggt Gly	1104
tac Tyr 370	gcg Ala	acg Thr	ctg Leu	aac Asn	cgc Arg	gac Asp 375	aac Asn	aca Thr	ggt Gly	ggt Gly	gcc Ala 380	ggt Gly	gcc Ala	ggt Gly	gcc Ala	1152

ggt gaa aat ccc acc gag agg agc agc ttc ttc tgc cta gag tac ttt	1200
Gly Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe	
385 390 395 400	
ccc agc aag atg ctg aga acg ggc aac aac ttt gag ttt acc tac aac	1248
Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn	
405 410 415	
ttt gag gag gtg ccc ttc cac tcc agc ttc gct ccc agt cag aac ctg	1296
Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu	
420 425 430	
ttc aag ctg gcc aac ccg ctg gtg gac cag tac ttg tac cgc ttc gtg	1344
Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val	
435 440 445	
agc aca aat aac act ggc gga gtc cag ttc aac aag aac ctg gcc ggg	1392
Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly	
450 455 460	
aga tac gcc aac acc tac aaa aac tgg ttc ccg ggg ccc atg ggc cga	1440
Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg	
465 470 475 480	
acc cag ggc tgg aac ctg ggc tcc ggg gtc aac cgc gcc agt gtc agc	1488
Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser	
485 490 495	
gcc ttc gcc acg acc aat agg atg gag ctc gag ggc gcg agt tac cag	1536
Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln	
500 505 510	
gtg ccc ccg cag ccg aac ggc atg acc aac aac ctc cag ggc agc aac	1584
Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn	
515 520 525	
acc tat gcc ctg gag aac act atg atc ttc aac agc cag ccg gcg aac	1632
Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn	
530 535 540	
ccg ggc acc acc gcc acg tac ctc gag ggc aac atg ctc atc acc agc	1680
Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser	
545 550 555 560	
gag agc gag acg cag ccg gtg aac cgc gtg gcg tac aac gtc ggc ggg	1728
Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly	
565 570 575	
cag atg gcc acc aac aac cag agc tcc acc act gcc ccc gcg acc ggc	1776
Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly	
580 585 590	
acg tac aac ctc cag gaa atc gtg ccc ggc agc gtg tgg atg gag agg	1824
Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg	
595 600 605	
gac gtg tac ctc caa gga ccc atc tgg gcc aag atc cca gag acg ggg	1872

Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	Glu	Thr	Gly	
610						615					620					
gcg	cac	ttt	cac	ccc	tct	ccg	gcc	atg	ggc	gga	ttc	gga	ctc	aaa	cac	1920
Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met	Gly	Gly	Phe	Gly	Leu	Lys	His	
625					630				635						640	
cca	ccg	ccc	atg	atg	ctc	atc	aag	aac	acg	cct	gtg	ccc	gga	aat	atc	1968
Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	
				645					650					655		
acc	agc	ttc	tcg	gac	gtg	ccc	gtc	agc	agc	ttc	atc	acc	cag	tac	agc	2016
Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	
			660					665					670			
acc	ggg	cag	gtc	acc	gtg	gag	atg	gag	tgg	gag	ctc	aag	aag	gaa	aac	2064
Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	
		675					680					685				
tcc	aag	agg	tgg	aac	cca	gag	atc	cag	tac	aca	aac	aac	tac	aac	gac	2112
Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	
	690					695					700					
ccc	cag	ttt	gtg	gac	ttt	gcc	ccg	gac	agc	acc	ggg	gaa	tac	aga	acc	2160
Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Thr	
705					710					715					720	
acc	aga	cct	atc	gga	acc	cga	tac	ctt	acc	cga	ccc	ctt	taa			2202
Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
				725					730							

<210> 6
 <211> 733
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 6

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

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Gly Gly Ala Gly Ala Gly Ala
370 375 380

Gly Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu
420 425 430

Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val
435 440 445

Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 7
<211> 2202
<212> DNA
<213> Artificial

<220>

<223> Cap2/5 - 454

<220>

<221> CDS

<222> (1)..(2202)

<220>

<221> misc_feature

<222> (1333)..(1356)

<223> immune evasion repeat sequence

<400> 7

acg	gct	gcc	gac	ggt	tat	cta	ccc	gat	tgg	ttg	gag	gac	act	ctc	tct	48
Thr	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Thr	Leu	Ser	
1				5					10					15		

gaa	gga	ata	aga	cag	tgg	tgg	aag	ctc	aaa	cct	ggc	cca	cca	cca	cca	96
Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro	
			20					25					30			

aag	ccc	gca	gag	cgg	cat	aag	gac	gac	agc	agg	ggt	ctt	gtg	ctt	cct	144
Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro	
		35					40					45				

ggg	tac	aag	tac	ctc	gga	ccc	ttc	aac	gga	ctc	gac	aag	gga	gag	ccg	192
Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
	50					55					60					

gtc	aac	gag	gca	gac	gcc	gcg	gcc	ctc	gag	cac	gac	aaa	gcc	tac	gac	240
Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
65					70					75					80	

cgg	cag	ctc	gac	agc	gga	gac	aac	ccg	tac	ctc	aag	tac	aac	cac	gcc	288
Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala	
			85					90						95		

gac	gcg	gag	ttt	cag	gag	cgc	ctt	aaa	gaa	gat	acg	tct	ttt	ggg	ggc	336
Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
			100					105					110			

aac	ctc	gga	cga	gca	gtc	ttc	cag	gcg	aaa	aag	agg	gtt	ctt	gaa	cct	384
Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
		115					120					125				

ctg	ggc	ctg	gtt	gag	gaa	cct	gtt	aag	acg	gcc	cct	acc	gga	aag	cgg	432
Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Thr	Gly	Lys	Arg	
	130					135					140					

ata	gac	gac	cac	ttt	cca	aaa	aga	aag	aag	gct	cgg	acc	gaa	gag	gac	480
Ile	Asp	Asp	His	Phe	Pro	Lys	Arg	Lys	Lys	Ala	Arg	Thr	Glu	Glu	Asp	
145					150					155					160	

tcc	aag	cct	tcc	acc	tcg	tca	gac	gcc	gaa	gct	gga	ccc	agc	gga	tcc	528
Ser	Lys	Pro	Ser	Thr	Ser	Ser	Asp	Ala	Glu	Ala	Gly	Pro	Ser	Gly	Ser	
				165					170					175		

cag	cag	ctg	caa	atc	cca	gcc	caa	cca	gcc	tca	agt	ttg	gga	gct	gat	576
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gln	Gln	Leu	Gln	Ile	Pro	Ala	Gln	Pro	Ala	Ser	Ser	Leu	Gly	Ala	Asp	
			180					185					190			
aca	atg	tct	gcg	gga	ggt	ggc	ggc	cca	ttg	ggc	gac	aat	aac	caa	ggc	624
Thr	Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro	Leu	Gly	Asp	Asn	Asn	Gln	Gly	
		195					200					205				
gcc	gat	gga	gtg	ggc	aat	gcc	tcg	gga	gat	tgg	cat	tgc	gat	tcc	acg	672
Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	
	210					215					220					
tgg	atg	ggg	gac	aga	gtc	gtc	acc	aag	tcc	acc	cga	acc	tgg	gtg	ctg	720
Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu	
225					230					235					240	
ccc	agc	tac	aac	aac	cac	cag	tac	cga	gag	atc	aaa	agc	ggc	tcc	gtc	768
Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	
			245						250					255		
gac	gga	agc	aac	gcc	aac	gcc	tac	ttt	gga	tac	agc	acc	ccc	tgg	ggg	816
Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	
			260					265					270			
tac	ttt	gac	ttt	aac	cgc	ttc	cac	agc	cac	tgg	agc	ccc	cga	gac	tgg	864
Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	
		275					280					285				
caa	aga	ctc	atc	aac	aac	tac	tgg	ggc	ttc	aga	ccc	cgg	tcc	ctc	aga	912
Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	
	290					295					300					
gtc	aaa	atc	ttc	aac	att	caa	gtc	aaa	gag	gtc	acg	gtg	cag	gac	tcc	960
Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	
305					310					315					320	
acc	acc	acc	atc	gcc	aac	aac	ctc	acc	tcc	acc	gtc	caa	gtg	ttt	acg	1008
Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	
				325					330					335		
gac	gac	gac	tac	cag	ctg	ccc	tac	gtc	gtc	ggc	aac	ggg	acc	gag	gga	1056
Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	
			340					345					350			
tgc	ctg	ccg	gcc	ttc	cct	ccg	cag	gtc	ttt	acg	ctg	ccg	cag	tac	ggc	1104
Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	
		355					360						365			
tac	gcg	acg	ctg	aac	cgc	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	
	370					375					380					
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	
385					390					395					400	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	
				405					410					415		

agc ttc gct ccc agt cag aac ctg ttc aag ctg gcc aac ccg ctg gtg	1296
Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val	
420 425 430	
gac cag tac ttg tac cgc ttc gtg agc aca aat aac ggt ggt gcc ggt	1344
Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Gly Gly Ala Gly	
435 440 445	
gcc ggt gcc ggt act ggc gga gtc cag ttc aac aag aac ctg gcc ggg	1392
Ala Gly Ala Gly Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly	
450 455 460	
aga tac gcc aac acc tac aaa aac tgg ttc ccg ggg ccc atg ggc cga	1440
Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg	
465 470 475 480	
acc cag ggc tgg aac ctg ggc tcc ggg gtc aac cgc gcc agt gtc agc	1488
Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser	
485 490 495	
gcc ttc gcc acg acc aat agg atg gag ctc gag ggc gcg agt tac cag	1536
Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln	
500 505 510	
gtg ccc ccg cag ccg aac ggc atg acc aac aac ctc cag ggc agc aac	1584
Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn	
515 520 525	
acc tat gcc ctg gag aac act atg atc ttc aac agc cag ccg gcg aac	1632
Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn	
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ccg ggc acc acc gcc acg tac ctc gag ggc aac atg ctc atc acc agc	1680
Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser	
545 550 555 560	
gag agc gag acg cag ccg gtg aac cgc gtg gcg tac aac gtc ggc ggg	1728
Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly	
565 570 575	
cag atg gcc acc aac aac cag agc tcc acc act gcc ccc gcg acc ggc	1776
Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly	
580 585 590	
acg tac aac ctc cag gaa atc gtg ccc ggc agc gtg tgg atg gag agg	1824
Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg	
595 600 605	
gac gtg tac ctc caa gga ccc atc tgg gcc aag atc cca gag acg ggg	1872
Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly	
610 615 620	
gcg cac ttt cac ccc tct ccg gcc atg ggc gga ttc gga ctc aaa cac	1920
Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His	
625 630 635 640	
cca ccg ccc atg atg ctc atc aag aac acg cct gtg ccc gga aat atc	1968

Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	
				645					650					655		
acc	agc	ttc	tcg	gac	gtg	ccc	gtc	agc	agc	ttc	atc	acc	cag	tac	agc	2016
Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	
			660					665					670			
acc	ggg	cag	gtc	acc	gtg	gag	atg	gag	tgg	gag	ctc	aag	aag	gaa	aac	2064
Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	
		675					680					685				
tcc	aag	agg	tgg	aac	cca	gag	atc	cag	tac	aca	aac	aac	tac	aac	gac	2112
Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	
	690					695					700					
ccc	cag	ttt	gtg	gac	ttt	gcc	ccg	gac	agc	acc	ggg	gaa	tac	aga	acc	2160
Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Thr	
705					710				715						720	
acc	aga	cct	atc	gga	acc	cga	tac	ctt	acc	cga	ccc	ctt	taa			2202
Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
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 <212> PRT
 <213> Artificial

<220>
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<400> 8

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Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		
Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			
Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				
Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80
Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Gly Gly Ala Gly
435 440 445

Ala Gly Ala Gly Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
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Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
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Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
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<212> DNA
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<220>
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<222> (1) .. (2202)

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 gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca 96
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct 144
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg 192
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac 240
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc 288
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc 336
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct 384
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag cgg 432
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
 130 135 140
 ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac 480
 Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
 145 150 155 160
 tcc aag cct tcc acc tcg tca gac gcc gaa gct gga ccc agc gga tcc 528
 Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
 165 170 175
 cag cag ctg caa atc cca gcc caa cca gcc tca agt ttg gga gct gat 576
 Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
 180 185 190
 aca atg tct gcg gga ggt ggc ggc cca ttg ggc gac aat aac caa ggt 624
 Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
 195 200 205
 gcc gat gga gtg ggc aat gcc tcg gga gat tgg cat tgc gat tcc acg 672

Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	
210						215					220					
tgg	atg	ggg	gac	aga	gtc	gtc	acc	aag	tcc	acc	cga	acc	tgg	gtg	ctg	720
Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu	
225					230					235					240	
ccc	agc	tac	aac	aac	cac	cag	tac	cga	gag	atc	aaa	agc	ggc	tcc	gtc	768
Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	
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gac	gga	agc	aac	gcc	aac	gcc	tac	ttt	gga	tac	agc	acc	ccc	tgg	ggg	816
Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	
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tac	ttt	gac	ttt	aac	cgc	ttc	cac	agc	cac	tgg	agc	ccc	cga	gac	tgg	864
Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	
		275					280					285				
caa	aga	ctc	atc	aac	aac	tac	tgg	ggc	ttc	aga	ccc	cgg	tcc	ctc	aga	912
Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	
	290					295					300					
gtc	aaa	atc	ttc	aac	att	caa	gtc	aaa	gag	gtc	acg	gtg	cag	gac	tcc	960
Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	
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Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	
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gac	gac	gac	tac	cag	ctg	ccc	tac	gtc	gtc	ggc	aac	ggg	acc	gag	gga	1056
Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	
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Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	
		355					360					365				
tac	gcg	acg	ctg	aac	cgc	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	
	370					375					380					
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	
385					390					395					400	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	
				405					410					415		
agc	ttc	gct	ccc	agt	cag	aac	ctg	ttc	aag	ctg	gcc	aac	ccg	ctg	gtg	1296
Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	
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gac	cag	tac	ttg	tac	cgc	ttc	gtg	agc	aca	aat	aac	act	ggc	gga	gtc	1344
Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	
		435					440					445				

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aga tac gcc aac acc tac aaa aac tgg ttc ccg ggg ccc atg ggc cga Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg 465 470 475 480	1440
acc cag ggc tgg aac ctg ggc tcc ggg gtc aac cgc gcc agt gtc agc Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser 485 490 495	1488
gcc ttc gcc acg acc aat agg atg gag ctc gag ggc gcg agt tac cag Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln 500 505 510	1536
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acc tat gcc ctg gag aac act atg atc ttc aac agc cag ccg gcg aac Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn 530 535 540	1632
ccg ggc acc acc gcc acg tac ctc gag ggc aac atg ctc atc acc agc Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser 545 550 555 560	1680
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cag atg gcc acc aac aac cag agc tcc acc act gcc ccc gcg acc ggc Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly 580 585 590	1776
acg tac aac ctc cag gaa atc gtg ccc ggc agc gtg tgg atg gag agg Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg 595 600 605	1824
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gcg cac ttt cac ccc tct ccg gcc atg ggc gga ttc gga ctc aaa cac Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His 625 630 635 640	1920
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acc ggg cag gtc acc gtg gag atg gag tgg gag ctc aag aag gaa aac	2064

Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	
		675					680					685				
tcc	aag	agg	tgg	aac	cca	gag	atc	cag	tac	aca	aac	aac	tac	aac	gac	2112
Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	
		690				695					700					
ccc	cag	ttt	gtg	gac	ttt	gcc	ccg	gac	agc	acc	ggg	gaa	tac	aga	acc	2160
Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Thr	
705					710					715					720	
acc	aga	cct	atc	gga	acc	cga	tac	ctt	acc	cga	ccc	ctt	taa			2202
Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
				725					730							

<210> 10
 <211> 733
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 10

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

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Gly Gly Ala Gly Ala Gly Ala Gly Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 11
<211> 2202
<212> DNA
<213> Artificial

<220>
<223> Cap2/5 - 502

<220>
<221> CDS
<222> (1)..(2202)

<220>
<221> misc_feature
<222> (1465)..(1488)
<223> immune evasion repeat sequence

<400> 11
acg gct gcc gac ggt tat cta ccc gat tgg ttg gag gac act ctc tct
Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca	96
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro	
20 25 30	
aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct	144
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro	
35 40 45	
ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg	192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro	
50 55 60	
gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac	240
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp	
65 70 75 80	
cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc	288
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala	
85 90 95	
gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc	336
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly	
100 105 110	
aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct	384
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro	
115 120 125	
ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag ccg	432
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg	
130 135 140	
ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac	480
Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp	
145 150 155 160	
tcc aag cct tcc acc tcg tca gac gcc gaa gct gga ccc agc gga tcc	528
Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser	
165 170 175	
cag cag ctg caa atc cca gcc caa cca gcc tca agt ttg gga gct gat	576
Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp	
180 185 190	
aca atg tct gcg gga ggt ggc ggc cca ttg ggc gac aat aac caa ggt	624
Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly	
195 200 205	
gcc gat gga gtg ggc aat gcc tcg gga gat tgg cat tgc gat tcc acg	672
Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr	
210 215 220	
tgg atg ggg gac aga gtc gtc acc aag tcc acc cga acc tgg gtg ctg	720
Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu	
225 230 235 240	
ccc agc tac aac aac cac cag tac cga gag atc aaa agc ggc tcc gtc	768

Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	
				245					250					255		
gac	gga	agc	aac	gcc	aac	gcc	tac	ttt	gga	tac	agc	acc	ccc	tgg	ggg	816
Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	
			260					265					270			
tac	ttt	gac	ttt	aac	cgc	ttc	cac	agc	cac	tgg	agc	ccc	cga	gac	tgg	864
Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	
		275					280					285				
caa	aga	ctc	atc	aac	aac	tac	tgg	ggc	ttc	aga	ccc	cgg	tcc	ctc	aga	912
Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	
	290					295					300					
gtc	aaa	atc	ttc	aac	att	caa	gtc	aaa	gag	gtc	acg	gtg	cag	gac	tcc	960
Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	
305					310					315					320	
acc	acc	acc	atc	gcc	aac	aac	ctc	acc	tcc	acc	gtc	caa	gtg	ttt	acg	1008
Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	
				325					330					335		
gac	gac	gac	tac	cag	ctg	ccc	tac	gtc	gtc	ggc	aac	ggg	acc	gag	gga	1056
Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	
			340					345					350			
tgc	ctg	ccg	gcc	ttc	cct	ccg	cag	gtc	ttt	acg	ctg	ccg	cag	tac	ggc	1104
Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	
		355					360					365				
tac	gcg	acg	ctg	aac	cgc	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	
	370					375					380					
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	
385					390					395					400	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	
				405					410					415		
agc	ttc	gct	ccc	agt	cag	aac	ctg	ttc	aag	ctg	gcc	aac	ccg	ctg	gtg	1296
Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	
			420					425					430			
gac	cag	tac	ttg	tac	cgc	ttc	gtg	agc	aca	aat	aac	act	ggc	gga	gtc	1344
Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	
		435					440					445				
cag	ttc	aac	aag	aac	ctg	gcc	ggg	aga	tac	gcc	aac	acc	tac	aaa	aac	1392
Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	
	450					455					460					
tgg	ttc	ccg	ggg	ccc	atg	ggc	cga	acc	cag	ggc	tgg	aac	ctg	ggc	tcc	1440
Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	
465					470					475					480	

ggg gtc aac cgc gcc agt gtc agc ggt ggt gcc ggt gcc ggt gcc ggt	1488
Gly Val Asn Arg Ala Ser Val Ser Gly Gly Ala Gly Ala Gly Ala Gly	
485 490 495	
gcc ttc gcc acg acc aat agg atg gag ctc gag ggc gcg agt tac cag	1536
Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln	
500 505 510	
gtg ccc ccg cag ccg aac ggc atg acc aac aac ctc cag ggc agc aac	1584
Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn	
515 520 525	
acc tat gcc ctg gag aac act atg atc ttc aac agc cag ccg gcg aac	1632
Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn	
530 535 540	
ccg ggc acc acc gcc acg tac ctc gag ggc aac atg ctc atc acc agc	1680
Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser	
545 550 555 560	
gag agc gag acg cag ccg gtg aac cgc gtg gcg tac aac gtc ggc ggg	1728
Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly	
565 570 575	
cag atg gcc acc aac aac cag agc tcc acc act gcc ccc gcg acc ggc	1776
Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly	
580 585 590	
acg tac aac ctc cag gaa atc gtg ccc ggc agc gtg tgg atg gag agg	1824
Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg	
595 600 605	
gac gtg tac ctc caa gga ccc atc tgg gcc aag atc cca gag acg ggg	1872
Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly	
610 615 620	
gcg cac ttt cac ccc tct ccg gcc atg ggc gga ttc gga ctc aaa cac	1920
Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His	
625 630 635 640	
cca ccg ccc atg atg ctc atc aag aac acg cct gtg ccc gga aat atc	1968
Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile	
645 650 655	
acc agc ttc tcg gac gtg ccc gtc agc agc ttc atc acc cag tac agc	2016
Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser	
660 665 670	
acc ggg cag gtc acc gtg gag atg gag tgg gag ctc aag aag gaa aac	2064
Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn	
675 680 685	
tcc aag agg tgg aac cca gag atc cag tac aca aac aac tac aac gac	2112
Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp	
690 695 700	
ccc cag ttt gtg gac ttt gcc ccg gac agc acc ggg gaa tac aga acc	2160

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

acc aga cct atc gga acc cga tac ctt acc cga ccc ctt taa 2202
Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 12
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 12

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Gly Gly Ala Gly Ala Gly Ala Gly
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 13
<211> 2202
<212> DNA
<213> Artificial

<220>
<223> Cap2/5 - 663

<220>
<221> CDS
<222> (1)..(2202)

<220>
<221> misc_feature
<222> (1957)..(1980)
<223> immune evasion repeat sequence

<400> 13
acg gct gcc gac ggt tat cta ccc gat tgg ttg gag gac act ctc tct 48
Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca 96
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct 144
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro 50 55 60	192
gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp 65 70 75 80	240
cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala 85 90 95	288
gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly 100 105 110	336
aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro 115 120 125	384
ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag ccg Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg 130 135 140	432
ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp 145 150 155 160	480
tcc aag cct tcc acc tcg tca gac gcc gaa gct gga ccc agc gga tcc Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser 165 170 175	528
cag cag ctg caa atc cca gcc caa cca gcc tca agt ttg gga gct gat Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp 180 185 190	576
aca atg tct gcg gga ggt ggc ggc cca ttg ggc gac aat aac caa ggt Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly 195 200 205	624
gcc gat gga gtg ggc aat gcc tcg gga gat tgg cat tgc gat tcc acg Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr 210 215 220	672
tgg atg ggg gac aga gtc gtc acc aag tcc acc cga acc tgg gtg ctg Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu 225 230 235 240	720
ccc agc tac aac aac cac cag tac cga gag atc aaa agc ggc tcc gtc Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val 245 250 255	768
gac gga agc aac gcc aac gcc tac ttt gga tac agc acc ccc tgg ggg Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly 260 265 270	816
tac ttt gac ttt aac cgc ttc cac agc cac tgg agc ccc cga gac tgg	864

Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	
		275					280					285				
caa	aga	ctc	atc	aac	aac	tac	tgg	ggc	ttc	aga	ccc	cgg	tcc	ctc	aga	912
Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	
	290					295					300					
gtc	aaa	atc	ttc	aac	att	caa	gtc	aaa	gag	gtc	acg	gtg	cag	gac	tcc	960
Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	
305					310					315					320	
acc	acc	acc	atc	gcc	aac	aac	ctc	acc	tcc	acc	gtc	caa	gtg	ttt	acg	1008
Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	
				325					330					335		
gac	gac	gac	tac	cag	ctg	ccc	tac	gtc	gtc	ggc	aac	ggg	acc	gag	gga	1056
Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	
			340					345					350			
tgc	ctg	ccg	gcc	ttc	cct	ccg	cag	gtc	ttt	acg	ctg	ccg	cag	tac	ggc	1104
Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	
		355					360					365				
tac	gcg	acg	ctg	aac	cgc	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	
	370					375					380					
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	
385					390					395					400	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	
				405					410					415		
agc	ttc	gct	ccc	agt	cag	aac	ctg	ttc	aag	ctg	gcc	aac	ccg	ctg	gtg	1296
Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	
			420					425					430			
gac	cag	tac	ttg	tac	cgc	ttc	gtg	agc	aca	aat	aac	act	ggc	gga	gtc	1344
Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	
		435					440					445				
cag	ttc	aac	aag	aac	ctg	gcc	ggg	aga	tac	gcc	aac	acc	tac	aaa	aac	1392
Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	
	450					455					460					
tgg	ttc	ccg	ggg	ccc	atg	ggc	cga	acc	cag	ggc	tgg	aac	ctg	ggc	tcc	1440
Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	
465					470					475					480	
ggg	gtc	aac	cgc	gcc	agt	gtc	agc	gcc	ttc	gcc	acg	acc	aat	agg	atg	1488
Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	
				485					490					495		
gag	ctc	gag	ggc	gcg	agt	tac	cag	gtg	ccc	ccg	cag	ccg	aac	ggc	atg	1536
Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	
			500					505					510			

acc aac aac ctc cag ggc agc aac acc tat gcc ctg gag aac act atg	1584
Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met	
515 520 525	
atc ttc aac agc cag ccg gcg aac ccg ggc acc acc gcc acg tac ctc	1632
Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu	
530 535 540	
gag ggc aac atg ctc atc acc agc gag agc gag acg cag ccg gtg aac	1680
Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn	
545 550 555 560	
cgc gtg gcg tac aac gtc ggc ggg cag atg gcc acc aac aac cag agc	1728
Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser	
565 570 575	
tcc acc act gcc ccc gcg acc ggc acg tac aac ctc cag gaa atc gtg	1776
Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val	
580 585 590	
ccc ggc agc gtg tgg atg gag agg gac gtg tac ctc caa gga ccc atc	1824
Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile	
595 600 605	
tgg gcc aag atc cca gag acg ggg gcg cac ttt cac ccc tct ccg gcc	1872
Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala	
610 615 620	
atg ggc gga ttc gga ctc aaa cac cca ccg ccc atg atg ctc atc aag	1920
Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys	
625 630 635 640	
aac acg cct gtg ccc gga aat atc acc agc ttc tcg ggt ggt gcc ggt	1968
Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Gly Gly Ala Gly	
645 650 655	
gcc ggt gcc ggt gac gtg ccc gtc agc agc ttc atc acc cag tac agc	2016
Ala Gly Ala Gly Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser	
660 665 670	
acc ggg cag gtc acc gtg gag atg gag tgg gag ctc aag aag gaa aac	2064
Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn	
675 680 685	
tcc aag agg tgg aac cca gag atc cag tac aca aac aac tac aac gac	2112
Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp	
690 695 700	
ccc cag ttt gtg gac ttt gcc ccg gac agc acc ggg gaa tac aga acc	2160
Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr	
705 710 715 720	
acc aga cct atc gga acc cga tac ctt acc cga ccc ctt taa	2202
Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu	
725 730	

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<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 14

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Gly Gly Ala Gly
645 650 655

Ala Gly Ala Gly Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 15
<211> 2202
<212> DNA
<213> Artificial

<220>
<223> Cap2/5 - 708

<220>
<221> CDS
<222> (1)..(2202)

<220>
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<222> (2092)..(2115)
<223> immune evasion repeat sequence

<400> 15
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Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca 96
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct 144
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg 192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac 240
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala 85 90 95	288
gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly 100 105 110	336
aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro 115 120 125	384
ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag cgg Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg 130 135 140	432
ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp 145 150 155 160	480
tcc aag cct tcc acc tcg tca gac gcc gaa gct gga ccc agc gga tcc Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser 165 170 175	528
cag cag ctg caa atc cca gcc caa cca gcc tca agt ttg gga gct gat Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp 180 185 190	576
aca atg tct gcg gga ggt ggc ggc cca ttg ggc gac aat aac caa ggt Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly 195 200 205	624
gcc gat gga gtg ggc aat gcc tcg gga gat tgg cat tgc gat tcc acg Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr 210 215 220	672
tgg atg ggg gac aga gtc gtc acc aag tcc acc cga acc tgg gtg ctg Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu 225 230 235 240	720
ccc agc tac aac aac cac cag tac cga gag atc aaa agc ggc tcc gtc Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val 245 250 255	768
gac gga agc aac gcc aac gcc tac ttt gga tac agc acc ccc tgg ggg Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly 260 265 270	816
tac ttt gac ttt aac cgc ttc cac agc cac tgg agc ccc cga gac tgg Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp 275 280 285	864
caa aga ctc atc aac aac tac tgg ggc ttc aga ccc cgg tcc ctc aga Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg 290 295 300	912
gtc aaa atc ttc aac att caa gtc aaa gag gtc acg gtg cag gac tcc	960

Val 305	Lys	Ile	Phe	Asn	Ile 310	Gln	Val	Lys	Glu	Val 315	Thr	Val	Gln	Asp	Ser 320	
acc	acc	acc	atc	gcc	aac	aac	ctc	acc	tcc	acc	gtc	caa	gtg	ttt	acg	1008
Thr	Thr	Thr	Ile	Ala 325	Asn	Asn	Leu	Thr	Ser 330	Thr	Val	Gln	Val	Phe 335	Thr	
gac	gac	gac	tac	cag	ctg	ccc	tac	gtc	gtc	ggc	aac	ggg	acc	gag	gga	1056
Asp	Asp	Asp	Tyr 340	Gln	Leu	Pro	Tyr	Val 345	Val	Gly	Asn	Gly	Thr 350	Glu	Gly	
tgc	ctg	ccg	gcc	ttc	cct	ccg	cag	gtc	ttt	acg	ctg	ccg	cag	tac	ggc	1104
Cys	Leu	Pro 355	Ala	Phe	Pro	Pro	Gln	Val 360	Phe	Thr	Leu	Pro 365	Gln	Tyr	Gly	
tac	gcg	acg	ctg	aac	cgc	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala 370	Thr	Leu	Asn	Arg	Asp 375	Asn	Thr	Glu	Asn	Pro 380	Thr	Glu	Arg	Ser	
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser 385	Phe	Phe	Cys	Leu	Glu 390	Tyr	Phe	Pro	Ser	Lys 395	Met	Leu	Arg	Thr 400	Gly	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe 405	Thr	Tyr	Asn	Phe	Glu 410	Glu	Val	Pro	Phe	His 415	Ser	
agc	ttc	gct	ccc	agt	cag	aac	ctg	ttc	aag	ctg	gcc	aac	ccg	ctg	gtg	1296
Ser	Phe	Ala 420	Pro	Ser	Gln	Asn	Leu	Phe 425	Lys	Leu	Ala	Asn	Pro 430	Leu	Val	
gac	cag	tac	ttg	tac	cgc	ttc	gtg	agc	aca	aat	aac	act	ggc	gga	gtc	1344
Asp	Gln	Tyr 435	Leu	Tyr	Arg	Phe	Val 440	Ser	Thr	Asn	Asn	Thr 445	Gly	Gly	Val	
cag	ttc	aac	aag	aac	ctg	gcc	ggg	aga	tac	gcc	aac	acc	tac	aaa	aac	1392
Gln	Phe 450	Asn	Lys	Asn	Leu	Ala 455	Gly	Arg	Tyr	Ala	Asn 460	Thr	Tyr	Lys	Asn	
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Trp 465	Phe	Pro	Gly	Pro	Met 470	Gly	Arg	Thr	Gln	Gly 475	Trp	Asn	Leu	Gly 480	Ser	
ggg	gtc	aac	cgc	gcc	agt	gtc	agc	gcc	ttc	gcc	acg	acc	aat	agg	atg	1488
Gly	Val	Asn	Arg	Ala 485	Ser	Val	Ser	Ala	Phe 490	Ala	Thr	Thr	Asn	Arg 495	Met	
gag	ctc	gag	ggc	gcg	agt	tac	cag	gtg	ccc	ccg	cag	ccg	aac	ggc	atg	1536
Glu	Leu	Glu	Gly 500	Ala	Ser	Tyr	Gln	Val 505	Pro	Pro	Gln	Pro	Asn 510	Gly	Met	
acc	aac	aac	ctc	cag	ggc	agc	aac	acc	tat	gcc	ctg	gag	aac	act	atg	1584
Thr	Asn 515	Asn	Leu	Gln	Gly	Ser	Asn 520	Thr	Tyr	Ala	Leu	Glu 525	Asn	Thr	Met	
atc	ttc	aac	agc	cag	ccg	gcg	aac	ccg	ggc	acc	acc	gcc	acg	tac	ctc	1632
Ile 530	Phe	Asn	Ser	Gln	Pro	Ala 535	Asn	Pro	Gly	Thr	Thr 540	Ala	Thr	Tyr	Leu	

gag ggc aac atg ctc atc acc agc gag agc gag acg cag ccg gtg aac	1680
Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn	
545 550 555 560	
cgc gtg gcg tac aac gtc ggc ggg cag atg gcc acc aac aac cag agc	1728
Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser	
565 570 575	
tcc acc act gcc ccc gcg acc ggc acg tac aac ctc cag gaa atc gtg	1776
Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val	
580 585 590	
ccc ggc agc gtg tgg atg gag agg gac gtg tac ctc caa gga ccc atc	1824
Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile	
595 600 605	
tgg gcc aag atc cca gag acg ggg gcg cac ttt cac ccc tct ccg gcc	1872
Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala	
610 615 620	
atg ggc gga ttc gga ctc aaa cac cca ccg ccc atg atg ctc atc aag	1920
Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys	
625 630 635 640	
aac acg cct gtg ccc gga aat atc acc agc ttc tcg gac gtg ccc gtc	1968
Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val	
645 650 655	
agc agc ttc atc acc cag tac agc acc ggg cag gtc acc gtg gag atg	2016
Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met	
660 665 670	
gag tgg gag ctc aag aag gaa aac tcc aag agg tgg aac cca gag atc	2064
Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile	
675 680 685	
cag tac aca aac aac tac aac gac ccc ggt ggt gcc ggt gcc ggt gcc	2112
Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gly Gly Ala Gly Ala Gly Ala	
690 695 700	
ggt cag ttt gtg gac ttt gcc ccg gac agc acc ggg gaa tac aga acc	2160
Gly Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr	
705 710 715 720	
acc aga cct atc gga acc cga tac ctt acc cga ccc ctt taa	2202
Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu	
725 730	

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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gly Gly Ala Gly Ala Gly Ala
690 695 700

Gly Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 17
<211> 2202
<212> DNA
<213> Artificial

<220>
<223> Cap2/5 - 751

<220>
<221> CDS
<222> (1)..(2202)

<220>
<221> misc_feature
<222> (2176)..(2199)
<223> immune evasion repeat sequence

<400> 17
acg gct gcc gac ggt tat cta ccc gat tgg ttg gag gac act ctc tct 48
Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

gaa gga ata aga cag tgg tgg aag ctc aaa cct ggc cca cca cca cca 96
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

aag ccc gca gag cgg cat aag gac gac agc agg ggt ctt gtg ctt cct 144
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

ggg tac aag tac ctc gga ccc ttc aac gga ctc gac aag gga gag ccg 192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

gtc aac gag gca gac gcc gcg gcc ctc gag cac gac aaa gcc tac gac 240
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

cgg cag ctc gac agc gga gac aac ccg tac ctc aag tac aac cac gcc 288
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

gac gcg gag ttt cag gag cgc ctt aaa gaa gat acg tct ttt ggg ggc 336
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

aac ctc gga cga gca gtc ttc cag gcg aaa aag agg gtt ctt gaa cct	384
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro	
115 120 125	
ctg ggc ctg gtt gag gaa cct gtt aag acg gcc cct acc gga aag cgg	432
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg	
130 135 140	
ata gac gac cac ttt cca aaa aga aag aag gct cgg acc gaa gag gac	480
Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp	
145 150 155 160	
tcc aag cct tcc acc tcg tca gac gcc gaa gct gga ccc agc gga tcc	528
Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser	
165 170 175	
cag cag ctg caa atc cca gcc caa cca gcc tca agt ttg gga gct gat	576
Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp	
180 185 190	
aca atg tct gcg gga ggt ggc ggc cca ttg ggc gac aat aac caa ggt	624
Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly	
195 200 205	
gcc gat gga gtg ggc aat gcc tcg gga gat tgg cat tgc gat tcc acg	672
Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr	
210 215 220	
tgg atg ggg gac aga gtc gtc acc aag tcc acc cga acc tgg gtg ctg	720
Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu	
225 230 235 240	
ccc agc tac aac aac cac cag tac cga gag atc aaa agc ggc tcc gtc	768
Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val	
245 250 255	
gac gga agc aac gcc aac gcc tac ttt gga tac agc acc ccc tgg ggg	816
Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly	
260 265 270	
tac ttt gac ttt aac cgc ttc cac agc cac tgg agc ccc cga gac tgg	864
Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp	
275 280 285	
caa aga ctc atc aac aac tac tgg ggc ttc aga ccc cgg tcc ctc aga	912
Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg	
290 295 300	
gtc aaa atc ttc aac att caa gtc aaa gag gtc acg gtg cag gac tcc	960
Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser	
305 310 315 320	
acc acc acc atc gcc aac aac ctc acc tcc acc gtc caa gtg ttt acg	1008
Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr	
325 330 335	
gac gac gac tac cag ctg ccc tac gtc gtc ggc aac ggg acc gag gga	1056

Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	
			340					345					350			
tgc	ctg	ccg	gcc	ttc	cct	ccg	cag	gtc	ttt	acg	ctg	ccg	cag	tac	ggc	1104
Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	
		355					360					365				
tac	gcg	acg	ctg	aac	cg	gac	aac	aca	gaa	aat	ccc	acc	gag	agg	agc	1152
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	
	370					375					380					
agc	ttc	ttc	tgc	cta	gag	tac	ttt	ccc	agc	aag	atg	ctg	aga	acg	ggc	1200
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	
385					390					395					400	
aac	aac	ttt	gag	ttt	acc	tac	aac	ttt	gag	gag	gtg	ccc	ttc	cac	tcc	1248
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	
			405						410					415		
agc	ttc	gct	ccc	agt	cag	aac	ctg	ttc	aag	ctg	gcc	aac	ccg	ctg	gtg	1296
Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	
			420					425					430			
gac	cag	tac	ttg	tac	cg	ttc	gtg	agc	aca	aat	aac	act	ggc	gga	gtc	1344
Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	
		435					440					445				
cag	ttc	aac	aag	aac	ctg	gcc	ggg	aga	tac	gcc	aac	acc	tac	aaa	aac	1392
Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	
	450					455					460					
tgg	ttc	ccg	ggg	ccc	atg	ggc	cga	acc	cag	ggc	tgg	aac	ctg	ggc	tcc	1440
Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	
465					470					475					480	
ggg	gtc	aac	cg	gcc	agt	gtc	agc	gcc	ttc	gcc	acg	acc	aat	agg	atg	1488
Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	
				485					490					495		
gag	ctc	gag	ggc	gcg	agt	tac	cag	gtg	ccc	ccg	cag	ccg	aac	ggc	atg	1536
Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	
			500					505					510			
acc	aac	aac	ctc	cag	ggc	agc	aac	acc	tat	gcc	ctg	gag	aac	act	atg	1584
Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	
		515					520					525				
atc	ttc	aac	agc	cag	ccg	gcg	aac	ccg	ggc	acc	acc	gcc	acg	tac	ctc	1632
Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	
	530					535					540					
gag	ggc	aac	atg	ctc	atc	acc	agc	gag	agc	gag	acg	cag	ccg	gtg	aac	1680
Glu	Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	
545					550					555					560	
cg	gtg	gcg	tac	aac	gtc	ggc	ggg	cag	atg	gcc	acc	aac	aac	cag	agc	1728
Arg	Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	
				565					570					575		

tcc acc act gcc ccc gcg acc ggc acg tac aac ctc cag gaa atc gtg	1776
Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val	
580 585 590	
ccc ggc agc gtg tgg atg gag agg gac gtg tac ctc caa gga ccc atc	1824
Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile	
595 600 605	
tgg gcc aag atc cca gag acg ggg gcg cac ttt cac ccc tct ccg gcc	1872
Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala	
610 615 620	
atg ggc gga ttc gga ctc aaa cac cca ccg ccc atg atg ctc atc aag	1920
Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys	
625 630 635 640	
aac acg cct gtg ccc gga aat atc acc agc ttc tcg gac gtg ccc gtc	1968
Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val	
645 650 655	
agc agc ttc atc acc cag tac agc acc ggg cag gtc acc gtg gag atg	2016
Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met	
660 665 670	
gag tgg gag ctc aag aag gaa aac tcc aag agg tgg aac cca gag atc	2064
Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile	
675 680 685	
cag tac aca aac aac tac aac gac ccc cag ttt gtg gac ttt gcc ccg	2112
Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro	
690 695 700	
gac agc acc ggg gaa tac aga acc acc aga cct atc gga acc cga tac	2160
Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr	
705 710 715 720	
ctt acc cga ccc ctt ggt ggt gcc ggt gcc ggt gcc ggt taa	2202
Leu Thr Arg Pro Leu Gly Gly Ala Gly Ala Gly Ala Gly	
725 730	

<210> 18
 <211> 733
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 18

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
690 695 700

Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705 710 715 720

Leu Thr Arg Pro Leu Gly Gly Ala Gly Ala Gly Ala Gly
725 730

<210> 19
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 236

<220>
<221> MISC_FEATURE
<222> (227)..(234)
<223> immune evasion repeat sequence

<400> 19

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Gly Ala Gly Ala Gly Ala Gly Gly Asp Arg Val Val Thr
225 230 235 240

Lys Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr
245 250 255

Arg Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Ser His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp
290 295 300

Gly Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr
340 345 350

Val Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln
355 360 365

Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn
370 375 380

Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu
420 425 430

Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val
435 440 445

Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 20
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 267

<220>
<221> MISC_FEATURE
<222> (256)..(263)
<223> immune evasion repeat sequence

<400> 20

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Gly
245 250 255

Gly Ala Gly Ala Gly Ala Gly Val Asp Gly Ser Asn Ala Asn Ala Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Ser His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp
290 295 300

Gly Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr
340 345 350

Val Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln
355 360 365

Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn
370 375 380

Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu
420 425 430

Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val
435 440 445

Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 21
<211> 733

<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 382

<220>
<221> MISC_FEATURE
<222> (378)..(385)
<223> immune evasion repeat sequence

<400> 21

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Gly Gly Ala Gly Ala Gly Ala
370 375 380

Gly Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu
420 425 430

Phe Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val
435 440 445

Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 22
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 454

<220>
<221> MISC_FEATURE
<222> (445)..(452)
<223> immune evasion repeat sequence

<400> 22

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Gly Gly Ala Gly
435 440 445

Ala Gly Ala Gly Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 23
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 467

<220>
 <221> MISC_FEATURE
 <222> (454)..(461)
 <223> immune evasion repeat sequence

<400> 23

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
 130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
 145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
 165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
 180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
 195 200 205

Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr			
	210					215					220							
Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu			
225					230					235					240			
Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val			
				245					250					255				
Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly			
			260					265					270					
Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp			
		275					280					285						
Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg			
	290					295					300							
Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser			
305					310					315					320			
Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr			
				325					330					335				
Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly			
			340					345					350					
Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly			
		355					360					365						
Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser			
	370					375					380							
Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly			
385					390					395					400			
Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser			
				405					410					415				
Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val			
			420					425					430					

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Gly Gly Ala Gly Ala Gly Ala Gly Leu Ala Gly
450 455 460

Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg
465 470 475 480

Thr Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 24
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 502

<220>
<221> MISC_FEATURE
<222> (489)..(496)
<223> immune evasion repeat sequence

<400> 24

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Gly Gly Ala Gly Ala Gly Ala Gly
485 490 495

Ala Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln
500 505 510

Val Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn
515 520 525

Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn
530 535 540

Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser
545 550 555 560

Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly
565 570 575

Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly
580 585 590

Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly
610 615 620

Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile
645 650 655

Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 25
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 663

<220>
<221> MISC_FEATURE
<222> (653)..(660)
<223> immune evasion repeat sequence

<400> 25

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Gly Gly Ala Gly
645 650 655

Ala Gly Ala Gly Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp
690 695 700

Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 26
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 708

<220>
<221> MISC_FEATURE
<222> (698)..(705)
<223> immune evasion repeat sequence

<400> 26

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gly Gly Ala Gly Ala Gly Ala
690 695 700

Gly Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr
705 710 715 720

Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 27
<211> 733
<212> PRT
<213> Artificial

<220>
<223> Cap2/5 - 751

<220>
<221> MISC_FEATURE
<222> (726)..(733)
<223> immune evasion repeat sequence

<400> 27

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
690 695 700

Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705 710 715 720

Leu Thr Arg Pro Leu Gly Gly Ala Gly Ala Gly Ala Gly
725 730

<210> 28
<211> 8
<212> PRT
<213> Artificial

<220>
<223> immune evasion repeat sequence

<400> 28

Gly Gly Ala Gly Ala Gly Ala Gly
1 5

<210> 29
<211> 54
<212> DNA
<213> Artificial

<220>
<223> Pr243

<400> 29
gattccacgt ggatgggtgg tgccggtgcc ggtgccggtg gggacagagt cgtc 54

<210> 30
<211> 54
<212> DNA
<213> Artificial

<220>
<223> Pr244

<400> 30
gacgactctg tccccaccgg caccggcacc ggcaccaccc atccacgtgg aatc 54

<210> 31
<211> 52
<212> DNA
<213> Artificial

<220>
<223> Pr245

<400> 31
caaaagcggc tccggtggtg ccggtgccgg tgccggtgtc gacggaagca ac 52

<210> 32
<211> 52

<212> DNA
 <213> Artificial

 <220>
 <223> Pr246

 <400> 32
 gttgcttccg tcgacaccgg caccggcacc ggcaccaccg gagccgcttt tg 52

 <210> 33
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr247

 <400> 33
 gaaccgcgac aacacaggtg gtgccggtgc cggtgccggt gaaaatccca ccgag 55

 <210> 34
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr248

 <400> 34
 ctcggtggga ttttcaccgg caccggcacc ggcaccacct gtgttgtcgc ggttc 55

 <210> 35
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr249

 <400> 35
 ggcaacaact ttgaggggtg tgccggtgcc ggtgccggtt ttacctacaa ctttg 55

 <210> 36
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr250

 <400> 36
 caaagttgta ggtaaaaccg gcaccggcac cggcaccacc ctcaaagttg ttgcc 55

<210> 37
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr251

 <400> 37
 gtgagcaciaa ataacggtgg tgccggtgcc ggtgccggtg ctggcggagt ccag 54

 <210> 38
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr252

 <400> 38
 ctggactccg ccagtaccgg caccggcacc ggcaccaccg ttatttgtgc tcac 54

 <210> 39
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr253

 <400> 39
 cagttcaaca agaacggtgg tgccggtgcc ggtgccggtc tggccgggag atac 54

 <210> 40
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr254

 <400> 40
 gtatctcccc gccagaccgg caccggcacc ggcaccaccg ttcttggtga actg 54

 <210> 41
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr255

 <400> 41
 cgcgccagtg tcagcgggtg tgccggtgcc ggtgccggtg ccttcgccac gacc 54

<210> 42
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr256

 <400> 42
 ggtcgtggcg aaggcaccgg caccggcacc ggcaccaccg ctgacactgg cgcg 54

 <210> 43
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr257

 <400> 43
 ctatgatctt caacagcggg ggtgccgggt ccggtgccgg tcagccggcg aaccc 55

 <210> 44
 <211> 55
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr258

 <400> 44
 gggttcgccg gctgaccggc accggcaccg gcaccaccgc tgttgaagat catag 55

 <210> 45
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr259

 <400> 45
 ggcaccaccg ccacgggtgg tgccgggtgcc ggtgccgggt acctcgaggg caac 54

 <210> 46
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> Pr260

<400> 46
gttgccctcg aggtaaccgg caccggcacc ggcaccaccc gtggcggtgg tgcc 54

<210> 47
<211> 53
<212> DNA
<213> Artificial

<220>
<223> Pr261

<400> 47
ccggcacgta caacggtggt gccggtgccg gtgccggtct ccaggaaatc gtg 53

<210> 48
<211> 53
<212> DNA
<213> Artificial

<220>
<223> Pr262

<400> 48
cacgatttcc tggagaccgg caccggcacc ggcaccaccg ttgtacgtgc cgg 53

<210> 49
<211> 52
<212> DNA
<213> Artificial

<220>
<223> Pr263

<400> 49
caccagcttc tcgggtggtg ccggtgccgg tgccggtgac gtgcccgta gc 52

<210> 50
<211> 52
<212> DNA
<213> Artificial

<220>
<223> Pr264

<400> 50
gctgacgggc acgtcaccgg caccggcacc ggcaccaccc gagaagctgg tg 52

<210> 51
<211> 56
<212> DNA
<213> Artificial

<220>

<223> Pr265

<400> 51
caactacaac gaccccggtg gtgccggtgc cggtgccggt cagtttgttg actttg 56

<210> 52
<211> 56
<212> DNA
<213> Artificial

<220>
<223> Pr266

<400> 52
caaagtccac aaactgaccg gcaccggcac cggcaccacc ggggtcgttg tagttg 56

<210> 53
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Pr280

<400> 53
cttaccgcac cccttggttg tgccggtgcc ggtgccggtt aagaccagc tttcttg 57

<210> 54
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Pr281

<400> 54
caagaaagct gggctottaac cggcaccggc accggcacca ccaaggggtc gggtaag 57

<210> 55
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Pr286

<400> 55
ggactccaag cttccacct c 21

<210> 56
<211> 20
<212> DNA
<213> Artificial

<220>		
<223>	Pr287	
<400>	56	
gccaacaacc tcacctccac		20
<210>	57	
<211>	20	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Pr288	
<400>	57	
ccagggcagc aacacctatg		20
<210>	58	
<211>	19	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Pr299	
<400>	58	
gcaggcacc gtggagatg		19
<210>	59	
<211>	22	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Pr315	
<400>	59	
gctgctttaa tgcctttgta tc		22
<210>	60	
<211>	20	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Pr316	
<400>	60	
aatgaaagcc atacgggaag		20
<210>	61	
<211>	725	

<212> PRT
<213> Artificial

<220>
<223> AAV2/5

<400> 61

Thr Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145 150 155 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
180 185 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
195 200 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
450 455 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
690 695 700

Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705 710 715 720

Leu Thr Arg Pro Leu
725