

62384479818-seql-000001
SEQUENCE LISTING

<110> Advaxis, Inc.
Petit, Robert
Eapen, Anil
Pujols, Mayo

<120> MANUFACTURING DEVICE AND PROCESS FOR PERSONALIZED DELIVERY
VECTOR-BASED IMMUNOTHERAPY

<130> 062384/479818

<150> US 62/184,125

<151> 2015-06-24

<150> US 62/342,037

<151> 2016-05-26

<160> 87

<170> PatentIn version 3.5

<210> 1

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> PEST amino acid sequence

<400> 1

Lys Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala
1 5 10 15

Ser Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys
20 25 30

<210> 2

<211> 529

<212> PRT

<213> Listeria monocytogenes

<400> 2

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu

62384479818-seql-000001

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

195

200

205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
 210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
 225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
 245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
 260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
 275 280 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
 290 295 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
 305 310 315 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
 340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
 355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
 370 375 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile

385 390 395 400

62384479818-seql-000001

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
50 55 60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65 70 75 80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
85 90 95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
100 105 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
115 120 125

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

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145 150 155 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
165 170 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
180 185 190

62384479818-seql-000001

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
195 200 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
275 280 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
290 295 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305 310 315 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
370 375 380

62384479818-seql-000001

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385 390 395 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
405 410 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
420 425 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp
435 440

<210> 4
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> LL0 fragment

<400> 4

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
50 55 60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65 70 75 80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn

85

90

95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
 100 105 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
 115 120 125

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

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
 145 150 155 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
 165 170 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
 180 185 190

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
 195 200 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
 210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
 225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
 245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
 260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn

275

280

285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
 290 295 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
 305 310 315 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
 340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
 355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
 370 375 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
 385 390 395 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
 405 410 415

<210> 5

<211> 14

<212> PRT

<213> *Listeria monocytogenes*

<400> 5

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

<210> 6

<211> 28

62384479818-seql-000001

<212> PRT

<213> *Listeria monocytogenes*

<400> 6

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

Gln Ser Ala Asp Glu Ser Thr Pro Gln Pro Leu Lys
20 25

<210> 7

<211> 20

<212> PRT

<213> *Listeria monocytogenes*

<400> 7

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

Glu Glu Leu Arg
20

<210> 8

<211> 33

<212> PRT

<213> *Listeria monocytogenes*

<400> 8

Arg Gly Gly Ile Pro Thr Ser Glu Glu Phe Ser Ser Leu Asn Ser Gly
1 5 10 15

Asp Phe Thr Asp Asp Glu Asn Ser Glu Thr Thr Glu Glu Glu Ile Asp
20 25 30

Arg

<210> 9

62384479818-seql-000001

<211> 17
<212> PRT
<213> Streptococcus pyogenes

<400> 9

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

Lys

<210> 10
<211> 17
<212> PRT
<213> Streptococcus equisimilis

<400> 10

Lys Gln Asn Thr Ala Asn Thr Glu Thr Thr Thr Thr Asn Glu Gln Pro
1 5 10 15

Lys

<210> 11
<211> 633
<212> PRT
<213> Artificial Sequence

<220>
<223> ActA protein

<400> 11

Met Arg Ala Met Met Val Val Phe Ile Thr Ala Asn Cys Ile Thr Ile
1 5 10 15

Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp Ser Glu Asp Ser Ser Leu
20 25 30

Asn Thr Asp Glu Trp Glu Glu Glu Lys Thr Glu Glu Gln Pro Ser Glu

35

40

45

Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala Arg Glu Val Ser Ser Arg
 50 55 60

Asp Ile Glu Glu Leu Glu Lys Ser Asn Lys Val Lys Asn Thr Asn Lys
 65 70 75 80

Ala Asp Leu Ile Ala Met Leu Lys Ala Lys Ala Glu Lys Gly Pro Asn
 85 90 95

Asn Asn Asn Asn Asn Gly Glu Gln Thr Gly Asn Val Ala Ile Asn Glu
 100 105 110

Glu Ala Ser Gly Val Asp Arg Pro Thr Leu Gln Val Glu Arg Arg His
 115 120 125

Pro Gly Leu Ser Ser Asp Ser Ala Ala Glu Ile Lys Lys Arg Arg Lys
 130 135 140

Ala Ile Ala Ser Ser Asp Ser Glu Leu Glu Ser Leu Thr Tyr Pro Asp
 145 150 155 160

Lys Pro Thr Lys Ala Asn Lys Arg Lys Val Ala Lys Glu Ser Val Val
 165 170 175

Asp Ala Ser Glu Ser Asp Leu Asp Ser Ser Met Gln Ser Ala Asp Glu
 180 185 190

Ser Thr Pro Gln Pro Leu Lys Ala Asn Gln Lys Pro Phe Phe Pro Lys
 195 200 205

Val Phe Lys Lys Ile Lys Asp Ala Gly Lys Trp Val Arg Asp Lys Ile
 210 215 220

Asp Glu Asn Pro Glu Val Lys Lys Ala Ile Val Asp Lys Ser Ala Gly

62384479818-seql-000001

225		230		235		240
Leu	Ile	Asp	Gln	Leu	Leu	Thr
			245			Lys
						Lys
						Lys
						Ser
						Glu
						Glu
						Val
						Asn
						Ala
						255
Ser	Asp	Phe	Pro	Pro	Pro	Thr
			260			Asp
						Glu
						Glu
						Leu
						Arg
						Leu
						Ala
						Leu
						270
Pro	Glu	Thr	Pro	Met	Leu	Leu
						Gly
						Phe
						Asn
						Ala
						Pro
						Thr
						Pro
						Ser
						Glu
						275
Pro	Ser	Ser	Phe	Glu	Phe	Pro
						Pro
						Pro
						Pro
						Thr
						Asp
						Glu
						Glu
						Leu
						Arg
						290
Leu	Ala	Leu	Pro	Glu	Thr	Pro
						Met
						Leu
						Leu
						Gly
						Phe
						Asn
						Ala
						Pro
						Ala
						305
Thr	Ser	Glu	Pro	Ser	Ser	Phe
						Glu
						Phe
						Pro
						Pro
						Pro
						Pro
						Thr
						Glu
						Asp
						325
Glu	Leu	Glu	Ile	Met	Arg	Glu
						Thr
						Ala
						Pro
						Ser
						Leu
						Asp
						Ser
						Ser
						Phe
						340
Thr	Ser	Gly	Asp	Leu	Ala	Ser
						Leu
						Arg
						Ser
						Ala
						Ile
						Asn
						Arg
						His
						Ser
						355
Glu	Asn	Phe	Ser	Asp	Phe	Pro
						Leu
						Ile
						Pro
						Thr
						Glu
						Glu
						Glu
						Leu
						Asn
						370
Gly	Arg	Gly	Gly	Arg	Pro	Thr
						Ser
						Glu
						Glu
						Phe
						Ser
						Ser
						Leu
						Asn
						Ser
						385
Gly	Asp	Phe	Thr	Asp	Asp	Glu
						Asn
						Ser
						Glu
						Thr
						Thr
						Glu
						Glu
						Glu
						Ile
						405
Asp	Arg	Leu	Ala	Asp	Leu	Arg
						Asp
						Arg
						Gly
						Thr
						Gly
						Lys
						His
						Ser
						Arg
						410
						415

420

425

430

Asn Ala Gly Phe Leu Pro Leu Asn Pro Phe Ile Ser Ser Pro Val Pro
 435 440 445

Ser Leu Thr Pro Lys Val Pro Lys Ile Ser Ala Pro Ala Leu Ile Ser
 450 455 460

Asp Ile Thr Lys Lys Ala Pro Phe Lys Asn Pro Ser Gln Pro Leu Asn
 465 470 475 480

Val Phe Asn Lys Lys Thr Thr Thr Lys Thr Val Thr Lys Lys Pro Thr
 485 490 495

Pro Val Lys Thr Ala Pro Lys Leu Ala Glu Leu Pro Ala Thr Lys Pro
 500 505 510

Gln Glu Thr Val Leu Arg Glu Asn Lys Thr Pro Phe Ile Glu Lys Gln
 515 520 525

Ala Glu Thr Asn Lys Gln Ser Ile Asn Met Pro Ser Leu Pro Val Ile
 530 535 540

Gln Lys Glu Ala Thr Glu Ser Asp Lys Glu Glu Met Lys Pro Gln Thr
 545 550 555 560

Glu Glu Lys Met Val Glu Glu Ser Glu Ser Ala Asn Asn Ala Asn Gly
 565 570 575

Lys Asn Arg Ser Ala Gly Ile Glu Glu Gly Lys Leu Ile Ala Lys Ser
 580 585 590

Ala Glu Asp Glu Lys Ala Lys Glu Glu Pro Gly Asn His Thr Thr Leu
 595 600 605

Ile Leu Ala Met Leu Ala Ile Gly Val Phe Ser Leu Gly Ala Phe Ile

610

615

620

Lys Ile Ile Gln Leu Arg Lys Asn Asn
625 630

<210> 12

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> truncated ActA protein

<400> 12

Met Arg Ala Met Met Val Val Phe Ile Thr Ala Asn Cys Ile Thr Ile
1 5 10 15

Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp Ser Glu Asp Ser Ser Leu
20 25 30

Asn Thr Asp Glu Trp Glu Glu Glu Lys Thr Glu Glu Gln Pro Ser Glu
35 40 45

Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala Arg Glu Val Ser Ser Arg
50 55 60

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

Ala Asp Leu Ile Ala Met Leu Lys Glu Lys Ala Glu Lys Gly Pro Asn
85 90 95

Ile Asn Asn Asn Asn Ser Glu Gln Thr Glu Asn Ala Ala Ile Asn Glu
100 105 110

Glu Ala Ser Gly Ala Asp Arg Pro Ala Ile Gln Val Glu Arg Arg His
115 120 125

62384479818-seql-000001

Pro Gly Leu Pro Ser Asp Ser Ala Ala Glu Ile Lys Lys Arg Arg Lys
130 135 140

Ala Ile Ala Ser Ser Asp Ser Glu Leu Glu Ser Leu Thr Tyr Pro Asp
145 150 155 160

Lys Pro Thr Lys Val Asn Lys Lys Lys Val Ala Lys Glu Ser Val Ala
165 170 175

Asp Ala Ser Glu Ser Asp Leu Asp Ser Ser Met Gln Ser Ala Asp Glu
180 185 190

Ser Ser Pro Gln Pro Leu Lys Ala Asn Gln Gln Pro Phe Phe Pro Lys
195 200 205

Val Phe Lys Lys Ile Lys Asp Ala Gly Lys Trp Val Arg Asp Lys Ile
210 215 220

Asp Glu Asn Pro Glu Val Lys Lys Ala Ile Val Asp Lys Ser Ala Gly
225 230 235 240

Leu Ile Asp Gln Leu Leu Thr Lys Lys Lys Ser Glu Glu Val Asn Ala
245 250 255

Ser Asp Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu Ala Leu
260 265 270

Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala Thr Ser Glu
275 280 285

Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg
290 295 300

Leu Ala Leu Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala
305 310 315 320

62384479818-seql-000001

Thr Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Glu Asp
325 330 335

Glu Leu Glu Ile Ile Arg Glu Thr Ala Ser Ser Leu Asp Ser Ser Phe
340 345 350

Thr Arg Gly Asp Leu Ala Ser Leu Arg Asn Ala Ile Asn Arg His Ser
355 360 365

Gln Asn Phe Ser Asp Phe Pro Pro Ile Pro Thr Glu Glu Glu Leu Asn
370 375 380

Gly Arg Gly Gly Arg Pro
385 390

<210> 13
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> truncated ActA protein

<400> 13

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

Ala Asn Cys Ile Thr Ile Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp
20 25 30

Ser Glu Asp Ser Ser Leu Asn Thr Asp Glu Trp Glu Glu Glu Lys Thr
35 40 45

Glu Glu Gln Pro Ser Glu Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala
50 55 60

Arg Glu Val Ser Ser Arg Asp Ile Lys Glu Leu Glu Lys Ser Asn Lys

65					70					75					80	
Val	Arg	Asn	Thr	Asn	Lys	Ala	Asp	Leu	Ile	Ala	Met	Leu	Lys	Glu	Lys	
				85					90					95		
Ala	Glu	Lys	Gly													
			100													
<210>	14															
<211>	639															
<212>	PRT															
<213>	Artificial Sequence															
<220>																
<223>	ActA protein															
<400>	14															
Met	Gly	Leu	Asn	Arg	Phe	Met	Arg	Ala	Met	Met	Val	Val	Phe	Ile	Thr	
1				5					10					15		
Ala	Asn	Cys	Ile	Thr	Ile	Asn	Pro	Asp	Ile	Ile	Phe	Ala	Ala	Thr	Asp	
			20					25					30			
Ser	Glu	Asp	Ser	Ser	Leu	Asn	Thr	Asp	Glu	Trp	Glu	Glu	Glu	Lys	Thr	
		35					40					45				
Glu	Glu	Gln	Pro	Ser	Glu	Val	Asn	Thr	Gly	Pro	Arg	Tyr	Glu	Thr	Ala	
	50					55					60					
Arg	Glu	Val	Ser	Ser	Arg	Asp	Ile	Glu	Glu	Leu	Glu	Lys	Ser	Asn	Lys	
65					70					75					80	
Val	Lys	Asn	Thr	Asn	Lys	Ala	Asp	Leu	Ile	Ala	Met	Leu	Lys	Ala	Lys	
				85					90					95		
Ala	Glu	Lys	Gly	Pro	Asn	Asn	Asn	Asn	Asn	Asn	Gly	Glu	Gln	Thr	Gly	
			100					105					110			

62384479818-seql-000001

Asn Val Ala Ile Asn Glu Glu Ala Ser Gly Val Asp Arg Pro Thr Leu
115 120 125

Gln Val Glu Arg Arg His Pro Gly Leu Ser Ser Asp Ser Ala Ala Glu
130 135 140

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

Ser Leu Thr Tyr Pro Asp Lys Pro Thr Lys Ala Asn Lys Arg Lys Val
165 170 175

Ala Lys Glu Ser Val Val Asp Ala Ser Glu Ser Asp Leu Asp Ser Ser
180 185 190

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

Lys Pro Phe Phe Pro Lys Val Phe Lys Lys Ile Lys Asp Ala Gly Lys
210 215 220

Trp Val Arg Asp Lys Ile Asp Glu Asn Pro Glu Val Lys Lys Ala Ile
225 230 235 240

Val Asp Lys Ser Ala Gly Leu Ile Asp Gln Leu Leu Thr Lys Lys Lys
245 250 255

Ser Glu Glu Val Asn Ala Ser Asp Phe Pro Pro Pro Pro Thr Asp Glu
260 265 270

Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro Met Leu Leu Gly Phe Asn
275 280 285

Ala Pro Thr Pro Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro
290 295 300

62384479818-seql-000001

Thr Asp Glu Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro Met Leu Leu
305 310 315 320

Gly Phe Asn Ala Pro Ala Thr Ser Glu Pro Ser Ser Phe Glu Phe Pro
325 330 335

Pro Pro Pro Thr Glu Asp Glu Leu Glu Ile Met Arg Glu Thr Ala Pro
340 345 350

Ser Leu Asp Ser Ser Phe Thr Ser Gly Asp Leu Ala Ser Leu Arg Ser
355 360 365

Ala Ile Asn Arg His Ser Glu Asn Phe Ser Asp Phe Pro Leu Ile Pro
370 375 380

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

Phe Ser Ser Leu Asn Ser Gly Asp Phe Thr Asp Asp Glu Asn Ser Glu
405 410 415

Thr Thr Glu Glu Glu Ile Asp Arg Leu Ala Asp Leu Arg Asp Arg Gly
420 425 430

Thr Gly Lys His Ser Arg Asn Ala Gly Phe Leu Pro Leu Asn Pro Phe
435 440 445

Ile Ser Ser Pro Val Pro Ser Leu Thr Pro Lys Val Pro Lys Ile Ser
450 455 460

Ala Pro Ala Leu Ile Ser Asp Ile Thr Lys Lys Ala Pro Phe Lys Asn
465 470 475 480

Pro Ser Gln Pro Leu Asn Val Phe Asn Lys Lys Thr Thr Thr Lys Thr
485 490 495

62384479818-seq1-000001

Val Thr Lys Lys Pro Thr Pro Val Lys Thr Ala Pro Lys Leu Ala Glu
500 505 510

Leu Pro Ala Thr Lys Pro Gln Glu Thr Val Leu Arg Glu Asn Lys Thr
515 520 525

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

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

Glu Met Lys Pro Gln Thr Glu Glu Lys Met Val Glu Glu Ser Glu Ser
565 570 575

Ala Asn Asn Ala Asn Gly Lys Asn Arg Ser Ala Gly Ile Glu Glu Gly
580 585 590

Lys Leu Ile Ala Lys Ser Ala Glu Asp Glu Lys Ala Lys Glu Glu Pro
595 600 605

Gly Asn His Thr Thr Leu Ile Leu Ala Met Leu Ala Ile Gly Val Phe
610 615 620

Ser Leu Gly Ala Phe Ile Lys Ile Ile Gln Leu Arg Lys Asn Asn
625 630 635

<210> 15

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> truncated ActA protein

<400> 15

Ala Thr Asp Ser Glu Asp Ser Ser Leu Asn Thr Asp Glu Trp Glu Glu

62384479818-seq1-000001

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

<210> 16
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> truncated ActA protein

<400> 16

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

62384479818-seq1-000001

Lys Ala Lys Ala Glu Lys Gly Pro Asn Asn Asn Asn Asn Asn Gly Glu
65 70 75 80

Gln Thr Gly Asn Val Ala Ile Asn Glu Glu Ala Ser Gly Val Asp Arg
85 90 95

Pro Thr Leu Gln Val Glu Arg Arg His Pro Gly Leu Ser Ser Asp Ser
100 105 110

Ala Ala Glu Ile Lys Lys Arg Arg Lys Ala Ile Ala Ser Ser Asp Ser
115 120 125

Glu Leu Glu Ser Leu Thr Tyr Pro Asp Lys Pro Thr Lys Ala Asn Lys
130 135 140

Arg Lys Val Ala Lys Glu Ser Val Val Asp Ala Ser Glu Ser Asp Leu
145 150 155 160

Asp Ser Ser Met Gln Ser Ala Asp Glu Ser Thr Pro Gln Pro Leu Lys
165 170 175

Ala Asn Gln Lys Pro Phe Phe Pro Lys Val Phe Lys Lys Ile Lys Asp
180 185 190

Ala Gly Lys Trp Val Arg Asp Lys
195 200

<210> 17
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> truncated ActA protein

<400> 17

Ala Thr Asp Ser Glu Asp Ser Ser Leu Asn Thr Asp Glu Trp Glu Glu

62384479818-seq1-000001

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

62384479818-seql-000001

195

200

205

Lys Ala Ile Val Asp Lys Ser Ala Gly Leu Ile Asp Gln Leu Leu Thr
210 215 220

Lys Lys Lys Ser Glu Glu Val Asn Ala Ser Asp Phe Pro Pro Pro Pro
225 230 235 240

Thr Asp Glu Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro Met Leu Leu
245 250 255

Gly Phe Asn Ala Pro Thr Pro Ser Glu Pro Ser Ser Phe Glu Phe Pro
260 265 270

Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro
275 280 285

Met Leu Leu Gly Phe Asn Ala Pro Ala Thr Ser Glu Pro Ser Ser
290 295 300

<210> 18

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<223> truncated ActA protein

<400> 18

Ala Thr Asp Ser Glu Asp Ser Ser Leu Asn Thr Asp Glu Trp Glu Glu
1 5 10 15

Glu Lys Thr Glu Glu Gln Pro Ser Glu Val Asn Thr Gly Pro Arg Tyr
20 25 30

Glu Thr Ala Arg Glu Val Ser Ser Arg Asp Ile Glu Glu Leu Glu Lys
35 40 45

62384479818-seql-000001

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

Lys Ala Lys Ala Glu Lys Gly Pro Asn Asn Asn Asn Asn Gly Glu
65 70 75 80

Gln Thr Gly Asn Val Ala Ile Asn Glu Glu Ala Ser Gly Val Asp Arg
85 90 95

Pro Thr Leu Gln Val Glu Arg Arg His Pro Gly Leu Ser Ser Asp Ser
100 105 110

Ala Ala Glu Ile Lys Lys Arg Arg Lys Ala Ile Ala Ser Ser Asp Ser
115 120 125

Glu Leu Glu Ser Leu Thr Tyr Pro Asp Lys Pro Thr Lys Ala Asn Lys
130 135 140

Arg Lys Val Ala Lys Glu Ser Val Val Asp Ala Ser Glu Ser Asp Leu
145 150 155 160

Asp Ser Ser Met Gln Ser Ala Asp Glu Ser Thr Pro Gln Pro Leu Lys
165 170 175

Ala Asn Gln Lys Pro Phe Phe Pro Lys Val Phe Lys Lys Ile Lys Asp
180 185 190

Ala Gly Lys Trp Val Arg Asp Lys Ile Asp Glu Asn Pro Glu Val Lys
195 200 205

Lys Ala Ile Val Asp Lys Ser Ala Gly Leu Ile Asp Gln Leu Leu Thr
210 215 220

Lys Lys Lys Ser Glu Glu Val Asn Ala Ser Asp Phe Pro Pro Pro Pro
225 230 235 240

62384479818-seql-000001

Thr Asp Glu Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro Met Leu Leu
245 250 255

Gly Phe Asn Ala Pro Thr Pro Ser Glu Pro Ser Ser Phe Glu Phe Pro
260 265 270

Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu Ala Leu Pro Glu Thr Pro
275 280 285

Met Leu Leu Gly Phe Asn Ala Pro Ala Thr Ser Glu Pro Ser Ser Phe
290 295 300

Glu Phe Pro Pro Pro Pro Thr Glu Asp Glu Leu Glu Ile Met Arg Glu
305 310 315 320

Thr Ala Pro Ser Leu Asp Ser Ser Phe Thr Ser Gly Asp Leu Ala Ser
325 330 335

Leu Arg Ser Ala Ile Asn Arg His Ser Glu Asn Phe Ser Asp Phe Pro
340 345 350

Leu Ile Pro Thr Glu Glu Glu Leu Asn Gly Arg Gly Gly Arg Pro Thr
355 360 365

Ser Glu
370

<210> 19
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>
<223> truncated ActA

<400> 19
atgcgtgcga tgatggtggt tttcattact gccaatgca ttacgattaa ccccgacata

60

62384479818-seql-000001

atatttgcag cgacagatag cgaagattct agtctaaca cagatgaatg ggaagaagaa	120
aaaacagaag agcaaccaag cgaggtaa at acgggaccaa gatacgaaac tgcacgtgaa	180
gtaagttcac gtgatattaa agaactagaa aaatcgaata aagtgagaaa tacgaacaaa	240
gcagacctaa tagcaatgtt gaaagaaaaa gcagaaaaag gtccaaatat caataataac	300
aacagtgaac aaactgagaa tgcggctata aatgaagagg cttcaggagc cgaccgacca	360
gctatacaag tggagcgtcg tcatccagga ttgccatcgg atagcgcagc ggaaattaaa	420
aaaagaagga aagccatagc atcatcggat agtgagcttg aaagccttac ttatccggat	480
aaaccaacaa aagtaaataa gaaaaaagtg gcgaaagagt cagttgcgga tgcttctgaa	540
agtgacttag attctagcat gcagtcagca gatgagtctt caccacaacc tttaaaagca	600
aaccaacaac catttttccc taaagtattt aaaaaaataa aagatgcggg gaaatgggta	660
cgtgataaaa tcgacgaaaa tcctgaagta aagaaagcga ttgttgataa aagtcagggg	720
ttaattgacc aattattaac caaaaagaaa agtgaagagg taaatgcttc ggacttcccg	780
ccaccaccta cggatgaaga gttaagactt gctttgccag agacaccaat gcttcttggt	840
tttaatgctc ctgctacatc agaaccgagc tcattcgaat ttccaccacc acctacggat	900
gaagagttaa gacttgcttt gccagagacg ccaatgcttc ttggttttta tgctcctgct	960
acatcgggaac cgagctcggt cgaattttcca ccgcctccaa cagaagatga actagaaatc	1020
atccgggaaa cagcatcctc gctagattct agttttacaa gaggggattt agctagtttg	1080
agaaatgcta ttaatcgcca tagtcaaaat ttctctgatt tcccaccaat cccaacagaa	1140
gaagagttga acgggagagg cggtagacca	1170

<210> 20
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E7 protein

<400> 20

62384479818-seql-000001

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30

Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45

Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80

Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95

Lys Pro

<210> 21
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> E7 protein

<400> 21

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

Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln Leu Ser
20 25 30

Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His

35

40

45

Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met
 50 55 60

Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala
 65 70 75 80

Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe
 85 90 95

Val Cys Pro Trp Cys Ala Ser Gln Gln
 100 105

<210> 22
 <211> 1263
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chimeric Her-2

<400> 22
 gagacccacc tggacatgct ccgccacctc taccagggct gccaggtggt gcagggaac 60
 ctggaactca cctacctgcc caccaatgcc agcctgtcct tcctgcagga tatccaggag 120
 gtgcagggct acgtgctcat cgctcacaac caagtgaggc aggtcccact gcagaggctg 180
 cggattgtgc gaggcacca gctctttgag gacaactatg ccctggccgt gctagacaat 240
 ggagacccgc tgaacaatac caccctgtc acaggggcct cccagaggag cctgcgggag 300
 ctgcagcttc gaagcctcac agagatcttg aaaggagggg tcttgatcca gcggaacccc 360
 cagctctgct accaggacac gattttgtgg aagaatatcc aggagtttgc tggctgcaag 420
 aagatctttg ggagcctggc atttctgccg gagagctttg atggggaccc agcctccaac 480
 actgccccgc tccagccaga gcagctccaa gtgtttgaga ctctggaaga gatcacaggt 540
 tacctataca tctcagcatg gccggacagc ctgcctgacc tcagcgtctt ccagaacctg 600

62384479818-seql-000001

caagtaatcc ggggacgaat tctgcacaat ggcgcctact cgctgaccct gcaagggctg 660
ggcatcagct ggctggggct gcgctcactg agggaaactgg gcagtggact ggccctcatc 720
caccataaca cccacctctg cttcgtgcac acggtgccct gggaccagct ctttcggaac 780
ccgcaccaag ctctgctcca cactgccaac cggccagagg acgagtgtgt gggcgagggc 840
ctggcctgcc accagctgtg cgcccagagg cagcagaaga tccggaagta cacgatgcgg 900
agactgctgc aggaaacgga gctggtggag ccgctgacac ctagcggagc gatgccaac 960
caggcgcaga tgcggatcct gaaagagacg gagctgagga aggtgaaggt gcttgatctt 1020
ggcgcttttg gcacagtcta caaggcatc tggatccctg atggggagaa tgtgaaaatt 1080
ccagtggcca tcaaagtgtt gagggaaaac acatcccca aagccaacaa agaaatctta 1140
gacgaagcat acgtgatggc tgggtgtgggc tccccatatg tctcccgctt tctgggcatc 1200
tgcctgacat ccacggtgca gctggtgaca cagcttatgc cctatggctg cctcttagac 1260
taa 1263

<210> 23
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Her-2 chimeric protein

<400> 23

Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln Val
1 5 10 15

Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu
20 25 30

Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala
35 40 45

His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg

62384479818-seq1-000001

50

55

60

Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn
65 70 75 80

Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly
85 90 95

Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly
100 105 110

Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile
115 120 125

Leu Trp Lys Asn Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly
130 135 140

Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn
145 150 155 160

Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu
165 170 175

Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro
180 185 190

Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu
195 200 205

His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp
210 215 220

Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile
225 230 235 240

His His Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln

62384479818-seql-000001

245

250

255

Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro
260 265 270

Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala
275 280 285

Arg Gly Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Gln
290 295 300

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

Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu Arg Lys Val Lys
325 330 335

Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile
340 345 350

Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg
355 360 365

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

Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile
385 390 395 400

Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly
405 410 415

Cys Leu Leu Asp
420

<210> 24

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

<220>
 <223> primer

<400> 24
 ggctcgagca tggagataca cc 22

<210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 25
 ggggactagt ttatggtttc tgagaaca 28

<210> 26
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 26
 gggggctagc cctcctttga ttagtatatt c 31

<210> 27
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 27
 ctccctcgag atcataatctt acttcac 28

<210> 28

62384479818-seql-000001

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

 <220>
 <223> primer

 <400> 28
 gactacaagg acgatgaccg acaagtgata acccgggatc taaataaatc cgttt 55

 <210> 29
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 29
 cccgtcgacc agctcttctt ggtgaag 27

 <210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 30
 gcggatccca tggagataca cctac 25

 <210> 31
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 31
 gctctagatt atggtttctg ag 22

 <210> 32

<211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 32
 ggggtctaga cctcctttga ttagtatatt c 31

<210> 33
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 33
 atcttcgcta tctgtcgccg cggcgcgtgc ttcagtttgt tgcgc 45

<210> 34
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 34
 gcgcaacaaa ctgaagcagc ggccgcggcg acagatagcg aagat 45

<210> 35
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 35
 tgtaggtgta tctccatgct cgagagctag gcgatcaatt tc 42

<210> 36

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

 <220>
 <223> primer

 <400> 36
 ggaattgatc gcctagctct cgagcatgga gatacaccta ca 42

 <210> 37
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 37
 aaacggattt atttagatcc cgggttatgg tttctgagaa ca 42

 <210> 38
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 38
 tgttctcaga aaccataacc cgggatctaa ataaatccgt tt 42

 <210> 39
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 39
 gggggtcgac cagctcttct tggatgaag 28

 <210> 40

62384479818-seql-000001

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

<220>
<223> phycoerythrin (PE)-conjugated E7 peptide

<400> 40

Arg Ala His Tyr Asn Ile Val Thr Phe
1 5

<210> 41
<211> 6523
<212> DNA
<213> Artificial Sequence

<220>
<223> plasmid pAdv142

<400> 41
cggagtgtat actggcttac tatgttggca ctgatgaggg tgtcagtga gtgcttcatg 60
tggcaggaga aaaaaggctg caccggtgcg tcagcagaat atgtgataca ggatatattc 120
cgcttcctcg ctactgact cgctacgctc ggctcgttcga ctgcggcgag cggaaatggc 180
ttacgaacgg ggcggagatt tcctggaaga tgccaggaag atacttaaca ggggaagtga 240
agggccgcgg caaagccgtt tttccatagg ctccgcccc ctgacaagca tcacgaaatc 300
tgacgctcaa atcagtgggtg gcgaaacccg acaggactat aaagatacca ggcgtttccc 360
cctggcggct ccctcgtgcg ctctcctgtt cctgcctttc gggtttaccgg tgcattccg 420
ctgttatggc cgcgtttgtc tcattccacg cctgacactc agttccgggt aggcagttcg 480
ctccaagctg gactgtatgc acgaaccccc cgttcagtcc gaccgctgcg cttatccgg 540
taactatcgt cttgagtcca acccggaag acatgcaaaa gcaccactgg cagcagccac 600
tggttaattga tttagaggag ttagtcttga agtcatgcgc cggttaaggc taaactgaaa 660
ggacaagttt tgggtgactgc gtcctccaa gccagttacc tcggttcaaa gagttggtag 720
ctcagagaac cttcgaaaaa ccgccctgca aggcgggtttt ttcgttttca gagcaagaga 780

62384479818-seql-000001

ttacgcgcag accaaaaacga tctcaagaag atcatcttat taatcagata aaatatttct	840
agccctcctt tgattagtat attcctatct taaagttact tttatgtgga ggcattaaca	900
tttgttaatg acgtcaaaag gatagcaaga ctagaataaa gctataaagc aagcatataa	960
tattgcgttt catctttaga agcgaatttc gccaatatta taattatcaa aagagagggg	1020
tggcaaacgg tatTTggcat tattaggTTa aaaaatgtag aaggagagtg aaacccatga	1080
aaaaaataat gctagTTTTt attacactta tattagTTag tctaccaatt gcgcaacaaa	1140
ctgaagcaaa ggatgcatct gcattcaata aagaaaattc aatttcatcc atggcaccac	1200
cagcatctcc gcctgcaagt cctaagacgc caatcgaaaa gaaacacgcg gatgaaatcg	1260
ataagtatat acaaggattg gattacaata aaaacaatgt attagtatac cacggagatg	1320
cagtgacaaa tgtgccgcca agaaaaggTT acaaagatgg aaatgaatat attgttTgtg	1380
agaaaaagaa gaaatccatc aatcaaaaata atgcagacat tcaagttgtg aatgcaattt	1440
cgagcctaac ctatccaggt gctctcgtaa aagcgaattc ggaattagta gaaaatcaac	1500
cagatgttct ccctgtaaaa cgtgattcat taacactcag cattgatttg ccaggTatga	1560
ctaatacaaga caataaaaata gttgtaaaaa atgccactaa atcaaacgTT aacaacgcag	1620
taaatacatt agtggaaga tggaatgaaa aatatgctca agcttatcca aatgtaagtg	1680
caaaaattga ttatgatgac gaaatggctt acagtgaatc acaattaatt gcgaaatttg	1740
gtacagcatt taaagctgta aataatagct tgaatgtaaa cttcggcgca atcagtgaag	1800
ggaaaatgca agaagaagtc attagTTTTa acaaatttTa ctataacgtg aatgtTaatg	1860
aacctacaag accttccaga tttttcggca aagctgttac taaagagcag ttgcaagcgc	1920
ttggagtga tgcagaaaaat cctcctgcat atatctcaag tgtggcgtat ggccgtcaag	1980
tttatttgaa attatcaact aattcccata gtactaaagt aaaagctgct tttgatgctg	2040
ccgtaagcgg aaaatctgtc tcaggTgatg tagaactaac aaatatcatc aaaaattctt	2100
ccttcaaagc cgtaatttTac ggaggTtccg caaaagatga agttcaaatc atcgacggca	2160
acctcggaga cttacgcgat attttgaaaa aaggcgctac ttttaatcga gaaacaccag	2220

62384479818-seql-000001

gagttcccat tgcttataca acaaacttcc taaaagacaa tgaattagct gttattaaaa	2280
acaactcaga atatattgaa acaacttcaa aagcttatac agatggaaaa attaacatcg	2340
atcactctgg aggatacggt gctcaattca acatttcttg ggatgaagta aattatgatc	2400
tcgagattgt gggaggctgg gagtgcgaga agcattccca accctggcag gtgcttgtgg	2460
cctctcgtgg cagggcagtc tgcggcgggtg ttctgggtgca cccccagtgg gtcctcacag	2520
ctgcccactg catcaggaac aaaagcgtga tcttgctggg tcggcacagc ctgtttcatc	2580
ctgaagacac aggccaggta tttcagggtca gccacagctt cccacacccg ctctacgata	2640
tgagcctcct gaagaatcga ttcctcaggc caggatgatga ctccagccac gacctcatgc	2700
tgctccgcct gtcagagcct gccgagctca cggatgctgt gaaggtcatg gacctgcccc	2760
cccaggagcc agcactgggg accacctgct acgcctcagg ctggggcagc attgaaccag	2820
aggagtctt gaccccaaag aaacttcagt gtgtggacct ccatgttatt tccaatgacg	2880
tgtgtgcgca agttcacctt cagaagggtga ccaagttcat gctgtgtgct ggacgctgga	2940
cagggggcaa aagcacctgc tcgggtgatt ctgggggccc acttgtctgt tatggtgtgc	3000
ttcaagggtat cacgtcatgg ggcagtgaac catgtgccct gcccgaaagg ctttcctgt	3060
acaccaaggt ggtgcattac cggaagtga tcaaggacac catcgtggcc aaccctaac	3120
ccggggccact aactcaacgc tagtagtgga tttaatccca aatgagccaa cagaaccaga	3180
accagaaaca gaacaagtaa cattggagtt agaaatggaa gaagaaaaaa gcaatgattt	3240
cgtgtgaata atgcacgaaa tcattgctta tttttttaaa aagcgatata ctagatataa	3300
cgaaacaacg aactgaataa agaatacaaa aaaagagcca cgaccagtta aagcctgaga	3360
aactttaact gcgagcctta attgattacc accaatcaat taaagaagtc gagacccaaa	3420
atttggtaaa gtatttaatt actttattaa tcagatactt aaatatctgt aaaccatta	3480
tatcgggttt ttgaggggat ttcaagtctt taagaagata ccaggcaatc aattaagaaa	3540
aacttagttg attgcctttt ttgttgtgat tcaactttga tcgtagcttc taactaatta	3600
attttcgtaa gaaaggagaa cagctgaatg aatatccctt ttgttgtaga aactgtgctt	3660

62384479818-seql-000001

catgacggct tgttaaagta caaatTTaaa aatagTaaaa ttcgctcaat cactaccaag	3720
ccaggTaaaa gTaaaggggc tatttttgcg tatcgctcaa aaaaaagcat gattggcgga	3780
cgtggcgttg ttctgacttc cgaagaagcg attcacgaaa atcaagatac atttacgcat	3840
tggacaccaa acgtttatcg ttatggtacg tatgcagacg aaaaccgttc atacactaaa	3900
ggacattctg aaaacaattt aagacaaatc aataccttct ttattgattt tgatattcac	3960
acggaaaaag aaactatttc agcaagcgat attttaacaa cagctattga tttaggTTTT	4020
atgcctacgt taattatcaa atctgataaa ggTtatcaag catattttgt tttagaaacg	4080
ccagtctatg tgacttcaaa atcagaattt aaatctgtca aagcagccaa aataatctcg	4140
caaaatatcc gagaatattt tggaaagtct ttgccagttg atctaacgtg caatcatttt	4200
gggattgctc gtataccaag aacggacaat gtagaatttt ttgatcccaa ttaccgttat	4260
tctttcaaag aatggcaaga ttggtctttc aaacaaacag ataataaggg ctttactcgt	4320
tcaagtctaa cggttttaag cggtacagaa ggcaaaaaac aagtagatga accctggttt	4380
aatctcttat tgcacgaaac gaaattttca ggagaaaagg gtttagtagg gcgcaatagc	4440
gttatgttta ccctctcttt agcctacttt agttcaggct attcaatcga aacgtgcgaa	4500
tataatatgt ttgagtttaa taatcgatta gatcaaccct tagaagaaaa agaagtaatc	4560
aaaattgtta gaagtgccta ttcagaaaac tatcaagggg ctaataggga atacattacc	4620
attctttgca aagcttgggt atcaagtgat ttaaccagta aagatttatt tgtccgtcaa	4680
gggtggttta aattcaagaa aaaaagaagc gaacgtcaac gtgttcattt gtcagaatgg	4740
aaagaagatt taatggctta tattagcgaa aaaagcgatg tatacaagcc ttatttagcg	4800
acgacaaaaa aagagattag agaagtgcta ggcatcctg aacggacatt agataaattg	4860
ctgaaggTtac tgaaggcgaa tcaggaaatt ttctttaaga ttaaaccagg aagaaatggt	4920
ggcattcaac ttgctagtgt taaatcattg ttgctatcga tcattaaatt aaaaaagaa	4980
gaacgagaaa gctatataaa ggcgctgaca gcttcgttta atttagaacg tacatttatt	5040
caagaaactc taaacaaatt ggcagaacgc cccaaaacgg acccacaact cgatttgttt	5100

62384479818-seq1-000001

agctacgata caggctgaaa ataaaacccg cactatgcca ttacatttat atctatgata	5160
cgtgttttgtt tttcttttgct ggctagctta attgcttata tttacctgca ataaaggatt	5220
tcttacttcc attatactcc catttttccaa aaacatacgg ggaacacggg aacttattgt	5280
acaggccacc tcatagttaa tggtttcgag ctttcctgca atctcatcca tggaaatata	5340
ttcatcccc tgccggccta ttaatgtgac ttttgtgccc ggcggatatt cctgatccag	5400
ctccaccata aattgggtcca tgcaaattcg gccggcaatt ttcaggcggtt ttcccttcac	5460
aaggatgtcg gtccctttca attttcggag ccagccgtcc gcatagccta caggcaccgt	5520
cccgatccat gtgtcttttt ccgctgtgta ctcggctccg tagctgacgc tctcgccttt	5580
tctgatcagt ttgacatgtg acagtgtcga atgcagggtta aatgccggac gcagctgaaa	5640
cggatatctcg tccgacatgt cagcagacgg gcgaaggcca tacatgccga tgccgaatct	5700
gactgcatta aaaaagcctt ttttcagccg gagtccagcg gcgctgttcg cgcagtggac	5760
cattagattc tttaacggca gcggagcaat cagctcttta aagcgctcaa actgcattaa	5820
gaaatagcct ctttcttttt catccgctgt cgcaaaatgg gtaaataccc ctttgcactt	5880
taaacgaggg ttgcggtcaa gaattgccat cacgttctga acttcttcct ctgtttttac	5940
accaagtctg ttcatccccg tatcgacctt cagatgaaaa tgaagagaac cttttttcgt	6000
gtggcgggct gcctcctgaa gccattcaac agaataacct gttaagggtca cgtcatactc	6060
agcagcgatt gccacatact ccgggggaac cgcgccaagc accaatatag gcgccttcaa	6120
tccctttttg cgcagtgaaa tcgcttcac caaaatggcc acggccaagc atgaagcacc	6180
tgcgtcaaga gcagcctttg ctgtttctgc atcaccatgc ccgtaggcgt ttgctttcac	6240
aactgccatc aagtggacat gttcaccgat atgttttttc atattgctga cattttcctt	6300
tatcgcggaac aagtcaatth ccgcccacgt atctctgtaa aaagggtttg tgctcatgga	6360
aaactcctct cttttttcag aaaatcccag tacgtaatta agtatttgag aattaattht	6420
atattgatta atactaagtt taccagttt tcacctaaaa aacaaatgat gagataatag	6480
ctccaaaggc taaagaggac tataccaact atttgttaat taa	6523

<210> 42
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 42
 cggaattcgg atccgcgcca aatcattggt tgattg 36

<210> 43
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 43
 gcgagtcgac gtcgggggta atcgtaatgc aattggc 37

<210> 44
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 44
 gcgagtcgac ccatacgacg ttaattcttg caatg 35

<210> 45
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 45
 gatactgcag ggatccttcc cttctcggtat atcagtcac 39

62384479818-seql-000001

<210> 46
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 46
 tgggatggcc aagaaattc 19

<210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 47
 ctaccatgtc ttccgttgct tg 22

<210> 48
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 48
 tgatctcgag acccacctgg acatgctc 28

<210> 49
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 49
 ctaccaggac acgattttgt ggaagaatat ccaggagttt gctggctgc 49

62384479818-seql-000001

<210> 50
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 50
 gcagccagca aactcctgga tattcttcca caaaatcgtg tcctggtag 49

<210> 51
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 51
 ctgccaccag ctgtgcgccc gagggcagca gaagatccgg aagtacacga 50

<210> 52
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 52
 gtggcccggg tctagattag tctaagaggc agccatagg 39

<210> 53
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 53
 ccgcctcgag gccgcgagca cccaagtg 28

<210> 54
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 54
 cgcgactagt ttaatcctct gctgtcacct c 31

 <210> 55
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 55
 ccgcctcgag tacctttcta cggacgtg 28

 <210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 56
 cgcgactagt ttactctggc cggttggcag 30

 <210> 57
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 57
 ccgcctcgag cagcagaaga tccggaagta c 31

62384479818-seql-000001

<210> 58
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 58
cgcgactagt ttaagcccct tcggagggtg

30

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> mapped HLA-A2 restricted epitopes located in extracellular
domains of the Her2/neu molecule

<400> 59

His Leu Tyr Gln Gly Cys Gln Val Val
1 5

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> mapped HLA-A2 restricted epitopes located in extracellular
domains of the Her2/neu molecule

<400> 60

Lys Ile Phe Gly Ser Leu Ala Phe Leu
1 5

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

62384479818-seql-000001

<220>

<223> mapped HLA-A2 restricted epitopes located in intracellular domains of the Her2/neu molecule

<400> 61

Arg Leu Leu Gln Glu Thr Glu Leu Val
1 5

<210> 62

<211> 535

<212> PRT

<213> Artificial Sequence

<220>

<223> His-tagged LLO

<400> 62

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
50 55 60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65 70 75 80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
85 90 95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
100 105 110

62384479818-seq1-000001

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
115 120 125

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

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145 150 155 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
165 170 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
180 185 190

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
195 200 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
275 280 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
290 295 300

62384479818-seq1-000001

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305 310 315 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
370 375 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385 390 395 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
405 410 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
420 425 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val
435 440 445

Gln His Lys Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe
450 455 460

Thr Ser Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr
465 470 475 480

Ala Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile
485 490 495

Asp Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp
500 505 510

Gly Thr Thr Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile
515 520 525

Glu His His His His His His
530 535

<210>	63
<211>	1551
<212>	DNA
<213>	Artificial Sequence

<220>
<223> gene encoding LL0 protein

<400>	63						
catatgaagg	atgcatctgc	attcaataaa	gaaaattcaa	tttcatccgt	ggcaccacca		60
gcatctccgc	ctgcaagtcc	taagacgcca	atcgaaaaga	aacacgcgga	tgaaatcgat		120
aagtatatac	aaggattgga	ttacaataaa	aacaatgtat	tagtatacca	cggagatgca		180
gtgacaaatg	tgccgccaag	aaaaggttac	aaagatggaa	atgaatatat	tgttgtggag		240
aaaaagaaga	aatccatcaa	tcaaaataat	gcagacattc	aagttgtgaa	tgcaatttcg		300
agcctaacct	atccaggtgc	tctcgtaaaa	gcgaattcgg	aattagtaga	aaatcaacca		360
gatgtttctc	ctgtaaaacg	tgattcatta	acactcagca	ttgatttgcc	aggtatgact		420
aatcaagaca	ataaaatagt	tgtaaaaaat	gccactaaat	caaacgttaa	caacgcagta		480
aatacattag	tggaaagatg	gaatgaaaaa	tatgctcaag	cttattcaaa	tgtaagtgca		540
aaaattgatt	atgatgacga	aatggcttac	agtgaatcac	aattaattgc	gaaatttggt		600
acagcattta	aagctgtaaa	taatagcttg	aatgtaaact	tcggcgcaat	cagtgaaggg		660
aaaatgcaag	aagaagtcac	tagtttttaa	caaatttact	ataacgtgaa	tgттаатgaa		720
cctacaagac	cttcagatt	tttcggcaaa	gctgttacta	aagagcagtt	gcaagcgctt		780
ggagtgaatg	cagaaaatcc	tcttgcata	atctcaagtg	tggcgtatgg	ccgtcaagtt		840

62384479818-seql-000001

tatttgaaat tatcaactaa ttcccatagt actaaagtaa aagctgcttt tgatgctgcc	900
gtaagcggaa aatctgtctc aggtgatgta gaactaaca ataatcatcaa aaattcttcc	960
ttcaaagccg taattttacgg aggttccgca aaagatgaag ttcaaatcat cgacggcaac	1020
ctcggagact tacgcgatat tttgaaaaaa ggcgctactt ttaatcgaga aacaccagga	1080
gttcccattg cttatacaac aaacttccta aaagacaatg aattagctgt tattaataaac	1140
aactcagaat atattgaaac aacttcaaaa gcttatacag atggaaaaat taacatcgat	1200
cactctggag gatacgttgc tcaattcaac atttcttggg atgaagtaaa ttatgacct	1260
gaaggtaacg aaattgttca acataaaaaac tggagcgaaa acaataaaaag caagctagct	1320
catttcacat cgtccatcta tttgcctggt aacgcgagaa atattaatgt ttacgctaaa	1380
gaatgcactg gtttagcttg ggaatggtgg agaacggtaa ttgatgaccg gaacttacca	1440
cttgtgaaaa atagaaatat ctccatctgg ggcaccacgc tttatccgaa atatagtaat	1500
aaagtagata atccaatcga acaccaccac caccaccact aataaggatc c	1551

<210> 64
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 64	
gctagctcat ttcacatcgt	20

<210> 65
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 65	
tcttcagct tcccaagcta aaccagtcgc ttcttttagcg taaacattaa tatt	54

<210> 66
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 66
 gaagcgactg gtttagcttg ggaagctgca agaacggtaa ttgatgaccg gaac 54

<210> 67
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 67
 ggatccttat tagtggtggt ggtggtggtg ttcgattgg 39

<210> 68
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> wild-type CBD sequence

<400> 68
 Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg
 1 5 10

<210> 69
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutated CBD sequence

<400> 69

Glu Ala Thr Gly Leu Ala Trp Glu Ala Ala Arg
 1 5 10

<210> 70

<211> 238

<212> DNA

<213> Artificial Sequence

<220>

<223> mutated NheI-BamHI fragment of Example 25

<400> 70

gctagctcat ttcacatcgt ccatctatTT gcctggtaac gcgagaaata ttaatgttta 60
 cgctaaagaa gcgactgggt tagcttggga agctgcaaga acggtaattg atgaccggaa 120
 cttaccactt gtgaaaaata gaaatatctc catctggggc accacgcttt atccgaaata 180
 tagtaataaa gtagataatc caatcgaaca ccaccaccac caccactaat aaggatcc 238

<210> 71

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> ctLL0, replacement sequence containing HLA-A2 restricted epitope
157-165 from NY-ESO-1

<400> 71

Glu Ser Leu Leu Met Trp Ile Thr Gln Cys Arg
 1 5 10

<210> 72

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 72

62384479818-seq1-000001

tctgcactgg gtgatccaca tcagcaggct ttcttttagcg taaacattaa tatt 54

<210> 73
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 73
gaaagcctgc tgatgtggat caccagtcg agaacggtaa ttgatgaccg gaac 54

<210> 74
<211> 238
<212> DNA
<213> Artificial Sequence

<220>
<223> resulting NheI/BamHI fragment from Example 26

<400> 74
gctagctcat ttcacatcgt ccatctatctt gcctggtaac gcgagaaata ttaatgttta 60
cgctaaagaa agcctgctga tgtggatcac ccagtcgaga acggaattg atgaccggaa 120
cttaccactt gtgaaaaata gaaatatctc catctggggc accacgcttt atccgaaata 180
tagtaataaa gtagataatc caatcgaaca ccaccaccac caccactaat aaggatcc 238

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

<220>
<223> ovalbumin derived peptide

<400> 75

Ser Ile Ile Asn Phe Glu Lys Leu
1 5

<210> 76

62384479818-seql-000001

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 76
tcgtgtactt ccggatcttc tgctgccctc gggcgcacag ctggtggcag 50

<210> 77
<211> 7075
<212> DNA
<213> Artificial Sequence

<220>
<223> pAdv164 sequence

<400> 77
cggagtgtat actggcttac tatgttggca ctgatgaggg tgtcagtga gtccttcacg 60
tggcaggaga aaaaaggctg caccggcgcg tcagcagaat atgtgataca ggatatattc 120
cgcttcctcg ctactgact cgctacgctc ggctgcttga ctgcggcgag cggaaatggc 180
ttacgaacgg ggcggagatt tcctggaaga tgccaggaag atacttaaca gggaagtga 240
agggccgcgg caaagccgtt tttccatagg ctccgcccc ctgacaagca tcacgaaatc 300
tgacgctcaa atcagtggcg gcgaaacccg acaggactat aaagatacca ggcgtttccc 360
cctggcggct ccctcgtgcg ctctcctgtt cctgcctttc gggtttaccgg tgcattccg 420
ctgttatggc cgcgtttgtc tcattccacg cctgacactc agttccgggt aggcagttcg 480
ctccaagctg gactgtatgc acgaaccccc cgttcagtcc gaccgctgcg cttatccgg 540
taactatcgt cttgagtcca acccggaag acatgcaaaa gcaccactgg cagcagccac 600
tggttaattga tttagaggag ttagtcttga agtcatgcgc cggttaaggc taaactgaaa 660
ggacaagttt tggcgactgc gtcctccaa gccagttacc tcggttcaaa gagttggtag 720
ctcagagaac cttcgaaaaa ccgccctgca aggcggtttt ttcgttttca gagcaagaga 780
ttacgcgcag accaaaacga tctcaagaag atcatcttat taatcagata aaatatttct 840

62384479818-seql-000001

agccctcctt tgattagtat attcctatct taaagttact tttatgtgga ggcattaaca	900
tttgttaatg acgtcaaaag gatagcaaga ctagaataaa gctataaagc aagcatataa	960
tattgcgttt catctttaga agcgaatttc gccaatatta taattatcaa aagagagggg	1020
tggcaaacgg tatTTggcat tattaggTTa aaaaatgtag aaggagagtg aaacccatga	1080
aaaaaataat gctagTTTT attacactta tattagTTag tctaccaatt gcgcaacaaa	1140
ctgaagcaaa ggatgcatct gcattcaata aagaaaattc aatttcatcc atggcaccac	1200
cagcatctcc gcctgcaagt cctaagacgc caatcgaaaa gaaacacgcg gatgaaatcg	1260
ataagtatat acaaggattg gattacaata aaaacaatgt attagtatac cacggagatg	1320
cagtgacaaa tgtgccgcca agaaaaggTT acaaagatgg aaatgaatat attgttTgtg	1380
agaaaaagaa gaaatccatc aatcaaaata atgcagacat tcaagttgtg aatgcaattt	1440
cgagcctaac ctatccaggT gctctcgtaa aagcgaattc ggaattagta gaaaatcaac	1500
cagatgttct ccctgtaaaa cgtgattcat taacactcag cattgatttg ccaggTatga	1560
ctaatacaaga caataaaaata gttgtaaaaa atgccactaa atcaaacgTT aacaacgcag	1620
taaatacatt agtggaagaa tggaatgaaa aatatgctca agcttatcca aatgtaagtg	1680
caaaaattga ttatgatgac gaaatggctt acagtgaatc acaattaatt gcgaaatttg	1740
gtacagcatt taaagctgta aataatagct tgaatgtaaa cttcggcgca atcagtgaag	1800
ggaaaatgca agaagaagtc attagTTTT aacaaattta ctataacgtg aatgttaatg	1860
aacctacaag accttcaga tttttcggca aagctgttac taaagagcag ttgcaagcgc	1920
ttggagtga tgcagaaaaat cctcctgcat atatctcaag tgtggcgTat ggccgtcaag	1980
tttatttgaa attatcaact aattcccata gtactaaagt aaaagctgct tttgatgctg	2040
ccgtaagcgg aaaatctgtc tcaggTgatg tagaactaac aaatatcatc aaaaattctt	2100
ccttcaaagc cgtaatttac ggaggTtccg caaaagatga agttcaaatc atcgacggca	2160
acctcggaga cttacgcgat attttgaaaa aaggcgctac ttttaatcga gaaacaccag	2220
gagttcccat tgcttataca acaaacttcc taaaagacaa tgaattagct gttattaaaa	2280

62384479818-seq1-000001

acaactcaga atatattgaa acaacttcaa aagcttatac agatggaaaa attaacatcg	2340
atcactctgg aggatacggtt gctcaattca acatttcttg ggatgaagta aattatgatc	2400
tcgagaccca cctggacatg ctccgccacc tctaccaggg ctgccaggtg gtgcagggaa	2460
acctggaact cacctacctg cccaccaatg ccagcctgtc cttcctgcag gatatccagg	2520
agggtgcaggg ctacgtgctc atcgctcaca accaagtgag gcaggtccca ctgcagaggc	2580
tgcggattgt gcgaggcacc cagctctttg aggacaacta tgccctggcc gtgctagaca	2640
atggagaccc gctgaacaat accacccctg tcacaggggc ctcccagga ggcctgcggg	2700
agctgcagct tcgaagcctc acagagatct tgaaaggagg ggtcttgatc cagcgaacc	2760
cccagctctg ctaccaggac acgattttgt ggaagaatat ccaggagttt gctggctgca	2820
agaagatctt tgggagcctg gcatttctgc cggagagctt tgatggggac ccagcctcca	2880
acactgcccc gctccagcca gagcagctcc aagtgtttga gactctggaa gagatcacag	2940
gttacctata catctcagca tggccggaca gcctgcctga cctcagcgtc ttccagaacc	3000
tgcaagtaat ccggggacga attctgcaca atggcgccta ctcgctgacc ctgcaagggc	3060
tgggcatcag ctggctgggg ctgcgctcac tgagggaact gggcagtgga ctggccctca	3120
tccaccataa caccacctc tgcttcgtgc acacggtgcc ctgggaccag ctctttcgga	3180
acccgcacca agctctgctc cacactgcca accggccaga ggacgagtgt gtgggcgagg	3240
gcctggcctg ccaccagctg tgcgcccag ggacagagaa gatccggaag tacacgatgc	3300
ggagactgct gcaggaaacg gagctggtgg agccgctgac acctagcgga gcgatgcca	3360
accaggcgca gatgcggatc ctgaaagaga cggagctgag gaaggtaag gtgcttgat	3420
ctggcgcttt tggcacagtc tacaaggga tctggatccc tgatggggag aatgtgaaaa	3480
ttccagtggc catcaaagtg ttgagggaaa acacatcccc caaagccaac aaagaaatct	3540
tagacgaagc atacgtgatg gctggtgtgg gctccccata tgtctccgc cttctgggca	3600
tctgcctgac atccacggtg cagctggtga cacagcttat gccctatggc tgctcttag	3660
actaatctag acccgggcca ctaactcaac gctagtagtg gatttaatcc caaatgagcc	3720

62384479818-seql-000001

aacagaacca gaaccagaaa cagaacaagt aacattggag ttagaaatgg aagaagaaaa	3780
aagcaatgat ttcgtgtgaa taatgcacga aatcattgct tattttttta aaaagcgata	3840
tactagatat aacgaaacaa cgaactgaat aaagaataca aaaaaagagc cacgaccagt	3900
taaagcctga gaaactttta ctgcgagcct taattgatta ccaccaatca attaaagaag	3960
tcgagaccca aaatttggtg aagtatttaa ttactttatt aatcagatac ttaaatatct	4020
gtaaacccat tatatcgggt ttttgagggg atttcaagtc ttttaagaaga taccaggcaa	4080
tcaattaaga aaaacttagt tgattgcctt ttttgttgtg attcaacttt gatcgtagct	4140
tctaactaat taattttcgt aagaaaggag aacagctgaa tgaatatccc ttttgttgta	4200
gaaactgtgc ttcattgacgg cttgttaaag tacaaattta aaaatagtaa aattcgctca	4260
atcactacca agccaggtaa aagtaaaggg gctatttttg cgtatcgctc aaaaaaagc	4320
atgattggcg gacgtggcgt tgttctgact tccgaagaag cgattcacga aaatcaagat	4380
acatttacgc attggacacc aaacgtttat cgttatggta cgtatgcaga cgaaaaccgt	4440
tcatacacta aaggacattc tgaaaacaat ttaagacaaa tcaatacctt ctttattgat	4500
tttgatattc acacggaaaa agaaactatt tcagcaagcg atattttaac aacagctatt	4560
gatttaggtt ttatgcctac gttaattatc aaatctgata aaggttatca agcatatttt	4620
gttttagaaa cgccagtcta tgtgacttca aaatcagaat ttaaatctgt caaagcagcc	4680
aaaataatct cgcaaaatat ccgagaatat tttggaaagt ctttgccagt tgatctaacg	4740
tgcaatcatt ttgggattgc tcgtatacca agaacggaca atgtagaatt ttttgatccc	4800
aattaccgtt attctttcaa agaattggcaa gattggctt tcaaacaac agataataag	4860
ggctttactc gttcaagtct aacggtttta agcggtagag aaggcaaaaa acaagtagat	4920
gaaccctggt ttaatctctt attgcacgaa acgaaatttt caggagaaaa gggtttagta	4980
gggcgcaata gcgttatgtt taccctctct ttagcctact ttagttcagg ctattcaatc	5040
gaaacgtgcg aatataatat gtttgagttt aataatcgat tagatcaacc cttagaagaa	5100
aaagaagtaa tcaaaattgt tagaagtgcc tattcagaaa actatcaagg ggctaatagg	5160

62384479818-seql-000001

gaatacatta ccattctttg caaagcttgg gtatcaagtg atttaaccag taaagattta	5220
tttgtccgtc aagggtgggt taaattcaag aaaaaaagaa gcgaacgtca acgtgttcat	5280
ttgtcagaat ggaaagaaga tttaatggct tatattagcg aaaaaagcga tgtatacaag	5340
ccttatttag cgacgaccaa aaaagagatt agagaagtgc taggcattcc tgaacggaca	5400
ttagataaat tgctgaaggt actgaaggcg aatcaggaaa ttttctttaa gattaaacca	5460
ggaagaaatg gtggcattca acttgctagt gttaaatacat tgttgctatc gatcattaaa	5520
ttaaaaaaag aagaacgaga aagctatata aaggcgctga cagcttcgtt taatttagaa	5580
cgtacattta ttcaagaaac tctaacaaca ttggcagaac gccccaaaac ggaccacaa	5640
ctcgatttgt ttagctacga tacaggctga aaataaaacc cgcactatgc cattacattt	5700
atatctatga tacgtgtttg tttttctttg ctggctagct taattgctta tatttacctg	5760
caataaagga tttcttactt ccattatact cccattttcc aaaaacatac ggggaacacg	5820
ggaacttatt gtacaggcca cctcatagtt aatggtttcg agccttcctg caatctcatc	5880
catggaaata tattcatccc cctgccggcc tattaatgtg acttttgtgc ccggcggata	5940
ttcctgatcc agctccacca taaattgggtc catgcaaatt cggccggcaa ttttcaggcg	6000
ttttcccttc acaaggatgt cggtcctttt caattttcgg agccagccgt ccgcatagcc	6060
tacaggcacc gtcccgatcc atgtgtcttt ttccgctgtg tactcggctc cgtagctgac	6120
gctctcgcct tttctgatca gtttgacatg tgacagtgtc gaatgcaggg taaatgccgg	6180
acgcagctga aacggtatct cgtccgacat gtcagcagac gggcgaaggc catacatgcc	6240
gatgccgaat ctgactgcat taaaaaagcc ttttttcagc cggagtccag cggcgtgtt	6300
cgcgcagtgg accattagat tctttaacgg cagcggagca atcagctctt taaagcgctc	6360
aaactgcatt aagaaatagc ctctttcttt ttcattccgt gtcgcaaaat gggtaaatac	6420
ccctttgcac tttaaacgag gggtgcggtc aagaattgcc atcacgttct gaacttcttc	6480
ctctgttttt acaccaagtc tgttcatccc cgtatcgacc ttcagatgaa aatgaagaga	6540
accttttttc gtgtggcggg ctgcctcctg aagccattca acagaataac ctgttaaggt	6600

62384479818-seql-000001

cacgtcatatc tcagcagcga ttgccacata ctccggggga accgcgcaa gcaccaatat 6660
 aggcgcccttc aatcccctttt tgcgcagtga aatcgcttca tccaaaatgg ccacggccaa 6720
 gcatgaagca cctgcgtcaa gagcagcctt tgctgtttct gcatcaccat gcccgtaggc 6780
 gtttgctttc acaactgcca tcaagtggac atgttcaccg atatgttttt tcatattgct 6840
 gacattttcc tttatcgcg gacaagtcaat ttccgccac gtatctctgt aaaaaggttt 6900
 tgtgctcatg gaaaactcct ctcttttttt agaaaatccc agtacgtaat taagtatttg 6960
 agaattaatt ttatattgat taataactaag tttaccaggt tttcacctaa aaaacaaatg 7020
 atgagataat agctccaaag gctaaagagg actataccaa ctatttgta attaa 7075

<210> 78

<211> 1761

<212> DNA

<213> Artificial Sequence

<220>

<223> a nucleic acid sequence of PAK6

<400> 78

gggctgctca acgacatcca gaagttgtca gtcacagct ccaacaccct gcgtggccgc 60
 agccccacca gccggcggcg ggcacagtcc ctggggctgc tgggggatga gcaactgggcc 120
 accgaccag acatgtacct ccagagcccc cagtctgagc gcaactgaccc ccacggcctc 180
 tacctcagct gcaacggggg cacaccagca ggccacaagc agatgccgtg gcccagacca 240
 cagagcccac gggctcctgcc caatgggctg gctgcaaagg cacagtcctt gggccccgcc 300
 gagtttcagg gtgcctcgca gcgctgtctg cagctgggtg cctgcctgca gagtcccca 360
 ccaggagcct cgccccccac gggcaccaat aggcatggaa tgaaggctgc caagcatggc 420
 tctgaggagg cccggccaca gtcctgcctg gtgggctcag ccacaggcag gccagggtggg 480
 gaaggcagcc ctagccctaa gaccggggag agcagcctga agcgcaggct attccgaagc 540
 atgttcctgt ccaactgctgc cacagcccct ccaagcagca gcaagccagg ccctccacca 600
 cagagcaagc ccaactcctc tttccgaccg ccgcagaaag acaaccccc aagcctggtg 660

62384479818-seql-000001

gccaaggccc agtccttgcc ctcggaccag ccggtgggga ccttcagccc tctgaccact	720
tcggatacca gcagcccccga gaagtccctc cgcacagccc cggccacagg ccagcttcca	780
ggccggtcctt ccccagcggg atccccccgc acctggcacg cccagatcag caccagcaac	840
ctgtacctgc cccaggaccc cacggttgcc aagggtgccc tggctgggtga ggacacaggt	900
gttgtgacac atgagcagtt caaggctgcg ctcaggatgg tggaggacca gggtagcccc	960
cggctgctgc tggacagcta cgtgaagatt ggcgagggct ccaccggcat cgtctgcttg	1020
gcccgggaga agcactcggg ccgccagggtg gccgtcaaga tgatggacct caggaagcag	1080
cagcgcaggg agctgctctt caacgagggtg gtgatcatgc gggactacca gcacttcaac	1140
gtgggtggaga tgtacaagag ctacctgggtg ggcgaggagc tgtgggtgct catggagttc	1200
ctgcaggggag gagccctcac agacatcgtc tcccaagtca ggctgaatga ggagcagatt	1260
gccactgtgt gtgaggctgt gctgcaggcc ctggcctacc tgcattgctca ggggtgtcatc	1320
caccgggaca tcaagagtga ctccatcctg ctgaccctcg atggcagggt gaagctctcg	1380
gacttcggat tctgtgctca gatcagcaaa gacgtcccta agagggaagtc cctgggtggga	1440
accccctact ggatggctcc tgaagtgatc tccaggctctt tgtatgccac tgagggtggat	1500
atctgggtctc tgggcatcat ggtgattgag atggtagatg gggagccacc gtacttcagt	1560
gactccccag tgcaagccat gaagaggctc cgggacagcc cccacccaa gctgaaaaac	1620
tctcacaagg tctccccagt gctgcgagac ttcctggagc ggatgctgggt gcgggacccc	1680
caagagagag ccacagccca ggagctccta gaccaccct tctgctgca gacagggcta	1740
cctgagtgcc tgggtgcccct g	1761

<210> 79

<211> 587

<212> PRT

<213> Artificial Sequence

<220>

<223> an amino acid sequence of PAK6

<400> 79

62384479818-seql-000001

Gly Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr
1 5 10 15

Leu Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly
20 25 30

Leu Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln
35 40 45

Ser Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys
50 55 60

Asn Gly Gly Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro
65 70 75 80

Gln Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser
85 90 95

Leu Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu
100 105 110

Gly Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly
115 120 125

Thr Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala
130 135 140

Arg Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg Pro Gly Gly
145 150 155 160

Glu Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg
165 170 175

Leu Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser
180 185 190

62384479818-seql-000001

Ser Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe
195 200 205

Arg Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln
210 215 220

Ser Leu Pro Ser Asp Gln Pro Val Gly Thr Phe Ser Pro Leu Thr Thr
225 230 235 240

Ser Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr
245 250 255

Gly Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp
260 265 270

His Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr
275 280 285

Val Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His
290 295 300

Glu Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro
305 310 315 320

Arg Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly
325 330 335

Ile Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val
340 345 350

Lys Met Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn
355 360 365

Glu Val Val Ile Met Arg Asp Tyr Gln His Phe Asn Val Val Glu Met
370 375 380

62384479818-seql-000001

Tyr Lys Ser Tyr Leu Val Gly Glu Glu Leu Trp Val Leu Met Glu Phe
385 390 395 400

Leu Gln Gly Gly Ala Leu Thr Asp Ile Val Ser Gln Val Arg Leu Asn
405 410 415

Glu Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu Gln Ala Leu Ala
420 425 430

Tyr Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser
435 440 445

Ile Leu Leu Thr Leu Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe
450 455 460

Cys Ala Gln Ile Ser Lys Asp Val Pro Lys Arg Lys Ser Leu Val Gly
465 470 475 480

Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala
485 490 495

Thr Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val
500 505 510

Asp Gly Glu Pro Pro Tyr Phe Ser Asp Ser Pro Val Gln Ala Met Lys
515 520 525

Arg Leu Arg Asp Ser Pro Pro Pro Lys Leu Lys Asn Ser His Lys Val
530 535 540

Ser Pro Val Leu Arg Asp Phe Leu Glu Arg Met Leu Val Arg Asp Pro
545 550 555 560

Gln Glu Arg Ala Thr Ala Gln Glu Leu Leu Asp His Pro Phe Leu Leu
565 570 575

62384479818-seql-000001

Gln Thr Gly Leu Pro Glu Cys Leu Val Pro Leu
580 585

<210> 80
<211> 529
<212> PRT
<213> *Listeria monocytogenes*

<400> 80

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
50 55 60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65 70 75 80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
85 90 95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
100 105 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
115 120 125

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

62384479818-seq1-000001

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145 150 155 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
165 170 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
180 185 190

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
195 200 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
275 280 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
290 295 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305 310 315 320

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

62384479818-seq1-000001

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
370 375 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385 390 395 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
405 410 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
420 425 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val
435 440 445

Gln His Lys Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe
450 455 460

Thr Ser Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr
465 470 475 480

Ala Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile
485 490 495

Asp Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp
500 505 510

Gly Thr Thr Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile
515 520 525

Glu

<210> 81
 <211> 2048
 <212> DNA
 <213> *Listeria monocytogenes*

<400> 81
 taacgacgat aaagggacag caggactaga ataaagctat aaagcaagca tataatattg 60
 cgtttcatct ttagaagcga atttcgcca tattataatt atcaaaagag aggggtggca 120
 aacggtattt ggcattatta ggtaaaaaa tgtagaagga gagtgaaacc catgaaaaa 180
 ataatgctag tttttattac acttatatta gttagtctac caattgcgca acaaactgaa 240
 gcaaaggatg catctgcatt caataaagaa aattcaattt catccatggc accaccagca 300
 tctccgcctg caagtcctaa gacgccaatc gaaaagaaac acgcggatga aatcgataag 360
 tatatacaag gattggatta caataaaaac aatgtattag tataccacgg agatgcagtg 420
 acaaatgtgc cgccaagaaa aggttacaaa gatggaaatg aatatattgt tgtggagaaa 480
 aagaagaaat ccatcaatca aaataatgca gacattcaag ttgtgaatgc aatttcgagc 540
 ctaacctatc caggtgctct cgtaaaagcg aattcggaat tagtagaaaa tcaaccagat 600
 gttctccctg taaaacgtga ttcattaaca ctgagcattg atttgccagg tatgactaat 660
 caagacaata aaatcgttgt aaaaaatgcc actaaatcaa acgttaacaa cgcagtaa 720
 acattagtgg aaagatggaa tgaaaaatat gctcaagctt atccaaatgt aagtcaaaa 780
 attgattatg atgacgaaat ggcttacagt gaatcacaat taattgcgaa atttggta 840
 gcatttaaag ctgtaaataa tagcttgaat gtaaacttcg gcgcaatcag tgaaggga 900
 atgcaagaag aagtcattag ttttaacaa atttactata acgtgaatgt taatgaacct 960
 acaagacctt ccagatTTTT cggcaaagct gttactaaag agcagttgca agcgcttgga 1020
 gtgaatgcag aaaatcctcc tgcatatatc tcaagtgtgg cgtatggccg tcaagtttat 1080
 ttgaaattat caactaattc ccatagtact aaagtaaaag ctgcttttga tgctgccgta 1140

62384479818-seql-000001

agcggaaaat ctgtctcagg tgatgtagaa ctaacaaata tcatcaaaaa ttcttccttc	1200
aaagccgtaa ttacggagg ttccgcaaaa gatgaagttc aaatcatcga cggcaacctc	1260
ggagacttac gcgatatttt gaaaaaaggc gctactttta atcgagaaac accaggagtt	1320
cccattgctt atacaacaaa cttcctaaaa gacaatgaat tagctgttat taaaaacaac	1380
tcagaatata ttgaaacaac ttcaaaagct tatacagatg gaaaaattaa catcgatcac	1440
tctggaggat acgttgctca attcaacatt tcttgggatg aagtaaatta tgatcctgaa	1500
ggtaacgaaa ttgttcaaca taaaaactgg agcgaaaaca ataaaagcaa gctagctcat	1560
ttcacatcgt ccatctattt gccaggtaac gcgagaaata ttaatgttta cgctaaagaa	1620
tgactgggtt tagcttggga atgggtggaga acggtaattg atgaccggaa cttaccactt	1680
gtgaaaaata gaaatatctc catctggggc accacgcttt atccgaaata tagtaataaa	1740
gtagataatc caatcgaata attgtaaaag taataaaaaa ttaagaataa aaccgcttaa	1800
cacacacgaa aaaataagct tgttttgcac tcttcgtaaa ttattttggtg aagaatgtag	1860
aaacaggctt attttttaat ttttttagaa gaattaacaa atgtaaaaga atatctgact	1920
gtttatccat ataataaag catatcccaa agtttaagcc acctatagtt tctactgcaa	1980
aacgtataat ttagttccca catatactaa aaaacgtgtc cttactctc tctgtcagat	2040
tagttgta	2048

<210> 82
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 6x Histidine tag

<400> 82

His His His His His His
 1 5

<210> 83

62384479818-seql-000001

<211> 123
 <212> DNA
 <213> Human papillomavirus type 16

<400> 83
 cacgtagaca tttgtacttt ggaagacctg ttaatgggca cactaggaat tgtgtgcccc 60
 atctgttctc agaaaccata atctaccatg gctgaccta caggtagcaa tggggaagag 120
 ggt 123

<210> 84
 <211> 7461
 <212> DNA
 <213> Human papillomavirus type 92

<400> 84
 tattgttgcc aacaatcatc acgcataga aaaacacgta accgcctgcg ttataataca 60
 aacagctagt atataaatac aggcagtga agtggtccca tcacaatggc aaaacctcct 120
 tcggtgcagg aacttagaag acagtttagat attccattgg aggacatttt attgcattgt 180
 aatttttgtg aggctttttt aacatttgag gagctactgc aatttgatgc aaaaaattta 240
 aatttaattt ggaaggagaa ttatgcttat gcttgctgtg gtgcttgtgc taaacaagta 300
 gcagcaatag aaacaaaaca tttttatgag tatagtgtac aaggaaagga tgctatagaa 360
 agggactcag gtagtctttt gtgttggtta actgttagat gtaagttttg tttaagacat 420
 ttggattact tagagaaatt ggcagtttgt gcatcaggca ttccttttga tagagttaga 480
 ggagcttgga aggcagtgtg taggttttgt acagagatat gattgggaaa caggctacta 540
 taccagatat tgtgctggat ctgcaagacc ttgtccagcc cattgacctg cattgtgacg 600
 aagacttgct agaaaaatcag gaggaggagc ctgcacctca aagaatagac tacaagatag 660
 tttcctcgtg tgggtggctgc ggaattaagc ttcgaatttt tgcacgtgt acccaatttg 720
 gaattagaac tctgcaagac ctacttcttg aagaaatagc gttgctgtgt cctgactgca 780
 aaaatggcag ataaaggat agatcctaaa gaaggctgta gtacttggtg tttaatagaa 840
 gctgattgta gtgatgtaga tggggatttt gaaaagtat ttgacaaaga cacagactca 900

62384479818-seql-000001

gatatttcag atttattaga tgatggggac cttggggacg cagaattggg aaatcccca	960
gagctgctgt gcctgcagga gagagaggag agcgatctac agctgcagca gttaaaacga	1020
aagtatttta gtcctaaagc tgtttttacag cttagtccac aattggaatc tattactatt	1080
tcgcctcaac gcaaaagtaa gaggcgactg ttcgaggaac aggacagcgg acttgagctt	1140
tctttaactc atgaagctga agattctgtt gcggaagtgg aggtaccggg gtcaaaagat	1200
gacgtcccag aaactgtttc tgctacagca gaaactaagg gaagccaaaa caaagaacat	1260
tacaaacagt tactacagtg cagcaatgcg cgggctacat tgcttagtaa atttaaagct	1320
gcttttggtg ttagctttac agagttaacc agaagataca aaagtgataa tacatgttgc	1380
agagactggg caattattgt ctatgggttg caggatgaaa ttattgaagg ctcaaagcat	1440
ttatttcagc agcattgtga atatatttgg ttgcatgttt tatctccaat atctttgtat	1500
ttactatgtt ttaaaactgg aaaaagcaga aatactgtaa agaacttggt gatgtccatt	1560
ttaaagtgtg gggatgcaca gcttatagct gatccacccc agattcgag cgtagtagca	1620
gctttgtttt ggtacaaaga atctatgaat aaaaatgtat ataccatgg agaataccca	1680
gagtggatag caaatcaaac attgctttct catcaggaat atgaaacaca gcaatttgat	1740
ttaagtagaa tgattcagtg ggcatatgat aatgaatata ctgaggactc agatattgct	1800
tatcattatg caaaattagc agatgaagat tcaaagtctc gcgccttttt agctcataac	1860
agtcaggcaa aatttgtag agaatgtgga cagatggtaa ggcattataa aagaggagaa	1920
atgaaaaata tgagtatgtc agcctggatt tatactagat tgaaatcaat tgaaggacca	1980
ggccattggt cagacattgt taaatttata cgatttcagc agattaattt tataatgttt	2040
ctagatgtat tcaagcaatt tcttgccca gtacctaaaa gaaattgttt attaatttat	2100
ggtgcacctg attgtggcaa atcaatgttt tgtatgtctt taataaaggc cttaaaggga	2160
aaagttatat cgtttgtaaa tgctagaagt caattttggt tatctccatt agtagaatct	2220
aaaattgcac tactagatga tgccaccgag tgctgttggga attatattga taattattta	2280
agaaatggaa tagatggtaa catggtagt gtggattgta agcataaaaa tccgggtccaa	2340

62384479818-seql-000001

attagatttc caccattatt gattacatca aataataata taatgtctga tccaaagtat	2400
aaatatctgc atagtagaat taaagcattt gagtttgtaa ataagtttcc atttaaggac	2460
gatggcagtc ccttgtttga acttactgac caaagctgga aatctttttt tcaaaggctt	2520
tggaggcaat tagatctaag tgaccaagaa gacgaggggtg aggatggagg ctctcagcga	2580
ccgtttcaat gcactgcaag acaagttaat gacaatttat gaaagagcta gtgaatcctt	2640
aaaagatcaa attgaacatt ggaacttggt aagacaggag caggtgttat ttcattatgc	2700
cagacaaaga ggagtattgc gccttgggta tcagccagta cctgcattaa ctatttcaga	2760
ggctaaagct aaggaagcca ttgctatggt ttacattta gaagcattgc aaagatcacc	2820
ttacaaaaat gaaaaatgga cattagtaaa tacaagtgtg gaaacgtttc gcacaccccc	2880
agaaaattgt tttaaaaagg gccctaagac tattgaaata gtgtatgatg gcaatcctga	2940
aaatacaatg ttatacacta tttggacaca tatatatattt gaagatgacg aaggcaactg	3000
gcaaaagact gagggacatt tggactatca tggcgcctat tttatggatg gattaaataa	3060
acaatactat atcagatttg ctcaagacgc acgcagattt agtgaaactg gagaatggga	3120
agttaagttt aacaacgaaa ttttgtttgc tcctgttacc agctccacca actccgaaga	3180
agaaagggac cgacccgccc ctgccacaga ccccggtcc ctttcgcaga catccggagg	3240
acagtccccct gtacccactc aacggaagca accatctaaa ggaagggtacg ggcgaaaaga	3300
ctctgggtgct acaaccgcct ccaggggggat ccaaagacga ccgaaagcgt caccgaggag	3360
atcacgatcg cggtcaggat cgagatcggg atcacaagga gacgcgcgga ccctcctcac	3420
agtcagacgc ggagaacggg aacgggggaca aggaagggga caaggaagcc ggggtcgggg	3480
aaggagcggg gacagaagca ggagcgggag cagaagcagg agcgggagca ggagaaggag	3540
caggagcagg ggcaggagca ggaacggaag ggaacggggg agagcagcct ccagaggccg	3600
tagagggtac agcaacagga ggtcaagatc caaatctgtt ggcacaagtg gcataccacc	3660
tgagcaagtg ggaagcagcc tacaaggtgt tggtagacaa catagtggac gacttgcgag	3720
attattggac gacgctaggg atccccagt aattttgttg aaaggacaag ccaatactct	3780

62384479818-seql-000001

taagtgttat cgctacaggg ctaaagaaaa gtataaaggc tattatgatt gcttcagtac	3840
tacatggtca tgggtcagtg caggtagcaa cgatagaata ggacgctcta gaatgattat	3900
tagctttacc agtaaattctc aaagacaaat gtttttaagt attatgaaat taccaaaggg	3960
cgttgattgg tctcttgggt gctttgactc tatttaacac actaaccttt ctagtttttt	4020
tactaacaca tacgtttcaa tagaattggt aatgcatggc tcgcgcacgc agaacaaagc	4080
gtgattctgt tactaatatt tacaggacct gcaaagcagc aggcacctgc cccctgatg	4140
ttgttaataa agtggagcag actactgtag ctgatcaaat tttaaaatat ggcagcactg	4200
gtgtatTTTT tggaggTTTg ggaattggta caggaagagg cactggTggt agcactggat	4260
atggggccatt aggtgaaggg acgagtgtaa gagttggaaa tacaccacaca gttattaggc	4320
ctgctttTgt gcctgaggct ataggaccaa gtgaactaat acctattgac agtgtcaatc	4380
ctattgaccc cagtgttct tctatcatatc ctttaacaga gtcaacaggt cctgacctct	4440
taccaggTga aatagaaaca attgcagagg tgcattcctgc ccctgacata cctacagtag	4500
atacaccagt ggtgactggg ggcagaaact cgaatgctgt tctggaggTg gctgatccaa	4560
gtccaccac acgaaacaga gttagtagaa cacaatataa caatcctgca tttcaaatca	4620
tatctgaaac tacaccaagt gcgggggaaa cgtccctatc agaccaaatt gttgttcagt	4680
catttgatgg tggacaatat ataggTggt acccacctcc gcgatcagta gttgaaatag	4740
aattacaaga aattccctca caatattctt ttgaaatcga agagccaacc ccacctaggc	4800
aaacaagcac tcctgtcaga caggcacaac aaatggcctc agcattacgg agggctttat	4860
acaatagaag gttcacacag caggttcaag tggaagatcc aatgttttat agtagacctt	4920
ccaggTtagt taggtttcaa tttgataatc ctgtatttga agaagaagtt actcaggTgt	4980
ttgaaagaga cctagaaact atagaagagc ctcctgatag acaattttta gatgtacaaa	5040
aacttggtag gcctacctat gctgaaacac ctgcaggcta tataagggtt agcagacttg	5100
gcaaacgagc tactataagg accaggTctg gaactacaat aggcggTcag gtacattttt	5160
ttagggatat tagcagtatt gatactcaac cttctattga actgcaagtt cttgggggaac	5220

62384479818-seq1-000001

attctggcga tgctacaata gtccagggtc ctgtggaaag tacgttcgta aatattgatt	5280
tggaagagtt acctaattta gaggaaaatg tacacctaga atctgatgat atacttattg	5340
atgaagctat agaggatttt agtggtgccc aattagtgtt tggaaattct agaagatcaa	5400
atactgttac attacctgc tttgaaactg taagggaac ttcctttatat actgtagatt	5460
tagatggatt ccatgtgtct tatcctgaga gtagagcgta tccagaagtt attcctacag	5520
aaccagataa taccccaaca gtaataattc acacagaaga ttttagtggt gattattatc	5580
tacatcctag cttaaaatgg aagaaacgaa aacgggccta tttataattt tttgcagatg	5640
tcctattggc ttccagcaaa tggtaaggta tacttacccc cttcaacacc ggttgcaagg	5700
gtacaaagta cggatgaatt tggtcaaagg accaacatct tttatcatgc aaatagtgat	5760
cgcctgctga cagttggaca cccttatttt gaagtgagaa gctcagttga tccacatgat	5820
gtattagtgc ctaagggtgc agggaaatcag tttagagctt ttcgactgaa attaccagat	5880
cctaatagat ttgctttagc tgacatgtct gtttataatc cagacaagga aaggcttggt	5940
tggggctgca ggggattgga aatagggcga gggcagcctt taggtgttgg caccacaggt	6000
catccattat ttaataaggt attggacact gaaaatccaa ataagtacaa tactggaaca	6060
aaggatgaca gagtaaacac atcttttgat ccaaagcaaa ttcagttatt tgtttttagga	6120
tgtacaccat gcttaggtga acattgggac acagccttac catgtgctga aaagcaacca	6180
gatactgggg gatgcccacc attagagtta aaaaacactg ttatctctga tggagatatg	6240
gttgacatag gcttcggtaa tatgaatttt aaggccttat cagtaaccaa atctgacgta	6300
agtttgata tagtagactc cacatgtaaa tatccagact ttttaaagat gtcaaagat	6360
gtatatggca actcatgttt tttctatgga cgacgagaac aatgttatgt taggcatatg	6420
tttgtgcgcg gtggtgttgt gggtgatacc atcccagatg cagttgtaaa tgaagaccat	6480
aactttatgt tacctgcagc atccagtgac cagtctagaa gtcaaattgc cagttctatc	6540
tatttcccta ctgttagtgg gtcttttggt tccactgatg cacaattatt taatcgcca	6600
tattgggttac aaagagcaca aggccacaac aatgggtattt gctggagtaa tgaactgttt	6660

62384479818-seql-000001

ctgacagttt gtgataatac caggaatact aactttaata ttagtgtccc taaggaaggt	6720
ggtcaaataa ccgactatga ttcacaaaag attagagaat acactagaca tgttgaagaa	6780
tatgaaatat cactaatatt acaattatgt aaaattcctt tggaagctga gatattagct	6840
caaattaatg caatgaatcc aaatatTTTtg gaggactggc agttaggatt tgttcctact	6900
ccagataacc ctattcagga tgcatacaga tttattcatt ctaaagcaac accttgtcca	6960
gataaagcac aacctaaaga aagagaagat ccatgggccc catatacatt ttgggttgta	7020
gacttaactg aaaaattatc tttagattta gatcaatatt cattgggtag aaaattttta	7080
tttcaagctg gattaactaa tacatctgtt aatggcttta aaagaactag aagcagttct	7140
caaagaggta ctaaagcaaa aagaaaaagt aactaaaacg gtcagtattc tttattgaaa	7200
ataaaatttt tggaactcat gtgttatgag taatgattat tatctattct gactaactca	7260
aacatgttaa ccgcgcccgg tgtattcaat ataaacgctg atgggtacaag ttgtcaagga	7320
acttggcagt ctgaactaca gtgggtgcaa cacctggaag gcacacaaga tttgcgcgcc	7380
aaaactactt ggcagaacat ttcaccgata acggtaagat tttatcttta accgggtgcg	7440
gtcgttgggt tactgttttag g	7461

<210> 85

<211> 7815

<212> DNA

<213> Human papillomavirus type 1a

<400> 85

gttaactacc atcattcatt attctagtta caacaagaac ctaggagtta tatgccagaa	60
gtaagcctat aaaatacaca ggtaagactc tgcacaggac cagatggcga caccaatccg	120
gaccgtcaga cagctttccg aaagcctctg tatcccatat attgatgttt tattgccttg	180
taatttttgt aattattttt tgtctaatagc tgagaagctg ctttttgatc attttgattt	240
gcatcttgtc tggagagaca atttggtgtt tggatgctgt caagggtgtg ctagaactgt	300
tagcctattg gagtttgttt tatattatca ggagtcttat gaggtaccgg aaatagaaga	360
aattttggac agacctttat tgcaaattga actccgttgt gttacatgca taaaaaaact	420

62384479818-seql-000001

gagtgttgct gaaaaattgg aggttgtgtc aaacggagaa agagtgcata gagttagaaa	480
cagacttaaa gcaaagtgtg gtttgtgtcg cttgtatgct atataacaat ggtgggcgaa	540
atgccagcac taaaggacct ggttcttcaa cttgaaccaa gcgtcctaga tttagatctt	600
tattgttacg aggagggtgcc tcctgatgac atagaggagg agttagtgtc gcctcagcaa	660
ccttatgctg tcgttgcttc ctgtgcctat tgcgagaaac tggttcgatt gaccgtcctc	720
gcggatcaca gcgccattag acagctggag gaactccttc tgcgatcttt gaacatcgtg	780
tgcccactgt gcaccctaca gcgacagtaa aatggcagat aataaaggta ctgaaaacga	840
ttggtttttg gtggaggcga cagattgtga ggaaacgtta gaggaaacct cacttgggtga	900
cctagataat gtttcttgtg ttagcgactt atctgattta ttagacgagg cgccgcaaag	960
ccaggggaat tccctggaat tgttccacaa gcaagaatcg ctggaaagcg aacaggaact	1020
taatgcttta aaacgaaagt tactttacag tcctcaggcg agaagcgcg acgaaacaga	1080
cattgctagc attagtccta gattagaaac tatttctatt acaaagcaag acaaaaaaag	1140
gtatcgaagg caactgtttt ctcaggatga tagtggttta gagctatcgc tgcttcagga	1200
tgaaactgaa aatattgatg aatcgacaca ggtagatcaa cagcagaaag aacatactgg	1260
ggaagtggg gccgctggg tgaacatttt gaaagctagt aatatccg cgccattatt	1320
aagcagattt aaagatacgg ctggcgtcag ttttacagac ctgacgcggt cgtacaagag	1380
caacaaaacc tgttgtggag attgggtttt ggcagtttgg ggtgtccgtg aaaattta	1440
tgacagtgtg aaagaattat tgcaaacca ttgtgtgtat attcaattgg aacatgcagt	1500
aactgaaaaa aatagatttt tatttttatt ggtacgattt aaagcccaga aaagtagaga	1560
gactgtgata aaacttataa ccacaattct tccagttgat gctagctata ttttgtctga	1620
gcctcaaaaa tcaagaagtg tggctgctgc attattttgg tataaaagat ctatgtcttc	1680
aactgttttt acatggggta caactttgga gtggattgca cagcaaacc ttattaatca	1740
tcagttagat tccgaaagtc cttttgagct ttgtaaaatg gttcagtggg cctatgataa	1800
tggacataca gaagagtgtg aaattgcata ttattatgct gtttttagcag atgaggatga	1860

62384479818-seql-000001

aaatgcaagg gcattttctaa gctctaattc acaggcaaaa tatgtgaaag actgtgcaca	1920
aatggtaaga cactattttac gtgctgagat ggcacaaatg tctatgtcag agtggatttt	1980
tagaaaacta gataatgtag aaggttctgg taattggaaa gaaattgtaa gatttttaag	2040
atttcaagaa gttgaattta taagctttat gattgcattt aaagatttgt tatgtggtaa	2100
gccaaagaaa aactgtttgt taatatttgg acctccaaat acaggaaaat caatgttttg	2160
tacaagttta ttaaagttgt taggagggaa agtgatttca tactgtaaca gtaaaagtca	2220
gttttggttg cagcctctgg ctgatgctaa gatagggcta ttagatgatg caacaaagcc	2280
atgttgggat tatatggaca tttatatgag aaatgcattg gatggtaaca ctatttgtat	2340
tgatttaaaa catagagctc ctcaacaaat taaatgcccc cttttactta ttactagtaa	2400
tattgatgtt aaatcagata cctgttggat gtatttgcac agtagaatat cagcttttaa	2460
atttgctcat gagtttccat ttaaagacaa tggatgatcca ggattttcct taacagacga	2520
aaattggaaa tctttctttg aaaggttttg gcaacagtta gaattaagt accaagaaga	2580
cgagggaac gatggaaaac ctcagcagtc gcttagactt actgcaagag cagctaatga	2640
acctatatga acaggacagt aaattgatag aagatcaaata taagcagtgg aatctaatta	2700
gacaagaaca agttcttttc catttcgcca gaaaaaatgg ggtaatgaga attggattgc	2760
aggcagttcc atcttttagcg tcctcacagg agaaggcaaa gacagctatt gaaatgggtgt	2820
tacatttaga gtcttttaaag gactcacctt atggcacaga ggattgggtca cttcaagaca	2880
ctagcagaga gctgtttttg gcacccccag ctggcacctt caagaagagt ggcagcacac	2940
ttgaggttac ctatgacaat aaccctgata atcagacaag gcacacaatt tggaatcatg	3000
tgtattatca aaatggggac gatgtatgga gaaaagtatc cagtgggtgtt gatgctgtag	3060
gagtgtacta tttagaacac gatggctata aaaattatta tgtgttattt gctgaggagg	3120
cctctaagta cagcacaaca ggacaatatg ctgtaaatta caggggtaaa aggtttacaa	3180
atgttatgtc ttccactagc tccccaaggg ctgctggggc tcctgcagta cactccgact	3240
acccaaccct atccgagagt gacaccgccc agcaatcgac gtccatcgac tacaccgaac	3300

62384479818-seql-000001

tcccaggaca ggggggagacc tcgcagggtcc gacaaagaca gcagaaaaca cctgtacgca	3360
gacggcctta cggacggcga agatccagaa gtcccagagg tggaggacga agagaaggag	3420
aatcaacgcc ctctaggaca cccggatctg tcccttctgc gcgagacgtt ggaagtatac	3480
acacaacgcc tcaaaaggga cattcttcaa gacttagacg acttctgcag gaagcttggg	3540
atccacccgt ggtctgtgta aaaggggggtg ccaatcagct taagtgtctc aggtacagac	3600
ttaaagcatc tactcaagtt gactttgaca gcataagcac cacatggcat tggacagata	3660
gaaaaaacac cgagaggata ggtagtgcta gaatgttagt aaagtttatt gatgaggctc	3720
aacgagagaa gtttcttgag agagttgctt tgcccagatc agtgtctgtg tttttgggac	3780
agtttaaatgg gtcttaaaat taatggaagt tgattttgct tggacgtgtg tacatagtcc	3840
ctgtatatat tcccctccta cccccacata ccttgaagct tgcaacattg taacaaatgt	3900
atcgcttacg tagaaaacgc gctgccccca aagatatata cccctcatgc aaaatatcaa	3960
acacctgccc acctgacatt caaaataaaa ttgagcatac aacaattgct gataaaatat	4020
tgcaatatgg cagtctggga gtttttttgg gaggtttggg cattggaaca gccagaggct	4080
ctggaggaag aattggttat actcccctcg gtgagggtgg tgggggttaga gttgctactc	4140
gtccaactcc agtaaggcct acaataacctg tggaacacgt aggccccagt gaaattttcc	4200
ccatagatgt tgtagatcct acaggccctg ctgttattcc cctacaagat ttaggtagag	4260
acttcccaat accaactgtg caggttattg cagaaattca ccctatttct gacataccaa	4320
acattgttgc atcttcaaca aatgaaggag aatctgcat attagatgtg ttacgaggga	4380
atgcaaccat acgcactgtt tcaagaacac aatacaataa cccctctttc actgttgcac	4440
ctacatctaa tataagtgtg ggagaagcat caacatcaga tattgtattt gttagcaatg	4500
gttcagggtga cagggtgggtg ggcgaggata tccccttggg agaattaaac ttaggccttg	4560
aaacagacac atcttctgtt gtacaagaaa cagcattttc cagcagcaca ccaattgctg	4620
aaagaccctc ttttaggccc tcaagattct ataataggcg tctatatgaa caggtgcaag	4680
tacaagaccc taggttcggt gagcagccac agtcaatggg cacttttgat aatccagcat	4740

62384479818-seql-000001

ttgagccaga gcttgatgag gtgtctatta tcttccaaag agacttagat gctcttgctc	4800
agacaccagt gcctgaatth agagatgtag tttatctgag caagcccaca ttttcgcggg	4860
aaccaggggg acggttaagg gttagccgcc ttggcaaaag ttcaactatt cgtacacgcc	4920
tgggcacagc aattggcgcc agaaccact ttttctatga ttttaagttct attgctccag	4980
aagactcaat tgaattattg ccttttaggtg agcatagtca aacaacagtc attagttcca	5040
acttaggtga cacagcattt atacaaggtg agacagcaga ggatgactta gaagttatct	5100
ctttagaac accacaatta tattcagaag aagagctttt agacacaaac gaaagtgtgg	5160
gcgaaaatth gcaacttact attactaact cagagggtga ggthttctata ctagatttha	5220
cacaaagcag agtcaggcca ctttttgcca ctgaagatac tagcttgcat gtatattacc	5280
caaattcttc taaagggact ccaataatta atcctgaaga atcatttaca cttttggtta	5340
ttatagctct taacaactca acaggggatt ttgagttaca tcctagtctt agaaagcgtc	5400
gtaaaagagc ttatgtataa tgthttttcag atggctgtct ggthtaccagc gcagaataag	5460
ttctatcttc ctccccagcc catcactaga atcctgtcca ctgatgaata tgtaaccaga	5520
accaatctct tctaccatgc aacatctgaa cgtctactgc tggtcggaca tcctttgttt	5580
gagatctcca gtaatcaaac tgtaactata ccaaaagtgt caccaaagtc atttagagtt	5640
tttaggggtc gthtttgctga tccaaataga tttgcatttg gggataaggc aatthttaat	5700
ccagaaacag aaagattagt ttggggccta agagggatag agataggtag aggccagcct	5760
ttaggtatag gaataacggg ccacctctt ttaaataagt tagatgatgc agaaaatcca	5820
acaaattata ttaatactca tgcaaatgga gattctagac aaaatactgc ttttgatgca	5880
aaacagacac aaatgttcct cgtcggctgt actcctgctt caggatgaaca ctggacaagt	5940
agtcgttgcc cagggaaca agtgaaactt ggggactgcc ccagggtgca aatgatagag	6000
tctgtcatag aagatggatga catgatggat attggthttg gggctatgga ttttgctgct	6060
ttacagcaag acaagtctga tgtcccttha gatgttgthc aagcaacatg caaatatcct	6120
gattatatca gaatgaacca tgaagcctat ggcaactcta tgththththt tgcacgtcgc	6180

62384479818-seql-000001

gagcaaatgt ataccaggca cttttttact cgcggggggtt cggtgggtga taaggaggca	6240
gtcccacaaa gcctgtatatt aacagcagat gctgaaccaa gaacaacttt agcaacaaca	6300
aattatgtag gcacaccaag tggctctatg gtttcatctg atgtccaatt gtttaataga	6360
tcttactggc ttcagcgatg tcaaggccag aataatggca tttgctggag aaaccagtta	6420
tttattacag ttggagataa taccagagga acaagtttat ctatcagtat gaaaaacaat	6480
gcaagtacta catattccaa tgctaatttt aatgattttc taagacatac tgaagaattt	6540
gatctttctt ttatagttca gctttgtaaa gtaaagttaa ctcccgaata tctagcctac	6600
attcatacaa tggaccctaa tatatttagag gattggcaac tatctgtatc tcaaccacct	6660
accaatcctc tagaagatca atataggttt ttagggctct ccttggcagc aaaatgtcca	6720
gaacaggcgc ctctgagcc ccagactgat ccttatagtc aatataaatt ctgggaagtc	6780
gatctcacag aaaggatgtc cgaacaatta gaccaatttc cactaggaag gaaatttcta	6840
tatcaaagtg gcatgacaca acgtactgct actagttcca ccacaaagcg caaaacagtg	6900
cgtgtatcta cgtcagccaa gcgcaggcgt aaggcttagt atatattata tataactata	6960
tttattagta gattatttat tatatatatt tatattttta tactttttat acttgtttag	7020
ttctaaatag acatgtaaga ttacattag tataagtagg catgtattta cataaaatag	7080
tcttggaac cttttattag tgaaccatca ttacaatag tgacatcata gttcatctgc	7140
aattgctatt ccatcgttct tcacatattc tacagtagtg ttctctagat tgtattgcta	7200
ttttcctgtt aggcaacaaa caacatctgt acatggacca aacaaccac tttcatttta	7260
ttgtgctgca tatattccag attgttgagg atttatttgt ttagactccg gtgcattata	7320
cacaagtgtg cattttttgt gttctctgat tgattgtgtg ttattttcct gcaatatgca	7380
ataaaagtga gctgtccttt ctttttgta atccctccct actccaataa aaaatcccta	7440
cccctaaaat ctgtttgtgc tggttttatt aataattgcg ctcttttata taataagtac	7500
tattaacacc gcacccgttg tggctaatac cttatgggtat ttaaaagact acacctacag	7560
gatgtattgt cttcattgtt tatggtttac cgcgctccaa agacgggttg cccaaagacg	7620

62384479818-seql-000001

gtttgccaac cgcggttagg acttgtttca atttgctgcc aaacttatct ggtcgtgctc	7680
caacggggttt cctgccaagc acctaaaacg gtaggtgtgt actcttttca agaattaaca	7740
aaggagattt ctcccgcaa attagtttcg agcgaccgaa ttcggtcgta aaaatctaaa	7800
gtgatgattg ttgtt	7815

<210> 86
 <211> 7880
 <212> DNA
 <213> Human papillomavirus type 13

<400> 86	
gtttctaaca atcttaagtt taaaaaatag gtgggaccga aaacgggttt aaccgaaaac	60
ggtgatatat aaaccagccc aaaaattgag caagcggggc ataatggaaa gtgcaaatgc	120
ctccacgcct gcaaaaacta tagaccagtt gtgcaaggag tgcaaccttt ctatgcacag	180
cttgcaaatt ctatgcgtgt tctgcaggaa aaccctgtcc acggcagagg tttatgcatt	240
tcagtataag agtttatata tagtgtggcg aggacagttt ccatttgcgg cttgtgcatg	300
ctgcttagaa atacaaggaa agattaacca gtttaggcat tttgacttcg cgggatttgc	360
tgtaacagtt gaagaagaca caaagcagtc aattttggat gtgctaattc gctgctattt	420
atgccacaaa ccatttgtgtg aagtggagaa actaagacat attttgcaga aggcacgatt	480
tattaaatta aacagcagtt ggaaaggccg ctgttttcat tgctgggtcat catgcatgga	540
aaatatccta ccttaaaaga cattgtttta gagctgactc ctgaccctgt aggtctacat	600
tgcaatgagc aattagacag ctcagaagac gaggtggacg aacaagccac gcaagccacg	660
caagccacgc aacatagcac actattacaa tgctacaaaa tactaacgtc ctgtagtaaa	720
tgttgtagca acgtccggct ggtgggtggag tgtacaggac ctgacattca cgacctacac	780
gacctactgc tgggcacgct gaatatagtg tgccctttgt gtgcacaaaa aagctaacca	840
cgatggcaga ggatacaggt actaataatg aggggacggg atgctcagga tggtttttag	900
tagaggctgt agtagaacga acaactgggc acaaatatc agatgatgag gatgaaacag	960

62384479818-seql-000001

tggaagatag tgggttgat atggtggatt tcatagatga cagacctatt acacacaatt	1020
ccgtggaagc acaggcattg ttaaacgagc aggaggcgga tgctcattat gcggctgtgc	1080
aggacctaaa acgaaagtat ttaggcagtc catatgttag tcccctagga catgttgaac	1140
agtcagtgga ctgtgatata agtcctcgat tggacgctat aaaattaagt agaaattcta	1200
aaaaagtaaa gcgacggctg tttcaatcaa gggaaataac ggacagtgga tatggctatt	1260
ctgaagtgga agctgaaacg caggtagaga gaaatggcga accggaaaat gattgtgggg	1320
gtggtggaca cggaaggac aaagaggggg agggacaggt gcacacggaa gtgcacacag	1380
gcagccagat agaagagcac acagggacca cgcgggtgtt agaactcctt aatgtaagg	1440
atgtaagggc tacattgtat ggtaagtta aagactgtta tgggttatca ttacagatt	1500
taattagacc atttaaaagt gataaaacaa catgtgggga ctgggtgggt gcagcatttg	1560
gtatacatca tagtgtatca gaggcatttg aaaagttaat gcagccatta acaacatata	1620
tgcatataca atggcttaca aatgcatggg ggatgggtatt gttagtatta ataagattta	1680
aagtaaataa aagtagatgc acagtggcgc gaacactggc aacctttctt aatattcctg	1740
aggaccacat gttaattgaa cctcccaaaa taaaagcag tgtggcagca ttatactggt	1800
ttagaacagg tattttcta gctagtatag taactgggtga aacaccagaa tggataaaaa	1860
ggcaaacaat tgtagagcat ggacttgagc ataatacaatt taaattaact gaaatgggtgc	1920
agtgggcata tgataatgat ttttgtgatg aaagcgaaat agcatttgaa tatgcacaac	1980
gaggagattt tgattcaaat gccagggcatt ttttaaatag taattgtcag gcaaaatatg	2040
taaaagattg tgcaacaatg tgcaagcatt ataaaaatgc agaaatgaaa aaaatgtcta	2100
tgaaacaatg gataacatat agaagtaaaa aaatagagga agcaggaaat tggaaacca	2160
tagtacaatt tttaaggcat caaaatatag aatttattcc atttttaagt aaattaaaat	2220
tgtggcttca tggcacgcca aagaaaaact gtattgcaat agtggggcca ccagatacag	2280
gcaaatcatg tttttgcatg agcttaatta agtttttagg gggcacagta attagttatg	2340
taaattcaag tagccatttt tggctgcagc cattatgtaa tgcaaaggta gctttgctag	2400

62384479818-seql-000001

atgatgcaac gcagtcatgc tgggtatata tggacacata catgagaaat ttattagatg	2460
gcaatccaat gagcattgat agaaaacata agtctttagc attaataaaa tgtccgccat	2520
tattagtaac atctaagtga gacattacca aagatgacaa atataaatat ttgtatagta	2580
gagtaacaac acttacatth ccaaattccat tcccttttga cagaaatggg aatgcagtat	2640
atgagttgtc tgatgcaaac tggaaatggt tttttacaag attgtcagca agcctagata	2700
tacaggactc tgaggacgag gacgatggag acaatagcca agcatttaga tgcgtgccag	2760
gaacagttgt tagaactgta tgaagaaaat agtaatgaac ttaaaaaaca tataacaacat	2820
tggaaatgct taaggtaga aagtgtactc ttacacaaag cagccaaat gggcctaagc	2880
cacattggat tacaagtggt gccaccattg acagtatcac aagctaaggg acatgaggca	2940
attgaaatgc aaatgacttt agagacatta ctagagtctg agtttggat ggaaccatgg	3000
actttacaag atacaagtcg tgaaatgtgg ctaacacccc caaacgctg ttttaagaaa	3060
cagggacaaa ctgtggaagt aaaatatgac tgtaatacag acaatagaat ggattatgtg	3120
tcgtggacat acatatatgt gtttgacaca gataaatgga caaagggtgaa aggaatggta	3180
gattataaag ggttgtacta catacatgga aatttgaaaa catattatth agagtttgaa	3240
aaggaggcta aaaaatatgg ggaaacgtta caatgggaag tatgtattgg cagcacagtc	3300
atatgttctc ctgcatctgt atctagtact gtacaagaag tatccattgc tgggcctgct	3360
tcatactcca ccaccacctc cacacaggcc tccaccgcag tgcctgcag cgcctcgga	3420
gaatgtgtgc aagcgccgcc ttgtaaacga caacgaggac cttcacgtcc cattggaaac	3480
ccccagaaca cacaagcat tgttgtgtc acagactacg acaccctgga cagtgcaaac	3540
aacaacatca acgttaacca ttacaacaat aacaaaggac gggacaacag ttactgtgca	3600
gctacaccta tagttcaatt acaaggtagc tctaattgtc taaagtgttt tcgatataga	3660
ttacatgaaa aatataaaga tttatthttg ttagcatcat ctacatggca ttggaccgcc	3720
cctaataatt cacaaaaaca tgcactggta accttaacct atgtaaatga acaacaaaga	3780
caagacttht taaaaactgt aaaaatacct ccaaccataa cacataaact aggtthttatg	3840

62384479818-seql-000001

tcattgcaat tgttataaca gcatatattg tatgtaaata tttgttgtgt gtgtgtatat	3900
attgtaaatg gaatttatac ctgtggatgt tagtacacag gcaaccagca agtcattact	3960
gccacttgta attgcactta cagtgttgtgt agttagcatt ataacaatat tgtgcatatc	4020
agagttcctg gtgtacacaa acgttttagt actaacatta attttatatg tacttttgtg	4080
gcttttacta acaactccct tgcaattcta tttactaacc ctgtctcttt gctttcttcc	4140
tgcgttgtgt gtacaccaat atattttaca aacacaagaa taactataca caatgttaac	4200
ctgtactttt gatgatgggtg acacatgggtt gctattatgg ttaattttat catttattgt	4260
agccattcta gggttactgt tgctgtatat aagaactgga catatgcatt gccagtgtg	4320
gagtaaataa gtgggttttat attttgtgtg tattcattta attatggcac atagtagggc	4380
tcgcagacgc aaacgcgctt cagctacaca actatatcaa acttgtaagg cttctggaac	4440
atgtcctcct gatgttatac caaagggtga acaaaacact cttgcagata aaatattaaa	4500
gtggggcagt ttaggagtat tttttggggg gcttggcatt ggcacaggct ctggtactgg	4560
cggtaggact ggctatgtac cagtaggatc caccacacgc cctgccatat caactgggcc	4620
tactgcacgt cctcctattg ttgttgatac tgttgggcct acagaccctt ctattgtatc	4680
tttggtagag gaatcagcta ttattaattc tggagtacct gaccctttgc ctcccgttca	4740
tgggggtttt gaaatcacca catctcaatc agccactcca gcaatattgg atgtgtctgt	4800
tacaacacaa aacactacgt ccacaagtat atttagaaat cctgtttttt cagaaccttc	4860
tattacacaa tctcaacctt ctattgaaag tgggtgcacac gtgtttatat cgccatctac	4920
tatttcccct cattctacag aagacattcc tttagataca tttattgtat cttcctcaga	4980
tagtaatcct gcatcaagca cccctgttcc agcaactgtt gcacgtccac gtctaggcct	5040
ttacagtagg gccttacatc aagtacaggt tactgatcct gcctttttat cgtcgcccca	5100
acgccttata acctttgata accctacata tgaagggtgaa gatataagtt tgcagtttgc	5160
acacaatacc attcatgaac cccctgatga ggcatttatg gatattataa gactacatag	5220
gccagccata acatcacggc gtgggtcttgt taggttttagt agaattgggtc agaggggggtc	5280

62384479818-seq1-000001

tatgtatact cgaagcggca agcatatagg tggaagggtc catttcttta aggatatttc	5340
tcctatatct gcagctgcag aagaaataga attacacccc cttgtggctg ctgcacagga	5400
tcacagtgggt ttgtttgata tttatgcaga acctgaccct gaccctgtgg ctgtaaacac	5460
ctctgggtca ttgtcttctg cctccacacc atttgcacaa tcttctttgt cttccgcccc	5520
atggggtaat actactgttc ctctttcact accaggtgat atatttatac agcctgggtcc	5580
tgacataaca ttcccaactg cacctacagt aacgccttat aatcctgtta cgcctgcttt	5640
acctacaggt cctgttttta ttactgcttc tggattttat ttatatccta catggtatatt	5700
tacacgcaaa cgccgtaaac gtgtttcctt gttttttaca gatgtggcgg cctagtgaca	5760
acaaactata tgtgcctcct cccgcccctg tatcaaaagt aattactacg gatgcctatg	5820
ttacacgtac caacatattt tatcatgcta gcagttctag actacttgca gtgggaaatc	5880
cttattttcc tattaagaaa caaaacaaaa ctgttgtccc taaggatatct ggttatcagt	5940
ttagggatatt taaagttgta ttacctgacc ctaataaatt tgccctgcct gacacatcta	6000
tatttgactc aactagtcaa cgcttagtgt gggcctgtac aggttttagag gttggtaggg	6060
gtcaaccctt aggtgttgggt attagtgggtc atccattatt aaataaatat gatgatgtgg	6120
aaaattctgc aagttatgct gccaatcctg gtcaggataa tagggttaat gtggccatgg	6180
actataaaca aacacagtta tgttttagtg gctgtgcacc tccttttaggt gaacattggg	6240
gacagggcaa gcaatgtact ggtgtaaatg tacaacctgg agattgccct cctttagaat	6300
taattagtag tgtaattcag gatggtgaca tgggtggatac aggatttgga gccatgaatt	6360
ttgcggaatt gcaatctaataaatctgatg tgccactaga catatgcacg tccacatgca	6420
aatatcctga ctattttacaa atggctgcgg atccttatgg agacagatta ttttttatc	6480
tgcgaaagga acaaatgttt gcaaggcatt tctttaacag ggcaggctct gttggtgaac	6540
aaatcccagc agaattatat gttaagggtta gtaatacact ttctaatagt atttactata	6600
atactcccag tggctctctt gtgtcttctg aggcccagtt gttaataaaa cttatttgg	6660
tacaaaaggc ccagggacac aataatggta tatgttgggg caatcacttg tttgttactg	6720

62384479818-seq1-000001

tagttgatac tacacgcagt actaacatga ctgtgtgtgc agccactaca tcatctcttt	6780
cagacacata taaggccaca gaatataaac agtacatgcg acatgtagaa gaatttgatt	6840
tacaatttat ttttcaattg tgcactatta aattaactgc agaggttatg tcatatattc	6900
atactatgaa tcctacaatt ctagaagact ggaactttgg gctatctccc cctcctaag	6960
gaacattaga agacacatat agatatgtac aatctcaggc cataacgtgt caaaagccta	7020
cacctgataa agaaaaacag gatccgtatg cgggtcttag tttttgggag gttaatctta	7080
aggaaaagtt ttctagtga ctagatcagt atccccctgg cagaaagttt ttattacaaa	7140
caggcgttca gtctagggtcc cctattcgtg taggtaggaa acgtgctgca tctacatcta	7200
ctgccacacc tactacacgt aaaaaagcta aaaggaaata atagtttggt tatgattgtg	7260
tatgtatgtc acgtttgttt gtactgtatg tatgttgtgt actgtatgtg taatgttgta	7320
tgtatgtgca tgttacttat taaagaatgt gtgtgtgtgt ttgtatgcaa taaatcta	7380
ctgtgggtgc ctgttccacc ctatgagtaa gtggatgtt gtgtctcgtg tgggtgtttg	7440
tatactatac tataacatta gtgcaaccat tttgtaactt ttcttacatt ttacgtctcc	7500
atattaagtg caaccgattt cggttgctat tgtttctgcg accgatttgt tgcagcacgc	7560
tgtttatata atcttaccta ccgcctgcca aaattatcca ccgcttgcca aaatcaccca	7620
cacacctggc gttgctaggg cgcggttata tatatttact aaatcttact aatctttcta	7680
tcactcattt tacctttata acaatacttt tgcttttcaa gtacattttt gtacttacta	7740
gccaatgcct gaaaggtttt ttggctacca gcactacatt tttgtacagt taatgttaca	7800
tgtataaaat gagtaaccta aggtcacaca cctgcaaacc ggtatcgggt aaaacacacc	7860
ctctatagtt ccttataatt	7880

<210> 87

<211> 7931

<212> DNA

<213> Human papillomavirus type 11

<400> 87

cttaataaca atcttagttt aaaaaagagg agggaccgaa aacggttcaa ccgaaaacgg	60
---	----

62384479818-seql-000001

ttatatataa accagcccaa aaaattagca gacgaggcat tatggaaagt aaagatgcct	120
ccacgtctgc aacatctata gaccagttgt gcaagacggt taatctttct ttgcacactc	180
tgcaaattca gtgcgtgttt tgcaggaatg cactgaccac cgcagagata tatgcatatg	240
cctataagaa cctaaagggt gtgtggcgag acaactttcc ctttgacgcg tgtgcctgtt	300
gcttagaact gcaagggaaa attaaccaat atagacactt taattatgct gcatatgcac	360
ctacagtaga agaagaaacc aatgaagata ttttaaaagt gttaattcgt tgttacctgt	420
gtcacaagcc gttgtgtgaa atagaaaaac taaagcacat attgggaaag gcacgcttca	480
taaaactaaa taaccagtgg aagggtcgtt gcttacactg ctggacaaca tgcattggaag	540
acttgttacc cttaaaggata tagtactaga cctgcagcct cctgaccctg tagggttaca	600
ttgctatgag caattagaag acagctcaga agatgagggt gacaagggtg acaaacaaga	660
cgcacaacct ttaacacaac attaccaaatt actgacctgt tgctgtggat gtgacagcaa	720
cgtccgactg gttgtggagt gcacagacgg agacatcaga caactacaag accttttgct	780
gggcacacta aatatttgtgt gtcccatctg cgcacaaaaa ccataacaag gatggcggac	840
gattcaggta cagaaaatga ggggtcgggg tgtacaggat ggtttatggt agaagccata	900
gtagagcaca ctacaggtag acaaatatca gaagatgagg aagaggaggt ggaggacagt	960
gggtatgaca tgggtggactt tattgatgac aggcataatta cacaaaattc tgtggaagca	1020
caggcattgt ttaataggca ggaggcggat gctcattatg cgactgtgca ggacctaaaa	1080
cgaaagtatt taggcagtcc atatgtaagt cctataagca atgtagctaa tgcagtagaa	1140
agtgagataa gtccacgggt agacgccatt aaacttacaa cacagccaaa aaaggtaaag	1200
cgacggctgt ttgaaacacg ggaattaacg gacagtggat atggctattc tgaagtggaa	1260
gctgcaacgc aggtagagaa acatggcgac ccggaaaatg ggggagatgg tcaggaaagg	1320
gacacaggga gggacataga gggtaggggg gtggaacata gagaggcgga agcagtagac	1380
gacagcaccg gagagcatgc agacacatca ggaatattag aattactaaa atgtaaggat	1440
atacgatcta cattacatgg taagtttaaa gactgctttg ggctgtcatt tgttgattta	1500

62384479818-seql-000001

attaggccat ttaaaagtga tagaaccaca tgtgccgatt gggtggttgc aggatttgggt	1560
atacatcata gcatagcaga tgcatttcaa aagttaattg agccattaag tttatatgca	1620
catatacaat ggcttacaaa tgcattgggga atggtactat tagtattaat aaggtttaaa	1680
gtaaaataaga gcagatgtac cgtggcacgt acattaggta cgttattaaa tatacctgaa	1740
aatcacatgt taattgagcc tcctaaaata caaagtggcg tacgagccct gtattgggtt	1800
aggacaggca tttcaaatgc aagtacagtt ataggggagg cgccggaatg gataacgcgc	1860
cagaccgtta ttgaacatag tttggctgac agtcaattta aattaactga aatggtgcag	1920
tgggcatatg ataatgatat ttgtgaagaa agtgagatag catttgaata tgcacagcgt	1980
ggagactttg actccaatgc aagggccttt ttaaatagta atatgcaggc taaatatgta	2040
aaagattgtg caattatgtg cagacattat aaacatgcag aaatgaaaaa gatgtctatt	2100
aaacaatgga ttaagtatag gggactataa gttgacagt taggtaactg gaagccaatt	2160
gtgcagtttc taagacatca aaacatagaa tttattccat ttttaagcaa actaaaatta	2220
tggctgcacg gaacgccccaa aaaaaattgt atagccattg tagggccacc tgacactggg	2280
aagtcgtgct tttgcatgag ttttaattaag tttttggggg gaacagttat tagttatgtt	2340
aattcctgca gccatttctg gctacagcca ctaacggatg caaaagtggc attattggat	2400
gatgccacac aacctgttg gacatatatg gatacatata tgagaaacct attagatgggt	2460
aatcctatga gcatagatag aaaacataga gcattaacat taattaagt tccaccgcta	2520
ctggttacat caaatataga cattagcaaa gaggagaaat acaaatattt acatagtaga	2580
gttaccacat ttacatttcc aaatccattc ccctttgaca gaaatgggaa tgcagtatat	2640
gaactatcag atgcaaactg gaaatgtttc tttgaaagac tgtcgtccag cctagacatt	2700
gaggattcag aggacgagga agatggaagc aatagccaag cgttttagatg cgtgccagga	2760
tcagttgtta gaactttatg aagaaaacag tattgatata cacaaacaca ttatgcattg	2820
gaaatgcata cgattggaaa gtgtattact acacaaagca aaacaaatgg gcctgagcca	2880
catcgggtta caagtagtac caccattaac tgtgtcagag actaaaggac ataatgctat	2940

62384479818-seql-000001

tgaaatgcaa atgcatttag aatccttagc aaaaactcag tatgggtgtgg aaccttggac	3000
attacaggac accagttatg aaatgtggct aacaccaccc aaacgggtgct ttaaaaaaca	3060
gggaaatact gtggaggtaa aatttgatgg ctgtgaagac aatgtaatgg agtatgtggt	3120
atggacacat atatacctgc aggacaacga ctcattgggta aaagtaacta gttccgtaga	3180
tgccaagggc atatattata catgtggaca atttaaaaaca tattatgtaa attttaataa	3240
agaggcacia aagtattgga gtaccaatca ttgggaagta tggttatggca gcacagttat	3300
atgttctcct gcatctgtat ctagcactgt acgagaagta tccattgctg aacctactac	3360
atacaccccc gcacagacca ccgcccctac agtgtccgcc tgcaccacgg aagacggcgt	3420
gtcggcgccg cctaggaagc gagcacgtgg accgtccact aacaacaccc tgtgtgtggc	3480
caacatcaga tccgtggaca gtacaatcaa caacatcgtc actgacaatt acaacaagca	3540
ccaaagaagg aacaactgtc acagtgcagc tacgcctata gtgcaactgc aaggtgattc	3600
caattgttta aaatgtttta gatatagact gaatgacaaa tataaacatt tgtttgaatt	3660
agcatcttca acgtggcatt gggcctcacc tgaggcacca cataaaaatg caattgtaac	3720
attaacatat agcagtgagg aacaacgtca gcaattttta aacagtgtaa aaataccacc	3780
caccattagg cataaggtgg ggtttatgtc attacattta ttgtaaccat tacacctgta	3840
tatatgtata tgtgtacata acatacgtgt atggaggtag tgcctgtaca aattgctgca	3900
gcaacaacta caacattgat attgcctgtt gttattgcat ttgcagtatg tattcttagt	3960
attgtactta taatattaat atctgatttt gtagtatata catctgtgct ggtactaaca	4020
cttcttttat atttgctttt gtggctttta ttaacaaccc ctttgcaatt ctttttacta	4080
acactgtgtg tgtgctatth tcctgcctth tatatacaca tatacattgt gcaaacgcaa	4140
caataatggg gatgttaacc tgtcacttaa atgatgggtga tacatgggtg tttctgtggg	4200
tgthtactgc atttgthgta gctgtacttg gattgthgtt actacattac agggctgtac	4260
atgggtactga aaaaactaaa tgtgctaagt gtaaatcaaa ccgcaatact actgtggatt	4320
atgtgtatat gtcacatggg gataatggag attatgtgta catgaactag agtaaacctt	4380

62384479818-seq1-000001

ttttatacag tgtgtggtgt acgttagtta tatataatga aacctagggc acgcagacgt	4440
aaacgtgcgt cagccacaca actatatcaa acatgcaagg ccactggtac atgtcccca	4500
gatgtaattc ctaaagttga acatactact attgcagatc aaatattaaa atggggaagc	4560
ttaggggttt tttttggtgg gttaggtatt ggtacagggg ctggtagtgg cggtcgtgca	4620
gggtatatac ccttggaag ctctccaag cctgctatta ctggggggcc agcagcacgt	4680
ccgccagtgc ttgtggagcc tggtgcccct tccgatccct ccattgtgtc cttaattgag	4740
gagtctgcta ttattaatgc tgggtgcacct gaggtggtac cccctacaca ggggtggcttt	4800
actataacat catctgaatc gactacacct gctattttag atgtgtctgt taccaatcac	4860
actaccacta gtgtgtttca aaatcccctg ttacagaac cgtctgtaat acagcccaa	4920
ccacctgtgg aggccagtgg tcacatactt atatctgccc caacaataac atcccaacat	4980
gtagaagaca ttccactaga cacttttggt gtatcctcta gtgatagtgg acctacatcc	5040
agtactcctc ttcctcgtgc ttttcctcgg cctcgggtgg gtttgtatag tcgtgcctta	5100
cagcaggtag aggttacgga ccccgcttt ttgtccacgc cacagcgatt ggtaacttat	5160
gacaaccctg tctatgaagg agaagatgta agtttacaat ttacccatga gtctatccac	5220
aatgcacctg atgaagcatt tatggatatt attagactac atagaccagc tataacgtcc	5280
agacgggggtc ttgtgcgttt tagtcgcatt gggcaacggg ggtccatgta cacacgcagt	5340
ggacaacata taggtgcccg catacattat tttcaggaca tttcaccagt tacacaagct	5400
gcagaggaaa tagaactgca ccctctagtg gctgcagaaa atgacacgtt tgatatttat	5460
gctgaaccat ttgaccctat ccctgacct gtccaacatt ctgttacaca gtcttatctt	5520
acctccacac ctaataccct ttcacaatcg tggggtaata ccacagtccc attgtcaatc	5580
cctagtgact ggtttgtgca gtctgggcct gacataactt ttcctactgc atctatggga	5640
acacccttta gtctgtaac tcctgcttta cctacaggcc ctgtttttat tacaggttct	5700
gacttctatt tgcacacct atggtacttt gcacgcagac gccgtaaacg tattccctta	5760
ttttttacag atgtggcggc ctagcgacag cacagtatat gtgcctcctc ccaaccctgt	5820

62384479818-seql-000001

atccaagggtt gttgccacgg atgcgtatgt taaacgcacc aacatatattt atcatgccag	5880
cagttctaga ctcccttgctg tgggacatcc atattactct atcaaaaaag ttaacaaaac	5940
agttgtacca aagggtgtctg gatatacaata tagagtgttt aaggtagtgt tgccagatcc	6000
taacaagttt gcattacctg attcatccct gtttgacccc actacacagc gtttagtatg	6060
ggcgtgcaca gggttgagg taggcagggg tcaaccttta ggcgttggtg ttagtgggca	6120
tccattgcta aacaaatatg atgatgtaga aaatagtggg gggatatggg gtaatcctgg	6180
tcaggataat agggttaatg taggtatgga ttataaaca acccagctat gtatgggtggg	6240
ctgtgctcca ccgttaggtg aacattgggg taagggtaca caatgttcaa atacctctgt	6300
acaaaatggg gactgcccc cgttggaact tattaccagt gttatacagg atggggacat	6360
ggttgataca ggctttgggt ctatgaattt tgcagactta caaaccaata aatcggatgt	6420
tccccttgat atttgtggaa ctgtctgcaa atatcctgat tatttgcaaa tggctgcaga	6480
cccttatggg gatagggtgt ttttttattt gcgaaaggaa caaatgtttg ctagacactt	6540
ttttaatagg gccggtactg tgggggaacc tgtgcctgat gacctgttgg taaaaggggg	6600
taataacaga tcatctgtag ctagtagtat ttatgtacat acacctagt gctcattggg	6660
gtcttcagag gctcaattat ttaataaacc atattggctt caaaaggctc aggacataa	6720
caatgggtatt tgctggggaa accacttggt tgttactgtg gtagatacca cacgcagtac	6780
aaatatgaca ctatgtgcat ctgtgtctaa atctgtcaca tacactaatt cagattataa	6840
ggaatacatg cgccatgtgg aggagtttga ttacagttt atttttcaat tgtgtagcat	6900
tacattatct gcagaagtca tggcctatat acacacaatg aatccttctg ttttggagga	6960
ctggaacttt ggtttatcgc ctccaccaa tgggtacactg gaggatactt atagatatgt	7020
acagtcacag gccattacct gtcagaaacc cacacctgaa aaagaaaaac aggatcccta	7080
taaggatatg agtttttggg aggttaactt aaaagaaaag ttttcaagt aattagatca	7140
gtttcccctt ggacgtaagt ttttattgca aagtggatat cgaggacgga cgtctgctcg	7200
tacagggtata aagcgcccag ctgtgtctaa gccctctaca gccccaaac gaaaacgtac	7260

62384479818-seq1-000001

caaaacaaaa aagtaatata tgtgtgtcag tgtgttgtgt tatttatatg ttgttgtagt	7320
gtgtatatgt ttcttgtatt gtgtatatgt gtatatgttt gtgtatatgt gtatgttatg	7380
tatgttatgt tgttatgtat gtttgttgtt ttagtgtgtg tatatatattg tggaatgtgt	7440
atgtatgttt ttgtgcaata aacaattatt atgtgtgtcc tgttacaccc agtgactaag	7500
ttgtgttttg cacgcgccgt ttgtgttgcc ttcataattat attatatata ttgttaatat	7560
acctatacta tgttaccccc cccacttgc aaccgttttc gggtgccctt acatacactt	7620
acctcaaatt tgttataacg tgttttgtac taatcccata tgtttgtgtg caaggtacat	7680
attgccctgc caagtatctt gccacaaca cacctggcca gggcgcggta ttgcatgact	7740
aatgtacaat aaacctgtcg gtttgtacaa tgttgtggat tgcagccaaa ggtaaaaagc	7800
atTTTTggct tctagctgaa catttttgta cccttagtat attatgcaca ataccacaa	7860
aatgagtaac ctaaggtcac acacctgcaa ccggtttcgg ttaccacac cctacatatt	7920
tccttcttat a	7931